

# Package ‘NlsyLinks’

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**Type** Package

**Title** Utilities and kinship information for behavior genetics and developmental research using the NLSY.

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**Author** Will Beasley, Joe Rodgers, David Bard, Michael Hunter, and Kelly Meredith

**Maintainer** Will Beasley <wibeasley@hotmail.com>

**Description** Utilities and kinship information for behavior genetics and developmental research using the NLSY (<http://www.bls.gov/nls/>)

**URL** <https://r-forge.r-project.org/projects/nlsylinks/>

**Depends** R(>= 2.14.0),stats

**Imports** methods,lavaan

**Suggests** devtools,ggplot2,knitr,plyr,scales,testit,testthat,xtable

**License** GPL

**LazyData** TRUE

**VignetteBuilder** knitr

**Collate** 'AceEstimate.R' 'AceLavaanGroup.R' 'AceUnivariate.R' 'CleanSemAceDataset.R' 'ColumnUtilities.R' 'CreateAceEstimate.R' 'CreatePairLinksDoubleEntered.R' 'CreatePairLinksDoubleEnteredWithNoOutcomes.R' 'CreatePairLinksSingleEntered.R' 'CreateSpatialNeighbours.R' 'CreateSubjectTag.R' 'DeFriesFulker.R' 'ExtraOutcomes79Doc.R' 'Links79PairDoc.R' 'Links79PairExpandedDoc.R' 'NlsyLinks.R' 'ReadCsvNlsy79.R' 'RGroupSummary.R' 'ValidateOutcomeDataset.R' 'ValidatePairLinks.R' 'ValidatePairLinksAreSymmetric.R' 'SubjectDetails79Doc.R'

## R topics documented:

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NlsyLinks-package	<i>Utilities and kinship information for Behavior Genetics and Developmental research using the NLSY.</i>
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## Description

Utilities and kinship information for Behavior Genetics and Developmental research using the NLSY.

## Note

This package considers both Gen1 and Gen2 subjects. "Gen1" refers to subjects in the original NLSY79 sample (<http://www.bls.gov/nls/nlsy79.htm>). "Gen2" subjects are the biological children of the Gen1 females -ie, those in the NLSY79 Children and Young Adults sample (<http://www.bls.gov/nls/nlsy79ch.htm>).

## Author(s)

William Howard Beasley (Howard Live Oak LLC, Norman)  
 Joseph Lee Rodgers (Vanderbilt University, Nashville)  
 David Bard (University of Oklahoma Health Sciences Center, OKC)  
 Kelly Meredith (Oklahoma City University, OKC)  
 Michael D. Hunter (University of Oklahoma, Norman)  
 Maintainer: Will Beasley <[wibeasley@hotmail.com](mailto:wibeasley@hotmail.com)>

## References

This package's development was largely supported by the NIH Grant 1R01HD65865, "NLSY Kinship Links: Reliable and Valid Sibling Identification" (PI: Joe Rodgers). A more complete list of research articles using NLSY Kinship Links is maintained on our [repository's wiki](#).

Rodgers, Joseph Lee, & Kohler, Hans-Peter (2005). *Reformulating and simplifying the DF analysis model*. *Behavior Genetics*, 35 (2), 211-217.

Rodgers, J.L., Bard, D., Johnson, A., D'Onofrio, B., & Miller, W.B. (2008). *The Cross-Generational Mother-Daughter-Aunt-Niece Design: Establishing Validity of the MDAN Design with NLSY Fertility Variables*. *Behavior Genetics*, 38, 567-578.

D'Onofrio, B.M., Van Hulle, C.A., Waldman, I.D., Rodgers, J.L., Rathouz, P.J., & Lahey, B.B. (2007). *Causal inferences regarding prenatal alcohol exposure and childhood externalizing problems*. *Archives of General Psychiatry*, 64, 1296-1304.

Rodgers, J.L. & Doughty, D. (2000). *Genetic and environmental influences on fertility expectations and outcomes using NLSY kinship data*. In J.L. Rodgers, D. Rowe, & W.B. Miller (Eds.) *Genetic influences on fertility and sexuality*. Boston: Kluwer Academic Press.

Cleveland, H.H., Wiebe, R.P., van den Oord, E.J.C.G., & Rowe, D.C. (2000). *Behavior problems among children from different family structures: The influence of genetic self-selection*. *Child Development*, 71, 733-751.

Rodgers, J.L., Rowe, D.C., & Buster, M. (1999). *Nature, nurture, and first sexual intercourse in the USA: Fitting behavioural genetic models to NLSY kinship data*. *Journal of Biosocial Sciences*, 31.

