

# Package: NU.Learning (via r-universe)

September 2, 2024

**Version** 1.5

**Date** 2023-09-15

**Title** Nonparametric and Unsupervised Learning from Cross-Sectional  
Observational Data

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**Depends** R (>= 3.5.0), cluster, lattice

**Description** Especially when cross-sectional data are observational, effects of treatment selection bias and confounding are best revealed by using Nonparametric and Unsupervised methods to ``Design" the analysis of the given data ...rather than the collection of ``designed data". Specifically, the ``effect-size distribution" that best quantifies a potentially causal relationship between a numeric y-Outcome variable and either a binary t-Treatment or continuous e-Exposure variable needs to consist of BLOCKS of relatively well-matched experimental units (e.g. patients) that have the most similar X-confounder characteristics. Since our NU Learning approach will form BLOCKS by ``clustering" experimental units in confounder X-space, the implicit statistical model for learning is One-Way ANOVA. Within Block measures of effect-size are then either [a] LOCAL Treatment Differences (LTDs) between Within-Cluster y-Outcome Means (``new" minus ``control") when treatment choice is Binary or else [b] LOCAL Rank Correlations (LRCs) when the e-Exposure variable is numeric with (hopefully many) more than two levels. An Instrumental Variable (IV) method is also provided so that Local Average y-Outcomes (LAOs) within BLOCKS may also contribute information for effect-size inferences when X-Covariates are assumed to influence Treatment choice or Exposure level but otherwise have no direct effects on y-Outcomes. Finally, a ``Most-Like-Me" function provides histograms of effect-size distributions to aid Doctor-Patient (or Researcher-Society) communications about Heterogeneous Outcomes. Obenchain and Young (2013)

<[doi:10.1080/15598608.2013.772821](https://doi.org/10.1080/15598608.2013.772821)>; Obenchain, Young and Krstic  
(2019) <[doi:10.1016/j.yrtph.2019.104418](https://doi.org/10.1016/j.yrtph.2019.104418)>.

**License** GPL-2

**URL** <https://www.r-project.org>, <http://localcontrolstatistics.org>

**NeedsCompilation** no

**Date/Publication** 2023-09-30 22:52:43 UTC

**Repository** <https://rlobenchain.r-universe.dev>

**RemoteUrl** <https://github.com/cran/NU.Learning>

**RemoteRef** HEAD

**RemoteSha** acedfecc3976daa7617683c4ddb8085ae6ac5d47

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## Description

NU.Learning forms Local Treatment Differences (LTDs) or Local Rank Correlations (LRCs) within Clusters of experimental units (patients, etc.) who have been relatively well-matched on their baseline X-confounder characteristics. The resulting distribution of LTD/LRC effect-size estimates can be interpreted much like a Bayesian posterior. Yet these distributions have been formed, via Non-parametric and Unsupervised Preprocessing, in purely Objective Ways.

## Details

Package: NU.Learning  
Type: Package  
Version: 1.5  
Date: 2023-09-15  
License: GPL-2

### UNSUPERVISED LOCAL TREATMENT DIFFERENCES or LOCAL RANK CORRELATIONS:

Multiple calls to `ltdagg(K)` or `lrcagg(K)` for varying numbers of clusters,  $K$ , are typically made after first invoking `NUcluster()` to hierarchically cluster patients in X-space and invoking `NUsetup()` to specify a numeric y-Outcome variable and a numeric treatment choice or exposure level measure, `trex`.

### UNSUPERVISED INSTRUMENTAL VARIABLES = LOCAL AVERAGE y-OUTCOME EFFECTS:

An OBSERVED Propensity Score (PS) is defined here to be either (i) the local (within-cluster) fraction of experimental units (patients) receiving `trex==1` (new) rather than `trex==0` (control) or else (ii) a measure of "relative exposure" when the numeric `trex` measure has (many) more than 2 observed levels. Multiple calls to `ivadj(K)` for varying numbers of clusters,  $K$ , then yield alternative scatters of Local Average Outcomes (LAOs) for Clusters when plotted against their PS estimates and, thus, different possible linear fits or `smooth.splines()` yielding potentially different inferences about across-cluster Treatment or Exposure Effects.

### CONFIRMATION and SENSITIVITY ANALYSES of LOCAL EFFECT-SIZE DISTRIBUTIONS:

For a given value of  $K$  = Number of Clusters requested, the output object from `ltdagg(K)` or `lrcagg(K)` can be input to `confirm()` to use (nonparametric) permutation theory to display visual evidence (empirical CDF comparisons) concerning the Question: "Does x-matching Truly Matter?" The NULL hypothesis here is that the x-Covariates used in Clustering / Matching of Experimental Units are actually IGNORABLE. Evidence against this hypothesis is provided when the observed LOCAL Effect-Size Distribution clearly deviates from the purely RANDOM, NULL distribution computed (to any desired precision) by randomly PERMUTING cluster ID labels across experimental units. Furthermore, the statistical significance of differences between the observed and random NULL distributions can be estimated using `KSperm()`, which simulates the random permutation distribution of the Kolmogorov-Smirnov D-statistic when many tied values occur in both distributions being compared. Finally, the `NUcompare()` function helps users of NU.Learning decide which Number of Clusters,  $K$ , optimizes Variance-Bias trade-offs. Larger values of  $K$  tend to yield smaller clusters with better matches and, thus, potentially reduced BIAS. On the other hand, smaller values of  $K$  usually yield local effect-size estimates with much lower Variability (higher Precision).

"Most-Like-Me" HISTOGRAMS for DOCTOR-PATIENT discussions of PERSONALIZED MEDICINE:

For a specified vector, `xvec`, of numerical values of the X-confounder variables used in the current CLUSTERING of eUnits, display histograms of observed LTD or LRC effect-sizes for (i) all available patients and (ii) for the specified number, `NN`, of "Nearest-Neighbors" in X-confounder space of the TARGET eUnit ...i.e. `xvec` defines "Me".

### Author(s)

Bob Obenchain <wizbob@att.net>

### References

- McClellan M, McNeil BJ, Newhouse JP. (1994) Does More Intensive Treatment of Myocardial Infarction in the Elderly Reduce Mortality?: Analysis Using Instrumental Variables. *JAMA* **272**: 859-866.
- Obenchain RL. (2010) The Local Control Approach using JMP. Chapter 7 of **Analysis of Observational Health Care Data using SAS**, Cary, NC:SAS Press, pages 151-192.
- Obenchain RL, Young SS. (2013) Advancing Statistical Thinking in Observational Health Care Research. *J. Stat. Theory and Practice*, **7**: 456-469, doi:10.1080/15598608.2013.772821.
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confirm

*Confirm that Clustering in Covariate X-space yields an "adjusted" LTD/LRC effect-size Distribution*

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### Description

For a given Number of Clusters, `K`, `confirm()` compares the observed distribution of LTDs or LRCs from relatively well-matched experimental units with the corresponding distribution from Purely Random Clusterings of experimental units. The larger are differences between the (blue) observed empirical CDF of effect-sizes and the (red) Purely Random CDF, the more potentially IMPORTANT are the "adjustments" resulting from focussing upon clustering (matching) of experimental units in X-space.

**Usage**

```
confirm(x, reps=100, seed=12345)
```

**Arguments**

<code>x</code>	An output object from <code>ltdagg()</code> or <code>lrcagg()</code> for a specified number of clusters, <code>K</code> .
<code>reps</code>	Number of simulation Replications, each with the same number, <code>K</code> , and sizes, <code>N1, N2, ..., NK</code> of Purely Random clusters.
<code>seed</code>	This (arbitrary) integer argument will be passed to the R <code>set.seed()</code> function. Knowing the value of this seed makes the output from <code>confirm()</code> reproducible.

**Details**

Making calls to `confirm()` for `ltdagg()` or `lrcagg()` objects resulting from different choices of `K =` Numbers of Clusters help the analyst decide which observed LTD or LRC effect-size distributions are (or are not) meaningfully different from Purely Random. When the X-covariates used in `NU-cluster()` are truly "ignorable," then [i] all X-based clusters will be Purely Random, and [ii] both the number (`K`) and the sizes (`N1, N2, ..., NK`) of clusters formed will be meaningless and arbitrary. Thus the NU Strategy `confirm()` function simulates the empirical CDF for LTDs or LRCs resulting from purely random permutations of the Cluster ID numbers (`1, 2, ..., K`) assigned by `ltdagg()` or `lrcagg()`. Each permutation yields `K` artificial "clusters" of sizes `N1, N2, ..., NK`. Simulation results are accumulated for the total number of random permutations specified in the "`reps=`" argument of `confirm()`. Calls to `print.confirm()` and `plot.confirm()` provide information on comparisons of empirical CDFs for the Observed and Purely Random LTD/LRC distributions, including calculation of an observed two-sample Kolmogorov-Smirnov D-statistic using `stats::ks.test`. This is a non-standard use of `ks.test()` because the distributions being compared are DISCRETE; both contain many within-cluster TIED effect-size estimates. The p-value computed by `ks.test()` is not reported or saved because it is badly biased downwards due to TIED estimates. Researchers wishing to simulate a p-value for the observed KS D-statistic that is adjusted for TIES can invoke `KSperm(confirm())`.

**Value**

An output list object of class `confirm`:

<code>hiclus</code>	Hierarchical clustering object created by the designated method.
<code>dframe</code>	Name of data.frame containing X, <code>trex</code> & Y variables.
<code>trtm</code>	Name of numerical <code>trex</code> variable.
<code>yvar</code>	Name of numerical Y-outcome variable.
<code>reps</code>	Number of overall Replications, each with the same numbers of requested clusters.
<code>seed</code>	Integer argument passed to <code>set.seed()</code> . Knowing which seed value was used in the call to <code>confirm()</code> makes not only the NULL distribution of observed LTDs or LRCs reproducible but also makes the NULL distribution of D-statistics (adjusted for ties) from a subsequent call to <code>KSperm()</code> reproducible.
<code>nclus</code>	Number of clusters requested.
<code>units</code>	Number of experimental units or patients.

Type	1 ==> LTDs, otherwise LRCs.
NUmean	Weighted Local Mean across Clusters.
NUstde	Weighted Std. Error across Clusters.
RPmean	Weighted Random Permutation Mean across Clusters.
RPstde	Weighted Random Permutation Std. Error across Clusters.
KSobsD	Output from print(ks.test()).
NUdist	data.frame of 5 key variables for all experimental units.
dfconf	data.frame of lstat = LTD or LRC values of max(length) = reps*units.

**Author(s)**

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**References**

Obenchain RL. (2010) The Local Control Approach using JMP. Chapter 7 of **Analysis of Observational Health Care Data using SAS**, Cary, NC:SAS Press, pages 151-192.

Obenchain RL. (2023) **NU.Learning\_in\_R.pdf** <http://localcontrolstatistics.org>

**See Also**

[ltdagg](#) and [lrcagg](#).

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 ivadj

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*Instrumental Variable LAO Fitting and Smoothing*


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**Description**

For a given number of patient clusters in baseline X-covariate space and a specified Y-outcome variable, smooth the distribution of Local Average Outcomes (LAOs) plotted versus Within-Cluster Propensity-like Scores: the Treatment Selection Fraction or the Relative Exposure Level.

**Usage**

```
ivadj(x)
```

**Arguments**

x An output object from `ltdagg()` or `lrcagg()` using K Clusters in X-covariate space.

**Details**

Multiple invocations of `ivadj(ltdagg())` or `ivadj(lrcagg())` using varying numbers of clusters, K, can be made. Each invocation of `ivadj()` displays a linear `lm()` fit and a `smooth.spline()` fit to the scatter of LAO estimates plotted versus their within-cluster propensity-like score estimates.

**Value**

An output list object of class ivadj:

hclobj	Name of clustering object output by NUcluster().
dframe	Name of data.frame containing X, trtm & Y variables.
trtm	Name of the numeric treatment variable.
yvar	Name of the numeric outcome Y variable.
K	Number of Clusters Requested.
actclust	Number of Clusters actually produced.

**Author(s)**

Bob Obenchain <wizbob@att.net>

**References**

McClellan M, McNeil BJ, Newhouse JP. (1994) Does More Intensive Treatment of Myocardial Infarction in the Elderly Reduce Mortality?: Analysis Using Instrumental Variables. *JAMA* **272**: 859-866.

Obenchain RL. (2010) Local Control Approach using JMP. Chapter 7 of **Analysis of Observational Health Care Data using SAS**, Cary, NC: SAS Press, pages 151-192.

Obenchain RL. (2023) **NU.Learning\_in\_R.pdf** <http://localcontrolstatistics.org>

Rosenbaum PR, Rubin RB. (1983) The Central Role of the Propensity Score in Observational Studies for Causal Effects. *Biometrika* **70**: 41-55.

**See Also**

[ltdagg](#), [lrcagg](#) and [NUcompare](#).

**Examples**

```
# Running takes about 7 seconds...
data(pci15k)
xvars = c("stent", "height", "female", "diabetic", "acutemi", "ejfract", "ves1proc")
hclobj = NUcluster(pci15k, xvars)
NU.env = NUsetup(hclobj, pci15k, thin, surv6mo)
surv050 = ltdagg(50, NU.env)
iv050 = ivadj(surv050)
iv050
plot(iv050)
```

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KSperm	<i>Simulate a p-value for the significance of the Kolmogorov-Smirnov D-statistic from confirm().</i>
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### Description

For a given confirm() output object, KSperm() simulates the NULL distribution of LTDs or LRCs resulting from Purely Random Clusterings of experimental units within the parent data.frame. This NULL distribution is discrete because Local Effect-Size estimates are TIED within-clusters. The observed D-Statistic from confirm() is compared with new NULL order statistics computed by KSperm(), again using stats::ks.test. When KSperm() is called immediately after confirm() and the seed value used in confirm() is known, then both the simulated p-value and the additional NULL KS-D order statistics generated by KSperm() will all be reproducible.

### Usage

```
KSperm(x, reps=100)
```

### Arguments

x	An output object from confirm().
reps	This is the number of new NULL KS-D statistics to generated. Each experimental unit is used at most once within each full replication. No clusters will be empty, but some may be "uninformative".

### Details

The observed value of the Kolmogorov-Smirnov D-statistic from confirm() is used here, but its "p.value" from ks.test() is not because it is badly biased downwards. This bias results because the distribution of LTDs or LRCs across clusters is always discrete, due to TIED values within clusters that typically also vary in size. Thus, KSperm() generates "reps" additional, independent, NULL values of KS-D and saves their order statistics. Finally, KSperm() compares the Observed KS-D from confirm() with its simulated NULL order statistics to estimate an appropriately "adjusted" p-value, pv.adj. Note that the simulated pv.adj value estimate cannot be less than 1/(reps).