Rodgers, J.L., Rowe, D.C., & Li, C. (1994). *Beyond nature versus nurture: DF analysis of non-shared influences on problem behaviors*. *Developmental Psychology*, 30, 374-384.

## Examples

```
library(NlsyLinks) #Load the package into the current R session.
summary(Links79Pair) #Summarize the five variables.
hist(Links79Pair$R) #Display a histogram of the Relatedness values.
table(Links79Pair$R) #Create a table of the Relatedness values for the whole sample.
```

---

Ace

*Estimates the heritability of additive traits using a single variable.*

---

## Description

An ACE model is the foundation of most behavior genetic research. It estimates the additive heritability (with *a*), common environment (with *c*) and unshared heritability/environment (with *e*).

## Usage

```
AceUnivariate(method=c("DeFriesFulkerMethod1","DeFriesFulkerMethod3"),
  dataSet, oName_S1, oName_S2, rName="R",
  manifestScale="Continuous")

DeFriesFulkerMethod1(dataSet, oName_S1, oName_S2,
  rName="R")

DeFriesFulkerMethod3(dataSet, oName_S1, oName_S2,
  rName="R")
```

## Arguments

method	The specific estimation technique.
dataSet	The data.frame that contains the two outcome variables and the relatedness coefficient (corresponding to oName_S1, oName_S2, and rName)
oName_S1	The name of the outcome variable corresponding to the first subject in the pair. This should be a character value.
oName_S2	The name of the outcome variable corresponding to the second subject in the pair. This should be a character value.
rName	The name of the relatedness coefficient for the pair (this is typically abbreviated as R). This should be a character value.
manifestScale	Currently, only <i>continuous</i> manifest/outcome variables are supported.

## Details

The AceUnivariate function is a wrapper that calls DeFriesFulkerMethod1 or DeFriesFulkerMethod3. Future versions will incorporate methods that use latent variable models.

## Value

Currently, a list is returned with the arguments ASquared, CSquared, ESquared, and RowCount. In the future, this may be changed to an S4 class.

## Author(s)

Will Beasley

## References

Rodgers, Joseph Lee, & Kohler, Hans-Peter (2005). **Reformulating and simplifying the DF analysis model**. *Behavior Genetics*, 35 (2), 211-217.

## Examples

```
library(NlsyLinks) #Load the package into the current R session.
dsOutcomes <- ExtraOutcomes79
dsOutcomes$SubjectTag <- CreateSubjectTag(subjectID=dsOutcomes$SubjectID,
  generation=dsOutcomes$Generation)
dsLinks <- Links79Pair
dsLinks <- dsLinks[dsLinks$RelationshipPath=='Gen2Siblings', ] #Use only Gen2 Siblings (ie, NLSY79-C)
dsDF <- CreatePairLinksDoubleEntered(outcomeDataset=dsOutcomes, linksPairDataset=dsLinks,
  outcomeNames=c("MathStandardized", "HeightZGenderAge", "WeightZGenderAge"))

estimatedAdultHeight <- DeFriesFulkerMethod3(
  dataSet=dsDF,
  oName_S1="HeightZGenderAge_S1",
  oName_S2="HeightZGenderAge_S2")
estimatedAdultHeight #ASquared and CSquared should be 0.60 and 0.10 for this rough analysis.

estimatedMath <- DeFriesFulkerMethod3(
  dataSet=dsDF,
  oName_S1="MathStandardized_S1",
  oName_S2="MathStandardized_S2")
estimatedMath #ASquared and CSquared should be 0.85 and 0.045.
```

```
class(GetDetails(estimatedMath))
summary(GetDetails(estimatedMath))
```

---

AceEstimate-class	<i>Class "AceEstimate"</i>
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---

## Description

A class containing information about a single univariate ACE model.

## Objects from the Class

Objects can be created by calls of the form:

```
new("AceEstimate", aSquared, cSquared, eSquared, caseCount, unity, withinBounds, details, ...)
```

## Note

The contents of the `Details` list depends on the underlying estimation routine. For example, when the ACE model is estimated with a DF analysis, the output is an `lm` object, because the `lm` function was used (ie, the basical general linear model). Alternatively, if the user specified the `lavaan` package should estimate that ACE model, the output is a `lavaan` object.

## Examples

```
library(NlsyLinks) #Load the package into the current R session.

showClass("AceEstimate")
est <- CreateAceEstimate(.5, .2, .3, 40)
est
print(est)
```

---

AceLavaanGroup	<i>A simple multiple-group ACE model with the <b>lavaan</b> package.</i>
----------------	--

---

## Description

This function uses the **lavaan** package to estimate a univariate ACE model, using multiple groups. Each group has a unique value of *R* (i.e., the *Relatedness* coefficient).