### Value

An output list object of class KSperm:

hiclus	Hierarchical clustering object created by the designated method.
dframe	Name of data.frame containing X, t & Y variables.
trtm	Name of numerical treatment/exposure variable.
yvar	Name of numerical y-Outcome variable.
Type	1 ==> LTDs, otherwise LRCs.
reps	Number of overall Replications, each with the same number, K, of requested clusters.



nclus	Number of clusters requested.
units	Number of experimental units or patients.
obsD	Observed numerical value of KS D-statistic from confirm()
Dvec	Vector of order statistics for simulated NULL KS D-statistics.
pv.adj	Simulated p-value adjusted for TIES within discrete LTD/LRC distributions.

**Author(s)**

Bob Obenchain <wizbob@att.net>

**References**

- Obenchain RL. (2010) Local Control Approach using JMP. Chapter 7 of **Analysis of Observational Health Care Data using SAS**, Cary, NC:SAS Press, pages 151-192.
- Obenchain RL. (2019) **NU.Learning\_in\_R.pdf** <http://localcontrolstatistics.org>

**See Also**

[confirm](#), [ltdagg](#) and [lrcagg](#).

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lrcagg	<i>Calculate the observed Distribution of LRCs in NU.Learning</i>
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**Description**

For a given number, K, of Clusters of Experimental Units in baseline X-covariate space, lrcagg() calculates the observed distribution of "Local Rank Correlations" (LRCs) across Clusters ...where each LRC = cor(trex, Y, method = "spearman") within a Cluster, trex is a numeric measure of Exposure, and Y is a numeric measure of Outcome.

**Usage**

```
lrcagg(K, envir)
```

**Arguments**

K	Number of Clusters in baseline X-covariate space.
envir	R environment output by a previous call to NUsetup().

**Details**

Multiple calls to lrcagg(K) for varying numbers of clusters, K, are typically made after first invoking NUcluster() to hierarchically cluster patients in X-space and then invoking NUsetup() to specify a Y Outcome variable and a continuous, numerical treatment Exposure: trex. lrcagg() computes an observed LRC Distribution, updates information stored in its envir object, and outputs an object that is typically saved in the user's .GlobalEnv to allow subsequent use by print.lrcagg(), plot.lrcagg(), confirm() or KSperm(). Uninformative Clusters (those containing only 1 or 2 experimental units) contribute NA values to the LRctabl\$LRC and LRCdist\$LRC objects within the lrcagg() output list.

**Value**

An output list of 12 objects, of class Ircagg:

hclobj	Name of clustering dendrogram object created by NUcluster().
dframe	Name of data.frame containing X, trex & Y variables.
trex	Name of numerical treatment/exposure level variable.
yvar	Name of outcome Y variable.
K	Number of Clusters Requested.
actclust	Number of Clusters delivered.
LRCtbl	data.frame with 5 columns and K rows for Clusters.
LRCtbl\$c	Cluster ID Factor, "1", "2", ..., "K".
LRCtbl\$LRC	Numerical value of Local Treatment Difference for a Cluster.
LRCtbl\$w	Integer value of "weight" = Cluster Size.
LRCtbl\$LAO	Numerical value of within-cluster Local Average Outcome (Y-value).
LRCtbl\$PS	Numerical value of Local Relative Propensity for Exposure, 0.0 to 1.0.
LRCdist	data.frame with 5 columns and same number of rows as the data: dframe.
LRCdist\$c.K	Cluster ID Variable of the form: "c.K"
LRCdist\$ID	Observation ID Variable for the rows of the input dframe.
LRCdist\$y	Numerical values of Y-Outcomes for Experimental Units.
LRCdist\$t	Numerical values of Treatment-Exposure Levels for Experimental Units.
LRCdist\$LRC	Numerical values of the LRC for the Cluster containing each Unit.
infoclus	Integer value of Number of Informative Clusters.
infounits	Integer value of Number of Units within Informative Clusters.
LRCmean	Numerical value of $\text{mean}(\text{LRCdist}\$LRC)$ = Weighted Average of LRCtbl\$LRC values.
LRCstde	Numerical value of $\text{sqrt}(\text{var}(\text{LRCdist}\$LRC))$ = Weighted Standard Deviation of LRCtbl\$LRC values.

**Author(s)**

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**References**

- Obenchain RL. (2010) The Local Control Approach using JMP. Chapter 7 of **Analysis of Observational Health Care Data using SAS**, Cary, NC: SAS Press, pages 151-192.
- Obenchain RL. (2019) **NU.Learning\_in\_R.pdf** <http://localcontrolstatistics.org>

**See Also**

[ivadj](#), [ltdagg](#) and [NUcompare](#).

**Examples**

```

data(radon)
xvars = c("obesity", "over65", "cursmoke")
hclobj = NUcluster(radon, xvars)
e = NUsetup(hclobj, radon, lnradon, lcanmort)
lrc050 = lrcagg(50, e)
lrc050
plot(lrc050, e)

```

ltdagg

*Calculate the Observed Distribution of LTDs in NU.Learning***Description**

For a given number,  $K$ , of Clusters of Experimental Units in baseline  $X$ -covariate space, `ltdagg()` calculates the observed distribution of "Local Treatment Differences" (LTDs) of the form  $LTD = ((\text{mean}(Y) \text{ for units receiving } \text{trtm}==1) - (\text{mean}(Y) \text{ for units receiving } \text{trtm}==0))$ .

**Usage**

```
ltdagg(K, envir)
```

**Arguments**

<code>K</code>	Number of Clusters in baseline $X$ -covariate space.
<code>envir</code>	R environment output by a previous call to <code>NUsetup()</code> .

**Details**

Multiple calls to `ltdagg(K)` for varying numbers of clusters,  $K$ , are typically made after first invoking `NUcluster()` to hierarchically cluster patients in  $X$ -space and then invoking `NUsetup()` to specify a  $Y$  Outcome variable and a two-level, numerical treatment variable: `trtm`. `ltdagg()` computes an observed LTD Distribution, updates information stored in its `envir` object, and outputs an object that is typically saved in the user's `.GlobalEnv` to allow subsequent use by `print.ltdagg()`, `plot.ltdagg()`, `confirm()` or `KSperm()`. Uninformative Clusters (those containing either only `trtm==1` units or else only `trtm==0` units) contribute **NA** values to the `LTDtbl$LTD` and `LTDdist$LTD` objects within the `ltdagg()` output list object.

**Value**

An output list of 12 objects, of class `ltdagg`:

<code>hiclus</code>	Name of clustering object created by <code>NUcluster()</code> .
<code>dframe</code>	Name of data.frame containing $X$ , <code>trtm</code> & $Y$ variables.
<code>trtm</code>	Name of treatment factor variable.
<code>yvar</code>	Name of outcome $Y$ variable.

K	Number of Clusters Requested.
actclust	Number of Clusters delivered.
LTDtbl	data.frame with 5 columns and K rows for Clusters.
LTDtbl\$c	Cluster ID Factor, "1", "2", ..., "K".
LTDtbl\$LTD	Numerical value of Local Treatment Difference for a Cluster.
LTDtbl\$w	Integer value of "weight" = Cluster Size.
LTDtbl\$LAO	Numerical value of within-cluster Local Average Outcome (Y-value).
LTDtbl\$PS	Numerical value of Propensity Score = Local Fraction of Experimental Units receiving trtm==1; 0.0 <= PS <= 1.0.
LTDdist	data.frame with 5 columns and same number of rows as the data: dframe.
LTDdist\$c.K	Factor values within c("1", "2", ..., "K").
LTDdist\$ID	Observation ID Variable for the rows of the input dframe.
LTDdist\$y	Numerical value of the Y-Outcome for an Experimental Unit.
LTDdist\$t	Numerical value of trtm (0 or 1) for an Experimental Unit.
LTDdist\$LTD	Numerical value of the LTD for the Cluster containing each Exp. Unit.
infoclus	Integer value of Number of Informative Clusters.
infounits	Integer value of Number of Units within Informative Clusters.
LTDmean	Numerical value of mean(LTDdist\$LTD) = Weighted Average of LTDtbl\$LTD values.
LTDstde	Numerical value of sqrt(var(LTDdist\$LTD)) = Weighted Standard Deviation of LTDtbl\$LTD values.