## Usage

```
AceLavaanGroup(dsClean, estimateA=TRUE, estimateC=TRUE,
  printOutput=FALSE)
```

## Arguments

<code>dsClean</code>	The <code>data.frame</code> containing complete cases for the R groups to be included in the estimation.
<code>estimateA</code>	Should the <i>A</i> variance component be estimated? $A^2$ represents the proportion of variability due to a shared genetic influence.
<code>estimateC</code>	Should the <i>C</i> variance component be estimated? $C^2$ represents the proportion of variability due to a shared environmental influence.
<code>printOutput</code>	Indicates if the estimated parameters and fit statistics are printed to the console.

## Details

The variance component for *E* is always estimated, while the *A* and *C* estimates can be fixed to zero (when `estimateA` and/or `estimateC` are set to `FALSE`).

## Value

An `AceEstimate` object.

## Note

Currently, the variables in `dsClean` must be named O1, O2 and R; the letter ‘O’ stands for *Outcome*. This may not be as restrictive as it initially seems, because `dsClean` is intended to be produced by `CleanSemAceDataset`. If this is too restrictive for your uses, we’d like to hear about it (*please email wibeasley at hotmail period com*).

## Author(s)

Will Beasley

## References

The **lavaan** package is developed by Yves Rosseel at Ghent University. Three good starting points are the package home page (<http://lavaan.ugent.be/>), the documentation (<http://cran.r-project.org/web/packages/lavaan/>) and the JSS paper.

Rosseel, Yves (2012), **lavaan: An R Package for Structural Equation Modeling**. *Journal of Statistical Software*, 48, (2), 1-36.

## See Also

[CleanSemAceDataset](#). Further ACE model details are discussed in our package’s [vignettes](#).

## Examples

```
library(NlsyLinks) #Load the package into the current R session.
dsLinks <- Links79PairExpanded #Start with the built-in data.frame in NlsyLinks
dsLinks <- dsLinks[dsLinks$RelationshipPath=='Gen2Siblings', ] #Use only Gen2 Siblings (NLSY79-C)

oName_S1 <- "MathStandardized_S1" #Stands for Outcome1
oName_S2 <- "MathStandardized_S2" #Stands for Outcome2

dsGroupSummary <- RGroupSummary(dsLinks, oName_S1, oName_S2)
dsClean <- CleanSemAceDataset(dsDirty=dsLinks, dsGroupSummary, oName_S1, oName_S2)
```

```

ace <- AceLavaanGroup(dsClean)
ace

#Should produce:
# [1] "Results of ACE estimation: [show]"
#      ASquared      CSquared      ESquared      CaseCount
#      0.6681874      0.1181227      0.2136900 8390.0000000

library(lavaan) #Load the package to access methods of the lavaan class.
GetDetails(ace)

#Examine fit stats like Chi-Squared, RMSEA, CFI, etc.
fitMeasures(GetDetails(ace)) #The function 'fitMeasures' is defined in the lavaan package.

#Examine low-level details like each group's individual parameter estimates and standard errors.
summary(GetDetails(ace))

#Extract low-level details. This may be useful when programming simulations.
inspect(GetDetails(ace), what="converged") #The lavaan package defines 'inspect'.
inspect(GetDetails(ace), what="coef")

```

---

CleanSemAceDataset	<i>Produces a cleaned dataset that works well with when using SEM to estimate a univariate ACE model.</i>
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## Description

This function takes a ‘GroupSummary’ data.frame (which is created by the RGroupSummary function) and returns a data.frame that is used by the Ace function.

## Usage

```
CleanSemAceDataset(dsDirty, dsGroupSummary, oName_S1,
  oName_S2, rName = "R")
```

## Arguments

dsDirty	This is the data.frame to be cleaned.
dsGroupSummary	The data.frame containing information about which groups should be included in the analyses. It should be created by the RGroupSummary function.
oName_S1	The name of the manifest variable (in dsDirty) for the first subject in each pair.
oName_S2	The name of the manifest variable (in dsDirty) for the second subject in each pair.
rName	The name of the variable (in dsDirty) indicating the pair’s relatedness coefficient.

## Details

The function takes dsDirty and produces a new data.frame with the following features:

[A] Only three existing columns are retained: O1, O2, and R. They are assigned these names.

[B] A new column called GroupID is created to reflect their group membership (which is based on the R value). These values are sequential integers, starting at 1. The group with the weakest R is 1. The group with the strongest R has the largest GroupID (this is typically the MZ twins).

[C] Any row is excluded if it has a missing data point for O1, O2, or R.

[D] The data.frame is sorted by the R value. This helps program against the multiple-group SEM API sometimes.

### Value

A data.frame with one row per subject pair. The data.frame contains the following variables (which can NOT be changed by the user through optional parameters):

R	The pair's R value.
O1	The outcome variable for the first subject in each pair.
O2	The outcome variable for the second subject in each pair.
GroupID	Indicates the pair's group membership.

### Author(s)

Will Beasley

### Examples

```
library(NlsyLinks) #Load the package into the current R session.
dsLinks <- Links79PairExpanded #Start with the built-in data.frame in NlsyLinks
dsLinks <- dsLinks[dsLinks$RelationshipPath=='Gen2Siblings', ] #Use only NLSY79-C siblings

oName_S1 <- "MathStandardized_S1" #Stands for Outcome1
oName_S2 <- "MathStandardized_S2" #Stands for Outcome2
dsGroupSummary <- RGroupSummary(dsLinks, oName_S1, oName_S2)

dsClean <- CleanSemAceDataset( dsDirty=dsLinks, dsGroupSummary, oName_S1, oName_S2, rName="R" )
summary(dsClean)

dsClean$AbsDifference <- abs(dsClean$O1 - dsClean$O2)
plot(jitter(dsClean$R), dsClean$AbsDifference, col="gray70")
```

---

ColumnUtilities	<i>A collection of functions that helps data management data.frames, particularly those derived from NLSY Extracts.</i>
-----------------	---

---

### Description

A collection of functions that helps data management data.frames, particularly those derived from NLSY Extracts.

### Usage

```
VerifyColumnExists( dataFrame, columnName )

RenameColumn( dataFrame, oldColumnName, newColumnName )

RenameNlsyColumn( dataFrame, nlsyRNumber, newColumnName )
```



**Arguments**

<code>dataFrame</code>	The <code>data.frame</code> whose columns are to be verified or renamed.
<code>columnName</code>	The name of the column to verify is present in the <code>data.frame</code> .
<code>nlsyRNumber</code>	The name of the column to change.
<code>oldColumnName</code>	The name of the column to change.
<code>newColumnName</code>	The desired name of the column.

**Details**

The RNumber assigned by the NLS has a pattern. In the Nlsy79 Gen1 dataset, the names start with a 'R' or 'T' and are followed by seven digits (eg, R0000100). In the Nlsy79 Gen2 dataset, the names start with 'C' or 'Y' and are followed by seven digits (eg, C0007030, Y1994600).

In the NLS Investigator, a decimal is present in the RNumber (eg, R00001.00). When the Investigator saves the dataset as a CSV, the decimal is removed (eg, R0000100).

**Value**

**\*IMPORTANT\*** The `RenameColumn` and `RenameNlsyColumn` functions do not use side-effects to rename the `data.frame`. Instead, it returns a new `data.frame`. In the example below, notice the assignment to `ds`: `ds <- RenameNlsyColumn(...)`.

The `VerifyColumnExists` function check that exactly one column exists with the specified `columnName`. If so, the index of the column is returned. If not, an exception is thrown.

**Author(s)**

Will Beasley

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CreateAceEstimate	Instantiate an <a href="#">AceEstimate-class</a> object.
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---

**Description**

Creates an instance of the S4 class, `AceEstimate` instantiating arguments set the parameter values estimated by the ACE model.

**Usage**

```
CreateAceEstimate(aSquared, cSquared, eSquared,
  caseCount, details=list(), unityTolerance = 1e-11)
```

**Arguments**

<code>aSquared</code>	The proportion of variability due to a shared genetic influence (typically represented as $a^2$ , or sometimes $h^2$ ).
<code>cSquared</code>	The proportion of variability due to shared common environmental influence.
<code>eSquared</code>	The proportion of variability due to unexplained/residual/error influence.
<code>caseCount</code>	The number of cases used to estimate the model.
<code>unityTolerance</code>	Specifies how close the the sum of the ACE components should be to one, to be considered properly scaled to one.
<code>details</code>	A list that contains the modeling output and details.

## Details

The contents of the details list depends on the underlying estimation routine. For example, when the ACE model is estimated with a DF analysis, the output is an `lm` object, because the `lm` function was used (ie, the basical general linear model). Alternatively, if the user specified the `lavaan` package should estimate that ACE model, the output is a `lavaan` object.

## Value

An S4 object of `AceEstimate-class`.