### Author(s)

Bob Obenchain <wizbob@att.net>

### References

- Obenchain RL. (2010) Local Control Approach using JMP. Chapter 7 of **Analysis of Observational Health Care Data using SAS**, Cary, NC:SAS Press, pages 151-192.
- Obenchain RL. (2019) **NU.Learning\_in\_R.pdf** <http://localcontrolstatistics.org>

### See Also

[ivadj](#), [lrcagg](#) and [NUcompare](#).

### Examples

```
# Running takes more than 7 seconds...
data(pci15k)
xvars = c("stent", "height", "female", "diabetic", "acutemi", "ejfract", "ves1proc")
hclobj = NUcluster(pci15k, xvars)
NUe = NUsetup(hclobj, pci15k, thin, surv6mo)
surv050 = ltdagg(50, NUe)
surv050
plot(surv050, NUe)
```

---

mlme	<i>Create a «Most-Like-Me» data.frame for a specified X-Confounder vector: xvec</i>
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### Description

For a Given X-confounder Vector (xvec), sort all experimental units (eUnits) in an ltdagg() or lrcagg() output object into the strictly non-decreasing order of their distances from this X-Vector, which defines the TARGET eUnit: "Me". Plots of mlme() objects and displays of mlme.stats() are then used to Visualize and Summarize "Mini-" « LOCAL effect-size Distributions » for different Numbers of "Nearest Neighbor" eUnits.

### Usage

```
mlme(envir, hcl, NUagg, xvec )
```

### Arguments

envir	Environment output by a call to the NUsetup() function.
hcl	Name of a NUcluster() output object created using a cluster::diana or stats::hclust method.
NUagg	A data.frame object output by ltdagg() or lrcagg() containing LOCAL effect-size Estimates for eUnits within Clusters defined in X-covariate space.
xvec	A suitable vector of the Numerical values for the X-Confounder variables, used in the current CLUSTERING, that define the eUnit: "Me".

### Details

For example, in demo(radon), the eUnits are 2881 US "Counties", and the NUagg object is of type lrcagg() because radon exposure is a continuous variable. But, in demo(pci15k), the eUnits are 15487 "Patients," and the NUagg object is of type ltdagg() because treatment choice (thin) is Binary (0 = "No", 1 = "Yes").

### Value

An output list object of class mlme:

xvec	The xvec vector input to mlme().
Type	Either "LTD" or "LRC".
xvars	Names of the X-Confounder variables specified in NUsetup().
varx	The vector of Variances of the xvars variabes, used in rescaling distances.
outdf	The output data.frame of sorted "Nearest Neighbor" candidate eUnits.

### Author(s)

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**References**

Obenchain RL. NU.Learning-vignette. (2023) **NU.Learning\_in\_R.pdf** <http://localcontrolstatistics.org>

**See Also**

[plot.mlme](#), [print.mlme](#), [mlme.stats](#)

**Examples**

```
# Running takes about 7 seconds...
data(pci15k)
xvars = c("stent", "height", "female", "diabetic", "acutemi", "ejfract", "ves1proc")
hclobj = NUcluster(pci15k, xvars)
NU.env = NUsetup(hclobj, pci15k, thin, surv6mo)
surv0500 = ltdagg(500, NU.env)
xvec11870 = c( 0, 162, 1, 1, 0, 57, 1)
mlmeC5H = mlme(envir = NU.env, hcl = hclobj, NUagg = surv0500, xvec = xvec11870 )
plot(mlmeC5H) # using default "NN" and "breaks" settings...
```

---

mlme.stats

*Print Summary Statistics for One or More "Most-Like-Me" Histogram Pairs.*

---

**Description**

Print Summary Statistics for Local effect-size (LTD or LRC) Distributions associated with given Numbers of "Nearest-Neighbors" in X-confounder Space.

**Usage**

```
mlme.stats(x, NN = 50, ...)
```

**Arguments**

x	An object output by mlme.data().
NN	Number(s) of "Nearest Neighbors" displayed in Histogram(s). NN can be either a single integer like NN = 40 or a combination of integers like NN = c( 50, 250, 2500 ).
...	Other arguments passed on to print().

**Value**

NULL

**Author(s)**

Bob Obenchain <wizbob@att.net>

**See Also**

[plot.mlme, print.mlme, mlme](#)

---

NUcluster	<i>Hierarchical Clustering of experimental units (such as patients) in X-covariate Space</i>
-----------	--

---

**Description**

Form the full, hierarchical clustering tree (dendrogram) for all units (regardless of Treatment/Exposure status) using Mahalanobis distances computed from specified baseline X-covariate characteristics.

**Usage**

```
NUcluster(dframe, xvars, method="ward.D")
```

**Arguments**

dframe	Name of data.frame containing baseline X covariates.
xvars	List of names of X variable(s).
method	Hierarchical Clustering Method of "diana", "ward.D", "ward.D2", "complete", "average", "mcquitty", "median" or "centroid".

**Details**

The first step in applying NU.Learning to data is to hierarchically cluster experimental units in baseline X-covariate space ...thereby creating "Blocks" of relatively well-matched units. NUcluster first calls `stats::prcomp()` to calculate Mahalanobis distances using standardized and orthogonal Principal Coordinates. NUcluster then uses either the divisive `cluster::diana()` method or one of seven agglomerative methods from `stats::hclust()` to compute a dendrogram tree. The `hclust` function is based on Fortran code contributed to STATLIB by F. Murtagh.

**Value**

An output list object of class NUcluster, derived from `cluster::diana` or `stats::hclust`.

dframe	Name of data.frame containing all baseline X-covariates.
xvars	List of 1 or more X-variable names.
method	Hierarchical Clustering Method: "diana", "ward.D", "ward.D2", "complete", "average", "mcquitty", "median" or "centroid".
hclobj	Hierarchical clustering object created by the designated method.

**Author(s)**

Bob Obenchain <[wizbob@att.net](mailto:wizbob@att.net)>

## References

- Kaufman L, Rousseeuw PJ. (1990) **Finding Groups in Data. An Introduction to Cluster Analysis**. New York: John Wiley and Sons.
- Kereiakes DJ, Obenchain RL, Barber BL, et al. (2000) Abciximab provides cost effective survival advantage in high volume interventional practice. *Am Heart J* **140**: 603-610.
- Murtagh F. (1985) Multidimensional Clustering Algorithms. **COMPSTAT Lectures** 4.
- Obenchain RL. (2010) Local Control Approach using JMP. Chapter 7 of **Analysis of Observational Health Care Data using SAS**, Cary, NC:SAS Press, pages 151-192.
- Rubin DB. (1980) Bias reduction using Mahalanobis metric matching. *Biometrics* **36**: 293-298.

## See Also

[NUsetup](#), [ltdagg](#) and [lrcagg](#).

## Examples

```
data(radon)
xvars = c("obesity", "over65", "cursmoke")
hclobj = NUcluster(radon, xvars) # ...using default method = "ward.D"
plot(hclobj)
```

---

NUcompare

*Display NU Sensitivity Graphic for help in choice of K = Number of Clusters*

---

## Description

This function displays Box-Whisker diagrams that compare Treatment Effect-Size distributions for different values of  $K$  = Number of Clusters requested in X-covariate space. After an initial call to `NUsetup()`, the analyst typically makes multiple calls to either `ltdagg()` or `lrcagg()` for different values of  $K$ . The analyst then invokes `NUcompare()` to see how choice of  $K$  changes the location, spread and/or skewness of the distribution of Treatment Effect-Size estimates across Clusters. Variance-Bias trade-offs occur as  $K$  increases; large values of  $K$  may reduce Bias, but they definitely inflate the Variance of LTD and LRC distributions.

## Usage

```
NUcompare(envir)
```

## Arguments

`envir` R environment output by an earlier call to `NUsetup()`.



## Details

The third phase of NU.Learning is called EXPLORE and uses graphical Sensitivity Analyses to show how Treatment Effect-Size distributions change with choice of NU parameter settings. Choice of K = Number of Clusters requested is guided, primarily, by NUcompare() graphics. Equally important are the analyst's choices of (i) which [and how many] of the available baseline X-covariates to "adjust for" and (ii) which clustering algorithm and dissimilarity metric to use. Unfortunately, changing these latter choices requires the analyst to essentially "start over" ...i.e. invoking NUcluster() with changed arguments, followed by an invocation of NUsetup() with a different 1st argument. To change only one's choice of y-Outcome variable and/or the Treatment/Exposure variable, a new NUsetup() invocation is all that is needed.

## Value

NULL

## Author(s)

Bob Obenchain <wizbob@att.net>

## References

Obenchain RL. (2010) Local Control Approach using JMP. Chapter 7 of **Analysis of Observational Health Care Data using SAS**, Cary, NC: SAS Press, pages 151-192.

Obenchain RL. (2015) **NU\_Confirm\_Guidelines.pdf** <http://localcontrolstatistics.org>

Obenchain RL. (2023) **NU.Learning\_in\_R.pdf** <http://localcontrolstatistics.org>

Rubin DB. (1980) Bias reduction using Mahalanobis metric matching. *Biometrics* **36**: 293-298.

Tukey JW. (1977) **Exploratory Data Analysis**, New York: Addison-Wesley, Section 2C.

## See Also

[ltdagg](#), [ivadj](#) and [lrcagg](#).

## Examples

```
# Running takes more than 7 seconds...
data(pci15k)
xvars = c("stent", "height", "female", "diabetic", "acutemi", "ejfract", "ves1proc")
hclobj = NUcluster(pci15k, xvars)
NU.env = NUsetup(hclobj, pci15k, thin, surv6mo)
surv050 = ltdagg( 50, NU.env)
surv100 = ltdagg(100, NU.env)
surv200 = ltdagg(200, NU.env)
NUcompare(NU.env)
```

---

NUsetup	<i>Specify KEY parameters used in NU.Learning to "design" analyses of Observational Data.</i>
---------	---

---

### Description

Invoke NUsetup() to specify the name of the Hierarchical Clustering object output by NUcluster() and the name of the data.frame containing all desired X-covariates, the Treatment/Exposure variable and the Y-Outcome variable. It is ESSENTIAL to save the Environment output by NUsetup() as a named object within the user's .GlobalEnv space.

### Usage

```
NUsetup(hclobj, dframe, trex, yvar)
```

### Arguments

hclobj	Name of a NUcluster() output object created using a cluster::diana or stats::hclust method.
dframe	Name of the data.frame containing all X-covariates, the Treatment/Exposure variable and the Y-Outcome variable.
trex	Name of the numerical Treatment/Exposure variable.
yvar	Name of the numerical Y-Outcome variable.

### Value

The environment output by NUsetup() must be saved to the user's .GlobalEnv space. It's contents will be automatically updated by calls to other NU.Learning functions:

aggdf	data.frame with 4 columns and 1 row for each call to ltdagg() or lrcagg().
aggdf\$Label	Factor value of "LTD" or "LRC".
aggdf\$Blocks	K = integer Number of Clusters requested.
aggdf\$LTDmean or aggdf\$LRCmean	numerical value of cluster mean of LTD or LRC estimates.
aggdf\$LTDstde or aggdf\$LRCstde	numerical value of the within-cluster standard deviation.
boxdf	data.frame of 2 variables ...for input to boxplot() by NUcompare().
boxdf\$NUstat	LTD or LRC estimate for a single experimental unit from ltdagg() or lrcagg().
boxdf\$K	Number of Cluters used in forming the LTD or LRC estimate for each Experimental Unit.
Kmax	Maximum Number of Clusters so that Average Size will be $\geq 12$ experimental units.
LTDmax or LRCmax	Maximum Treatment Effect-Size estimate across Clusters.

LTDmin or LRCmin	Minimum Treatment Effect-Size estimate across Clusters.
NumLevels	Integer number of distinct Levels of the Treatment/Exposure variable: trex.
pars	Character data.frame with 4 columns and 1 row.
pars[1, 1]	Name of the diana or hclust object created by NUcluster().
pars[1, 2]	Name of data.frame containing the X, Treatment/Exposure and Y variables.
pars[1, 3]	Name of Treatment/Exposure variable within data.frame pars[1,2].
pars[1, 4]	Name of Y-outcome variable within data.frame pars[1,2].

**Author(s)**

Bob Obenchain <wizbob@att.net>

**References**

Obenchain RL. (2010) Local Control Approach using JMP. Chapter 7 of **Analysis of Observational Health Care Data using SAS**, Cary, NC:SAS Press, pages 151-192.

Obenchain RL. (2023) **NU.Learning\_in\_R.pdf** <http://localcontrolstatistics.org>

**See Also**

[ltdagg](#), [ivadj](#) and [lrcagg](#).

**Examples**

```
# Running takes about 7 seconds...
data(pci15k)
xvars = c("stent", "height", "female", "diabetic", "acutemi", "ejfract", "veslproc")
hclobj = NUcluster(pci15k, xvars)
NUe = NUsetup(hclobj, pci15k, thin, surv6mo)
ls.str(NUe)
```

---

pci15k	<i>Six-month Survival, Cardiac cost and Baseline Covariate data for 15,487 PCI patients.</i>
--------	--

---

**Description**

Using observational data on 996 patients who received a Percutaneous Coronary Intervention (PCI) at Ohio Heart Health, Lindner Center, Christ Hospital, Cincinnati (Kereiakes et al, 2000), we generated this much larger dataset via "plasmode simulation."

**Usage**

```
data(pci15k)
```

## Format

A data frame of 11 variables on 15,487 patients; no NAs.

**patid** Patient ID number: 1 to 15487.

**surv6mo** Binary PCI Survival variable: 1 => Survival for at least 6 months following PCI, 0 => Survival for less than 6 months.

**cardcost** Cardiac related costs incurred within 6 months of patient's initial PCI; numeric value in 1998 dollars; costs were truncated by death for the 404 patients with surv6mo == 0.

**thin** Numeric treatment selection indicator: thin = 0 implies usual PCI care alone; thin = 1 implies usual PCI care augmented by either planned or rescue treatment with a new blood thinning agent.