## Author(s)

Will Beasley

---

CreatePairLinks	<i>Creates a pairs linking file.</i>
-----------------	--------------------------------------

---

## Description

Creates a linking file for BG designs using this file structure (e.g., DF analysis, other ACE modeling). A DF analysis requires a double-entered file that contains the R value for the pair, and their two outcome variable values.

`CreatePairLinksDoubleEnteredWithNoOutcomes` is intended to be a primarily a helper function for `CreateSpatialNeighbours`.

## Usage

```
CreatePairLinksDoubleEntered(outcomeDataset,
  linksPairDataset, outcomeNames, linksNames =
  c("ExtendedID", "R", "RelationshipPath"),
  validateOutcomeDataset = TRUE, subject1Qualifier =
  "_S1", subject2Qualifier = "_S2")
```

```
CreatePairLinksSingleEntered(outcomeDataset,
  linksPairDataset, outcomeNames, linksNames =
  c("ExtendedID", "R", "RelationshipPath"),
  validateOutcomeDataset = TRUE, subject1Qualifier =
  "_S1", subject2Qualifier = "_S2")
```

```
CreatePairLinksDoubleEnteredWithNoOutcomes(linksPairDataset,
  linksNames = c("ExtendedID", "R", "RelationshipPath"))
```

## Arguments

`outcomeDataset` A data frame containing the outcome variable(s)

`linksPairDataset`

A data frame containing the SubjectTags of each subject in the pair and their R coefficient.

`outcomeNames` The column names of the outcome variable(s)

linksNames	The column names desired to be present in the newly created data frame. SubjectTag_S1 and SubjectTag_S2 are included automatically.
validateOutcomeDataset	Indicates if characteristics of the outcomeDataset should be validated.
subject1Qualifier	Indicates how the outcome variable for the pair's first subject is distinguished from the other subject. The default is _S1.
subject2Qualifier	Indicates how the outcome variable for the pair's second subject is distinguished from the other subject. The default is _S2.

**Author(s)**

Will Beasley

**References**

For more information about a DF analysis, see Rodgers, Joseph Lee, & Kohler, Hans-Peter (2005). *Reformulating and simplifying the DF analysis model*. *Behavior Genetics*, 35 (2), 211-217.

**Examples**

```
dsSingleLinks <- data.frame(
  ExtendedID=c(1, 1, 1, 2),
  SubjectTag_S1=c(101, 101, 102, 201),
  SubjectTag_S2=c(102, 103, 103, 202),
  R=c(.5, .25, .25, .5),
  RelationshipPath=rep("Gen2Siblings", 4)
)
dsSingleOutcomes <- data.frame(
  SubjectTag=c(101, 102, 103, 201, 202),
  DV1=c(11, 12, 13, 41, 42),
  DV2=c(21, 22, 23, 51, 52))
dsDouble <- CreatePairLinksDoubleEntered(
  outcomeDataset=dsSingleOutcomes,
  linksPairDataset=dsSingleLinks,
  outcomeNames=c("DV1", "DV2"),
  validateOutcomeDataset=TRUE)
dsDouble #Show the 8 rows in the double-entered pair links
summary(dsDouble) #Summarize the variables

ValidatePairLinksAreSymmetric(dsDouble) #Should return TRUE.
```

---

**CreateSpatialNeighbours**

*Distances between related family members, formatted for spatial analysis.*

---

**Description**

This helper function formats the LinksPair datasets so it can be used in some types of spatial analyses. The **spdep** (Spatial Dependence) uses a sparse matrix (actually a [data.frame](#)) to represent neighbours.

**Usage**

```
CreateSpatialNeighbours(linksPairsDoubleEntered)
```

**Arguments**

`linksPairsDoubleEntered`

A `data.frame` containing the links, preferably created by a function like [CreatePairLinksDoubleEntered](#).

**Details**

There is one row per unique pair of subjects, *respecting order*. This has twice as many rows as [Links79Pair](#) and [Links79PairExpanded](#) (which have one row per unique pair of subjects, *irrespective of order*).

`CreateSpatialNeighbours` accepts any paired relationships in a `data.frame`, as long as it contains the columns `SubjectTag_S1`, `SubjectTag_S2`, and `R`. See [Links79Pair](#) for more details about these columns.

**Value**

An S3 `spatial.neighbours` object to work with functions in the **spdep** package.

`SubjectTag_S1` is renamed 'from'.

`SubjectTag_S2` is renamed 'to'.

`R` is renamed 'weight'.

The attribute `region.id` specifies each unique `SubjectTag`.

The attribute `n` specifies the number of unique subjects.

**Note**

Notice the British variant of 'neighbours' is used, to be consistent with the `spatial.neighbour` class in the **spdep** package.