**stent** Coronary stent deployment; numeric, with 1 meaning YES and 0 meaning NO.

**height** Height in centimeters; numeric integer from 133 to 198.

**female** Female gender; numeric, with 1 meaning YES and 0 meaning NO.

**diabetic** Diabetes mellitus diagnosis; numeric, with 1 meaning YES and 0 meaning NO.

**acutemi** Acute myocardial infarction within the previous 7 days; numeric, with 1 meaning YES and 0 meaning NO.

**ejfrac** Left ejection fraction; numeric value from 17 percent to 77 percent.

**ves1proc** Number of vessels involved in the patient's initial PCI procedure; numeric integer from 0 to 5.

## References

Kereiakes DJ, Obenchain RL, Barber BL, et al. Abciximab provides cost effective survival advantage in high volume interventional practice. *Am Heart J* 2000; **140**: 603-610.

Gadbury GL, Xiang Q, Yang L, Barnes S, Page GP, Allison DB. Evaluating Statistical Methods Using Plasmode Data Sets in the Age of Massive Public Databases: An Illustration Using False Discovery Rates. *PLOS Genetics* 2008; **4**: 1-8, e1000098 (Open Access).

Obenchain RL. (2023) **NU.Learning\_in\_R.pdf** <http://localcontrolstatistics.org>

## Examples

```
data(pci15k)
str(pci15k)
```

---

plot.ivadj	<i>Display an Instrumental Variable (LAO) plot with Linear and smooth.spline Fits</i>
------------	---

---

## Description

For a given number of patient clusters, K, in baseline X-covariate space and a specified Y-outcome variable, display the distribution of Local Average Outcomes (LAOs) plotted versus Within-Cluster Propensity-like Scores: Treatment Selection Fractions or Relative Exposure Levels.

**Usage**

```
## S3 method for class 'ivadj'
plot(x, maxsiz = 0.15, ...)
```

**Arguments**

**x** An object output by ivadj() for K given Clusters in baseline X-covariate space.

**maxsiz** Radius of the Circle plotting symbol for the largest Cluster. Usually < 0.6

**...** Other arguments passed on to plot().

**Value**

NULL

**Author(s)**

Bob Obenchain <wizbob@att.net>

**See Also**

[plot.ltdagg](#), [plot.lrcagg](#)

---

plot.lrcagg                    *Display Visualizations of an Observed LRC Distribution in NU.Learning*

---

**Description**

Display a Histogram, Box-Whisker Diagram and/or empirical Cumulative Distribution Function depicting the Observed Local Rank Correlation (LRC) Distribution across K Clusters.

**Usage**

```
## S3 method for class 'lrcagg'
plot(x, envir, show="all", breaks="Sturges", ...)
```

**Arguments**

**x** An object output by lrcagg() for K = Number of Clusters in baseline X-covariate space.

**envir** R environment output by a previous call to NUsetup().

**show** Choice of "all", "seq", "hist", "boxp", or "ecdf".

**breaks** Parameter setting for hist(); May be an integer value ...like 25 or 50.

**...** Other arguments passed on to plot().

**Value**

NULL

**Author(s)**

Bob Obenchain &lt;wizbob@att.net&gt;

**See Also**[plot.ltdagg](#)


---

plot.ltdagg	<i>Display Visualizations of an Observed LTD Distribution in NU.Learning</i>
-------------	--

---

**Description**

Display a Histogram, Box-Whisker Diagram and/or empirical Cumulative Distribution Function depicting the Observed Local Treatment Difference (LTD) Distribution across K Clusters.

**Usage**

```
## S3 method for class 'ltdagg'
plot(x, envir, show="all", breaks="Sturges", ...)
```

**Arguments**

x	An object output by ltdagg() for K = Number of Clusters in baseline X-covariate space.
envir	R environment output by a previous call to NUsetup().
show	Choice of "all", "seq", "hist", "boxp", or "ecdf".
breaks	Parameter setting for hist(); May be an integer value ...like 25 or 50.
...	Other arguments passed on to plot().

**Value**

NULL

**Author(s)**

Bob Obenchain &lt;wizbob@att.net&gt;

**See Also**[plot.lrcagg](#)

---

plot.mlme	<i>Display a Pair (or Pairs) of Histograms showing LOCAL effect-sizes for Patients "Most-Like-Me".</i>
-----------	--

---

### Description

Display Pair(s) of Histograms of Local effect-size (LTD or LRC) Distributions for a specified Number (or combinations of Numbers) of "Nearest-Neighbors in X-confounder Space.

### Usage

```
## S3 method for class 'mlme'  
plot(x, NN=50, breaks=50, ...)
```

### Arguments

x	An object output by mlme().
NN	Number(s) of Nearest Neighbors displayed in Bottom Histogram(s). NN can be a single integer like NN = 40 or a combination of integers like NN = c( 50, 250, 2500 ).
breaks	Integer number of breaks in the Top Histogram for the full LTD or LRC distribution. Because the Bottom Histogram may include only a few Nearest Neighbors, it is always displayed using breaks = "Sturges".
...	Other arguments passed on to plot().

### Value

NULL

### Author(s)

Bob Obenchain <wizbob@att.net>

### See Also

[mlme.stats](#), [print.mlme](#), [mlme](#)

pmdata

*Particulate Matter, Mortality and Other data for 2980 US Counties***Description**

This data.frame combines 122 variables from the 5 sources referenced below. Several PM variables appear to be predictions from EPA "CMAQ" models rather than values from validated measuring instruments. NU.Learning concepts are illustrated in demo(pmdata) using Clustering of 2973 Counties and Parishes within the contiguous 48 US States and Washington, D.C.

**Usage**

```
data(pmdata)
```

**Format**

This data.frame contains 122 variables for 2,980 US counties. A total of 738 "NA"s imply that only about two tenths of one percent of these 363,560 values are missing.

**fips** Federal Information Processing Standard code; 4 or 5 digits; 2980 unique values

**C50** Cluster ID Number between 1 and 50. Total of 50 unique values

**LRC50** Local (Spearman) Rank Correlation between Bvoc and AACRmort within Cluster

**County** County or Parish name is a Factor variable (character code)

**State** State name is a 2-Character Factor code; 49 unique levels

**Deaths** CDC: Total number of Deaths in the County in 2016

**Population** CDC: Total population of County in 2016

**CRmort** CDC: Crude Rate of Circulatory-Respiratory Mortality for the County in 2016

**CrudeL95** CDC: Lower 95% confidence limit for Crude Rate of CR Mortality

**CrudeU95** CDC: Upper 95% confidence limit for Crude Rate of CR Mortality

**CrudeSE** CDC: Standard Error for Crude Rate of CR Mortality

**AACRmort** CDC: Age Adjusted Rate of Circulatory-Respiratory Mortality in 2016

**AACRL95** CDC: Lower 95% confidence limit for Age Adjusted Rate of CR Mortality

**AACRU95** CDC: Upper 95% confidence limit for Age Adjusted Rate of CR Mortality

**AACR\_SE** CDC: Standard Error for Age Adjusted Rate of CR Mortality

**TotDeathPct** CDC: Total Death Percentage - Circulatory-Respiratory Mortality in 2016

**lat** EPA: County Latitude used in EPA "CMAQ" model calculations

**long** EPA: County Longitude used in EPA "CMAQ" model calculations

**RHpct** EPA: Relative Humidity Percentage for 2016

**SFCtmpC** EPA: Surface Temperature in Degrees Centigrade for 2016

**NO2** EPA: Nitrogen Dioxide level (NO2.ppbV) for 2016

**O3** EPA: Ozone level (O3.ppbV) for 2016



**pmCL** EPA: Chlorine level in Particulate Matter (PM25\_CL.ugm3) for 2016  
**pmEC** EPA: Ethylene Carbonate level in Particulate Matter (PM25\_EC.ugm3) for 2016  
**pmNA** EPA: Sodium level in Particulate Matter (PM25\_NA.ugm3) for 2016  
**pmMG** EPA: Magnesium level in Particulate Matter (PM25\_MG.ugm3) for 2016  
**pmK** EPA: Potassium level in Particulate Matter (PM25\_K.ugm3) for 2016  
**pmCA** EPA: Calcium level in Particulate Matter (PM25\_CA.ugm3) for 2016  
**pmNH4** EPA: Ammonium level in Particulate Matter (PM25\_NH4.ugm3) for 2016  
**pmNO3** EPA: Nitrate level in Particulate Matter (PM25\_NO3.ugm3) for 2016  
**pmOC** EPA: Organic Compounds in pmTOT [fine particulate matter] (PM25\_OC.ugm3) for 2016  
**pmOM** EPA: OM compounds in pmTOT (PM25\_OM.ugm3) for 2016  
**pmOTHR** EPA: Other Compounds in pmTOT (PM25\_OTHR.ugm3) for 2016  
**pmSO4** EPA: Sulfate Compounds in pmTOT (PM25\_SO4.ugm3) for 2016  
**pmFE** EPA: Ferrous Compounds in pmTOT (PM25\_FE.ugm3) for 2016  
**pmSI** EPA: Silicon Compounds in pmTOT (PM25\_SI.ugm3) for 2016  
**pmTI** EPA: Titanium Compounds in pmTOT (PM25\_TI.ugm3) for 2016  
**pmMN** EPA: Manganese Compounds in pmTOT (PM25\_MN.ugm3) for 2016  
**pmAL** EPA: Aluminum Compounds in pmTOT (PM25\_AL.ugm3) for 2016  
**pmUNSPCRS** EPA: UNSPCRS Compounds in pmTOT (PM25\_UNSPCRS.ugm3) for 2016  
**pmPOA** EPA: Primary Organic Aerosols in pmTOT (PM25\_POA.ugm3) for 2016  
**pmSOA** EPA: Secondary Organic Aerosols in pmTOT (PM25\_SOA.ugm3) for 2016; pmSOA = Avoc+Bvoc  
**pmGLY** EPA: Glycemic Secondary Organic Aerosols in pmTOT (PM25\_GLYSOA.ugm3) for 2016  
**pmOLGB** EPA: OLGB compounds in pmTOT (PM25\_OLGB.ugm3) for 2016  
**pmISOP** EPA: ISOP compounds in pmTOT (PM25\_ISOP.ugm3) for 2016  
**pmEPOX** EPA: EPOX compounds in pmTOT (PM25\_EPOX.ugm3) for 2016  
**pmSQT** EPA: SQT compounds in pmTOT (PM25\_SQT.ugm3) for 2016  
**pmMTN** EPA: MTN compounds in pmTOT (PM25\_MTN.ugm3) for 2016  
**pmMT** EPA: MT compounds in pmTOT (PM25\_MT.ugm3) for 2016  
**pmTOT** EPA: Total (fine) Particulate Matter (PM25\_TOT.ugm3) for 2016  
**SFCtmpK** EPA: Surface Temperature in Degrees Kelvin for 2016  
**CardioRes** CDC: Cardio Respiratory Rate (rate I00J98.per100000.cdc) for 2016  
**POPcdc** CDC: County Population (population.cdc) for 2016  
**POP5yracs** CDC: 5yracs Population (population.people.5yracs) for 2016  
**PREMdeath** Premature Deaths per 100K Residents ...UWPHI for 2018  
**POFHealth** Poor or Fair Health rate (Poor.or.fair.health) ...UWPHI for 2018  
**PPHdays** Poor Physical Health days (Poor.physical.health.days) ...UWPHI for 2018  
**PMHdays** Poor Mental Health days (Poor.mental.health.days) ...UWPHI for 2018

**LBW** Low Birth Weight rate (Low.birthweight) ...UWPHI for 2018  
**ASmoke** Adult Smoking Percentage (Adult.smoking) ...UWPHI for 2018  
**AObes** Adult Obesity Percentage (Adult.obesity) ...UWPHI for 2018  
**FEnv** Food Environment Index (Food.environment.index) ...UWPHI for 2018  
**PhysInAct** Physical Inactivity (Physical.inactivity) ...UWPHI for 2018  
**ExercOPS** Access to Exercise Opportunities ...UWPHI for 2018  
**ExsDrink** Excessive Drinking Rate (Excessive.drinking) ...UWPHI for 2018  
**AIDrivD** Alcohol Impaired Driving Deaths ...UWPHI for 2018  
**STInfect** Sexually Transmitted Infections ...UWPHI for 2018  
**TBirths** Teenage Births (Teen.births) ...UWPHI for 2018  
**Uninsur** Uninsured Residences (Uninsured) ...UWPHI for 2018  
**PCDocs** Primary Care Physicians (Primary.care.physicians) ...UWPHI for 2018  
**Dentists** Dentists (Dentists) ...UWPHI for 2018  
**PrevntHS** Preventable Hospital Stays (Preventable.hospital.stays) ...UWPHI for 2018  
**DiabMNT** Diabetes Monitoring (Diabetes.monitoring) ...UWPHI for 2018  
**MammoSC** Mammography Screening (Mammography.screening) ...UWPHI for 2018  
**SomCOL** Some College Education (Some.college) ...UWPHI for 2018  
**UnEMP** Unemployment Rate (Unemployment) ...UWPHI for 2018  
**ChildPOV** Children Living in Poverty (Children.in.poverty) ...UWPHI for 2018  
**IncomIEQ** Income Inequality (Income.inequality) ...UWPHI for 2018  
**ChildSPH** Children In Single-Parent Households ...UWPHI for 2018  
**SocASOC** Social Associations (Social.associations) ...UWPHI for 2018  
**VioCRM** Violent Crime Rate (Violent.crime) ...UWPHI for 2018  
**InjyDths** Injury Death Rate (Injury.deaths) ...UWPHI for 2018  
**AirPolpm** Air Pollution Particulate Matter ...UWPHI for 2018  
**DrnkWtVi** Drinking Water Violations (Drinking.water.violations) ...UWPHI for 2018  
**SevrHOUS** Severe Housing Problems (Severe.housing.problems) ...UWPHI for 2018  
**DrivATW** Driving Alone to Work (Driving.alone.to.work) ...UWPHI for 2018  
**LComutA** Long Commute - Driving Alone to Work ...UWPHI for 2018  
**PAAM** Premature Age Adjusted Mortality ...UWPHI for 2018  
**FrqPhysD** Frequent Physical Distress ...UWPHI for 2018  
**FrqMentD** Frequent Mental Distress ...UWPHI for 2018  
**DiabPrev** Diabetes Prevalence (Diabetes.prevalence) ...UWPHI for 2018  
**FoodInSec** Food Insecurity (Food.insecurity) ...UWPHI for 2018  
**LimAHFood** Limited Access to Healthy Foods ...UWPHI for 2018  
**DrugOdDM** Drug Overdose Deaths Model predictions ...UWPHI for 2018  
**InsufSlp** Insufficient Sleep (Insufficient.sleep) ...UWPHI for 2018