**Author(s)**

Will Beasley and David Bard

**References**

Bard, D.E., Beasley, W.H., Meredith, K., & Rodgers, J.L. (2012). *Biometric Analysis of Complex NLSY Pedigrees: Introducing a Conditional Autoregressive Biometric (CARB) Mixed Model*. Behavior Genetics Association 42nd Annual Meeting. [[Slides](#)]

Bivand, R., Pebesma, E., & Gomez-Rubio, V. (2013). *Applied Spatial Data Analysis with R*. New York: Springer. (Especially Chapter 9.)

Banerjee, S., Carlin, B.P., & Gelfand, A.E. (2004). *Hierarchical Modeling and Analysis for Spatial Data*. Boca Raton: CRC Press.

Lawson, A.B (2013). *Bayesian Disease Mapping: Hierarchical Modeling in Spatial Epidemiology, Second Edition*. Boca Raton: CRC Press.

The **spdep** package documentation: [spdep: Spatial dependence: weighting schemes, statistics and models](#).

## Examples

```
dsLinksAll <- Links79Pair
dsLinksGen1Housemates <- dsLinksAll[dsLinksAll$RelationshipPath=="Gen1Housemates", ]
dsLinksGen2Siblings <- dsLinksAll[dsLinksAll$RelationshipPath=="Gen2Siblings", ]

spGen1 <- CreateSpatialNeighbours(dsLinksGen1Housemates)
spGen2 <- CreateSpatialNeighbours(dsLinksGen2Siblings)

head(spGen2)
#Returns:
#   from to weight
#3   201 202  0.50
#6   301 302  0.50
#7   301 303  0.50
#9   302 303  0.50
#24  401 403  0.25
#28  801 802  0.50

table(spGen2$weight)
#Returns:
#0.25 0.375  0.5  0.75    1
#3442  610 6997   12   27
```

---

CreateSubjectTag	<i>Creates a SubjectTag. This value uniquely identifies subjects, when both generations are included in the same dataset.</i>
------------------	---

---

## Description

A SubjectTag uniquely identify subjects. For Gen2 subjects, the SubjectTag is identical to their CID (ie, C00001.00 -the SubjectID assigned in the NLSY79-Children files). However for Gen1 subjects, the SubjectTag is their CaseID (ie, R00001.00), with "00" appended. This manipulation is necessary to identify subjects uniquely in inter-generational datasets. A Gen1 subject with an ID of 43 becomes 4300. The SubjectTags of her four children remain 4301, 4302, 4303, and 4304.

## Usage

```
CreateSubjectTag(subjectID, generation)
```

## Arguments

subjectID	The ID assigned by the NLSY. For Gen1 subjects, this will be their CaseID (ie, R00001.00). For Gen2 subjects, this will be their CID (ie, C00001.00).
generation	The generation of the subject. Values are either 1 or 2, representing Gen1 and Gen2.

## Details

For a fuller explanation of SubjectTag in context, see the [Links79Pair](#) dataset documentation.

**Value**

A integer value under normal circumstances. An error is thrown if the vectors `subjectID` and `generation` are different lengths. If either input vector has NA values, the respective output element(s) will be NA too.

**Author(s)**

Will Beasley

**See Also**

[Links79Pair](#)

**Examples**

```
library(NlsyLinks) #Load the package into the current R session.

#Typically these two vectors will come from a data frame.
subjectIDs <- c(71:82, 10001:10012)
generation <- c(rep(1, 12), rep(2, 12))

CreateSubjectTag(subjectIDs, generation)
#Returns 7100, ..., 8200, 10001, ..., 10012

#Use the ExtraOutcomes79 dataset, with numeric variables 'SubjectID' and 'Generation'.
ExtraOutcomes79$SubjectTag <- CreateSubjectTag(
  subjectID=ExtraOutcomes79$SubjectID,
  generation=ExtraOutcomes79$Generation
)
```

---

ExtraOutcomes79

*Extra outcome variables in the NLSY79*

---

**Description**

This dataset is provided primarily to facilitate documentation examples.

**Format**

A data frame with 11,495 observations on the following 6 variables. There is one row per subject.

**SubjectTag** The ID value assigned by NLS to the first subject. For Gen1 Subjects, this is their "CaseID" (ie, R00001.00). For Gen2 subjects, this is their "CID" (ie, C00001.00).

**SubjectID** The ID value assigned by NLS to the first subject. For Gen1 Subjects, this is their "CaseID" (ie, R00001.00). For Gen2 subjects, this is their "CID" (ie, C00001.00).

**Generation** The generation of the subject. Values are either 1 or 2, representing Gen1 and Gen2. Note that this variable is not a factor (in contrast with data frames like [Links79Pair](#)). This dataset is supposed to mimic the dataset provided by the researcher, which typically will not have been converted to a factor.

**HeightZGenderAge** The subject's height, standardized by gender and age (see Details).

**WeightZGenderAge** The subject's weight, standardized by gender and age (see Details).

**AfqtRescaled2006Gaussified** Armed Forces Qualification Test Score (Gen1 only; see Details).

**Afi** Self-reported age of first intercourse (Gen1 only; see Details).

**Afm** Self-reported age of first menstration (Gen1 only; see Details).

**MathStandardized** Standardized PIAT Math scores (Gen2 only; see Details).

## Details

The SubjectTag variable uniquely identify subjects. For Gen2 subjects, the SubjectTag is identical to their CID (ie, C00001.00 -the SubjectID assigned in the NLSY79-Children files). However for Gen1 subjects, the SubjectTag is their CaseID (ie, R00001.00), with "00" appended. This manipulation is necessary to identify subjects uniquely in inter-generational datasets. A Gen1 subject with an ID of 43 has a SubjectTag of 4300. The SubjectTags of her four children remain 4301, 4302, 4303, and 4304.

For Gen2, an NLSY79 variable of MathStandardized is C0580100.00.

Afi and Afm, values were simplified (to one value per subject) by Kelly Meredith in Sept 2010.

The variables for height and weight were manipulated in R files available in a [repository](#) available to the public. Find the appropriate subfolder, and view the HTML report for more details.

## Author(s)

Will Beasley

## Source

Gen1 information comes from the Summer 2013 release of the [NLSY79 sample](#). Gen2 information comes from the Summer 2013 release of the [NLSY79 Children and Young Adults sample](#). Data were extracted with the NLS Investigator (<https://www.nlsinfo.org/investigator/>).

## Examples

```
library(NlsyLinks) #Load the package into the current R session.
gen2Outcomes <- subset(ExtraOutcomes79, Generation==2) #Create a dataset of only Gen2 subjects.

#plot(ExtraOutcomes79) #Uncomment to see a large scatterplot matrix.
summary(ExtraOutcomes79)

oldPar <- par(mfrow=c(3,2))
hist(ExtraOutcomes79$Generation)
hist(ExtraOutcomes79$MathStandardized)
hist(ExtraOutcomes79$HeightZGenderAge)
hist(ExtraOutcomes79$WeightZGenderAge)
hist(ExtraOutcomes79$Afi)
hist(ExtraOutcomes79$Afm)
par(oldPar)
```

---

GetDetails-methods	<i>A generic function for extracting the Details slot of an object.</i>
--------------------	---

---

### Description

A generic function for extracting the Details slot of an AceEstimation object.

### Author(s)

Will Beasley

---

Links79Pair	<i>Kinship linking file for pairs of relatives in the NLSY79 and NLSY79 Children and Young Adults</i>
-------------	---

---

### Description

This dataset specifies the relatedness coefficient (ie, 'R') between subjects in the same extended family. Each row represents a unique relationship pair.

NOTE: Two variable names changed in November 2013. Subject1Tag and Subject2Tag became SubjectTag\_S1 and SubjectTag\_S2.

### Format

A data frame with 42,773 observations on the following 5 variables. There is one row per unique pair of subjects, irrespective of order.

**ExtendedID** Identity of the extended family of the pair; it corresponds to the HHID in the NLSY79. See References below.

**SubjectTag\_S1** Identity of the pair's first subject. See Details below.

**SubjectTag\_S2** Identity of the pair's second subject. See Details below.

**R** The pair's Relatedness coefficient. See Details below.

**RelationshipPath** Specifies the relationship category of the pair. This variable is a factor, with levels Gen1Housemates=1, Gen2Siblings=2, Gen2Cousins=3, ParentChild=4, AuntNiece=5.

### Details

The dataset contains Gen1 and Gen2 subjects. "Gen1" refers to subjects in the original NLSY79 sample (<http://www.bls.gov/nls/nlsy79.htm>). "Gen2" subjects are the biological children of the Gen1 females -ie, those in the NLSY79 Children and Young Adults sample (<http://www.bls.gov/nls/nlsy79ch.htm>).

Subjects will be in the same extended family if either: [1] they are Gen1 housemates, [2] they are Gen2 siblings, [3] they are Gen2 cousins (ie, they have mothers who are Gen1 sisters in the NLSY79, [4] they are mother and child (in Gen1 and Gen2, respectively), or [5] they are aunt/niece and nephew (in Gen1 and Gen2, respectively).