**UnInsAds** Uninsured Adults (Uninsured.adults) ...UWPHI for 2018  
**UnInsCls** Uninsured Children (Uninsured.children) ...UWPHI for 2018  
**HCareCost** Health Care Costs (Health.care.costs) ...UWPHI for 2018  
**OthPrimCP** Other Primary Care Providers ...UWPHI for 2018  
**MHHIncome** Median Household Income ...UWPHI for 2018  
**ChildFRPL** Children Eligible for Free or Reduced-Price Lunch ...UWPHI for 2018  
**Population** County Population (Population) ...UWPHI for 2018  
**AGELess18** Residents below 18 Years of Age ...UWPHI for 2018  
**A65oOVR** Residents 65 or Older (X..65.and.older) ...UWPHI for 2018  
**NHispAfA** Non-Hispanic African-American Residents ...UWPHI for 2018  
**AmINalsN** American Indian or Alaskan Natives ...UWPHI for 2018  
**Asian** Asian Residents (X..Asian) ...UWPHI for 2018  
**NHawOPI** Native Hawaiian and Other Pacific Islanders ...UWPHI for 2018  
**Hispanic** Hispanic Residents (X..Hispanic) ...UWPHI for 2018  
**NHispWht** Non-Hispanic White Residents ...UWPHI for 2018  
**LoProEngl** Low Proficiency in English (not.proficient.in.English) ...UWPHI for 2018  
**Females** Female Residents ...UWPHI for 2018  
**Rural** Rural Residents ...UWPHI for 2018  
**pmOA** EPA: Organic Aerosols in pmTOT (PM25\_OA.ugm3) for 2016  
**Avoc** EPA: Anthroprogenic [man-made] Volatile Organic Compounds in pmTOT for 2016  
**pmSEAspry** EPA: Sea Spray components in pmTOT (PM25\_SOAAVOC.ugm3) for 2016  
**pmDUST** EPA: Dust components in pmTOT (PM25\_DUST.ugm3) for 2016  
**pmNH4NO3** EPA: Ammonium Nitrate components in pmTOT (PM25\_NH4NO3.ugm3) for 2016  
**pmSOOT** EPA: Soot components in pmTOT (PM25\_SOOT.ugm3) for 2016  
**isop** EPA: SOA Isoprenes (PM25\_SOAISOPRENE.ugm3) for 2016  
**terp** EPA: SOA Terpenes (PM25\_SOATERPENE.ugm3) for 2016  
**Bvoc** EPA: Biogenic (natural) Volatile Organic Compounds for 2016; Bvoc = isop + terp

## References

Obenchain RL. and Young SS. (2022), EPA Particulate Matter Data - Analyses using Local Control Strategy. (24 pages, 22 figures) <https://doi.org/10.48550/arXiv.2209.05461>  
 Pye, H., Ward-Caviness, C., Murphy, B., Appel, K., and Seltzer, K. (2021). Secondary organic aerosol association with cardiorespiratory disease mortality in the united states. *Nature Communications*, 12.7215 <https://doi.org/10.1038/s41467-021-27484-1>  
 Pye, H. [EPA] (2021), Data For Secondary Organic Aerosol and Cardiorespiratory Disease Mortality. <https://doi.org/10.5281/zenodo.5713903>  
 University of Wisconsin, Population Health Institute. <https://uwphi.pophealth.wisc.edu> [UWPHI] [UWPHI@med.wisc.edu](mailto:UWPHI@med.wisc.edu)  
 Young SS. and Obenchain RL. (2022), "EPA particulate matter data...Analyses using Local Control Strategy" <https://doi.org/10.5061/dryad.63xsj3v58>

**Examples**

```
data(pmdata)
str(pmdata, list.len=122)
```

---

print.mlme	<i>Print Summary Statistics on Local effect-size Estimates for Patients "Most-Like-Me".</i>
------------	---

---

**Description**

Display "Most-Like-Me" Summary Statistics for LOCAL effect-size (LTD or LRC) Distributions of "Nearest-Neighbors" in X-confounder Space.

**Usage**

```
## S3 method for class 'mlme'
print(x, ...)
```

**Arguments**

x	An object output by mlme().
...	Other arguments passed on to print().

**Value**

NULL

**Author(s)**

Bob Obenchain <wizbob@att.net>

**See Also**

[mlme.stats](#), [plot.mlme](#), [mlme](#)

---

radon	<i>Radon exposure and lung cancer mortality data for 2,881 US counties in 46 States.</i>
-------	--

---

## Description

Federal EPA and state government agencies have been reporting observational data at the US County level since about 1980. The data given here include 5 potential X-confounder variables of the relationship between lung cancer mortality and radon exposure; they were amassed and checked by Goran Krstic, Fraser Health Authority, Vancouver, BC, Canada.

## Usage

```
data(radon)
```

## Format

A data frame of 11 variables for 2881 US counties. One Missing Value; row 778 for Shannon County, SD, fips == 46113, has hhincome == NA.

**fips** County FIPS code. Codes are 4 or 5 digit integers; 2881 unique values.

**state** State Factor variable (2-character codes); 46 unique levels.

**county** County or Parish Factor variable (character codes); 1703 unique levels.

**lcanmort** Lung Cancer Mortality rate (deaths per 100,000 person-years), 1980-2004.

**radon** County Radon Exposure level in picocuries per liter (pCi/L) for some unspecified period within 1986-1992; rounded to nearest single decimal place.

**lnradon** Natural logarithm of County Radon Exposure level. Radon levels reported as 0.0 for 10 US counties are Windsorized here to  $\ln(0.05)$ , which is roughly -3.

**obesity** Percentage of County Residents considered Obese (age adjusted), 2008.

**over65** Percentage of County Residents of Age 65 and over, 2000 Census.

**cursmoke** Percentage of County Residents who Currently Smoke, 1997-2003.

**evrsmoke** Percentage of County Residents who Ever Smoked, 1997-2003.

**hhincome** Average Median HouseHold Income in Thousands (\$1,000), 1989-2004.

## References

Krstic G, Obenchain RL. (2016) Radon dataset documentation and downloads. <http://localcontrolstatistics.org>

Obenchain RL. (2018) **RADON\_short.pdf** <http://localcontrolstatistics.org> 40 PPT Slides and Commentary in Notes Pages format.

## Examples

```
data(radon)
str(radon)
```

---

reveal.data	<i>Create a data.frame for use in Prediction of a LTD/LRC effect-size Distribution</i>
-------------	--

---

### Description

reveal.data() forms a data.frame by sorting and appending the LTD or LRC exposure effect-size measures from ltdagg() or lrcagg() – as well as a Cluster membership-number variable – to a copy of the data.frame specified in NUsetup(). In the fourth and final REVEAL Phase of NU.Learning, a stretch-goal is to predict variation in LTD/LRC effect-size distributions using the known (baseline) X-covariate characteristics of experimental units. For example, the data.frame output by reveal.data() is suitable for input to party::ctree() as well as to a number of other "less Visual" prediction methods available in **R**.

### Usage

```
reveal.data(x, clus.var="Clus", effe.var="eSiz")
```

### Arguments

x	An output object resulting from a call to ltdagg() or lrcagg().
clus.var	Quoted NAME for the Cluster-Number variable.
effe.var	Quoted NAME for the LTD/LRC effect-size variable.

### Value

The desired data.frame:

outdf	A data.frame containing clus.var, effe.var plus (X, trex & Y) variables.
-------	--

### Author(s)

Bob Obenchain <wizbob@att.net>

### References

Obenchain RL. (2023) **NU.Learning\_in\_R.pdf** <http://localcontrolstatistics.org>

### See Also

[ltdagg](#), [lrcagg](#), and [NUsetup](#).

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