The variables SubjectTag\_S1 and SubjectTag\_S2 uniquely identify subjects. For Gen2 subjects, the SubjectTag is identical to their CID (ie, C00001.00 -the SubjectID assigned in the NLSY79-Children files). However for Gen1 subjects, the SubjectTag is their CaseID (ie, R00001.00), with



"00" appended. This manipulation is necessary to identify subjects uniquely in inter-generational datasets. A Gen1 subject with an ID of 43 has a SubjectTag of 4300. The SubjectTags of her four children remain 4301, 4302, 4303, and 4304.

Level 5 of RelationshipPath (ie, AuntNiece) is gender neutral. The relationship could be either Aunt-Niece, Aunt-Nephew, Uncle-Niece, or Uncle-Nephew. If there's a widely-accepted gender-neutral term, please tell me.

An extended family with  $k$  subjects will have  $k(k-1)/2$  rows. Typically, Subject1 is older while Subject2 is younger.

MZ twins have  $R=1$ . DZ twins and full-siblings have  $R=.5$ . Half-siblings have  $R=.25$ . Typical first cousins have  $R=.125$ . Unrelated subjects have  $R=0$  (this occasionally happens for Gen1Housemates). Other  $R$  coefficients are possible.

There are several other uncommon possibilities, such as half-cousins ( $R=.0625$ ) and ambiguous aunt-nieces ( $R=.125$ ). The variable coding for genetic relatedness,  $R$ , in Links79Pair contains only the common values of  $R$  whose groups are likely to have stable estimates. However the variable RFull in Links79PairExpanded contains all  $R$  values. We strongly recommend using  $R$  in this data.frame. Move to RFull (or some combination) only if you have a good reason, and are willing to carefully monitor a variety of validity checks. Some of these excluded groups are too small to be estimated reliably.

Furthermore, some of these groups have members who are more strongly genetically related than their items would indicate. For instance, there are 41 Gen1 pairs who explicitly claim they are not biologically related (ie, RExplicit=0), yet their correlation for Adult Height is  $r=0.24$ . This is much higher than would be expected for two people sampled randomly; it is nearly identical to the  $r=0.26$  we observed among the 268 Gen1 half-sibling pairs who claim they share exactly 1 biological parent.

### Author(s)

Will Beasley

### Source

Gen1 information comes from the Summer 2013 release of the **NLSY79 sample**. Gen2 information comes from the Summer 2013 release of the **NLSY79 Children and Young Adults sample**. Data were extracted with the NLS Investigator (<https://www.nlsinfo.org/investigator/>).

The internal version for the links is Links2011V84.

### References

The NLSY79 variable HHID (ie, R00001.49) is the source for the ExtendedID variable. This is discussed at <http://www.nlsinfo.org/nlsy79/docs/79html/79text/hhcomp.htm>.

For more information on  $R$  (ie, the Relatedness coefficient), please see Rodgers, Joseph Lee, & Kohler, Hans-Peter (2005). **Reformulating and simplifying the DF analysis model**. *Behavior Genetics*, 35 (2), 211-217.

### See Also

The LinksPair79 dataset contains columns necessary for a basic BG analysis. The **Links79PairExpanded** dataset contains further information that might be useful in more complicated BG analyses.

A tutorial that produces a similar dataset is [http://www.nlsinfo.org/childya/nlsdocs/tutorials/linking\\_mothers\\_and\\_children/linking\\_mothers\\_and\\_children\\_tutorial.html](http://www.nlsinfo.org/childya/nlsdocs/tutorials/linking_mothers_and_children/linking_mothers_and_children_tutorial.html). It provides examples in SAS, SPSS, and STATA.

The current dataset (ie, Links79Pair) can be saved as a CSV file (comma-separated file) and imported into in other programs and languages. In the R console, type the following two lines of code:

```
library(NlsyLinks)
```

```
write.csv(Links79Pair, "C:/BGDirectory/Links79Pair.csv")
```

where "C:/BGDirectory/" is replaced by your preferred directory. Remember to use forward slashes instead of backslashes; for instance, the path "C:\BGDirectory\Links79Pair.csv" can be misinterpreted.

## Examples

```
library(NlsyLinks) #Load the package into the current R session.
summary(Links79Pair) #Summarize the five variables.
hist(Links79Pair$R) #Display a histogram of the Relatedness coefficients.
table(Links79Pair$R) #Create a table of the Relatedness coefficients for the whole sample.
```

```
#Create a dataset of only Gen2 sibs, and display the distribution of R.
gen2Siblings <- subset(Links79Pair, RelationshipPath=='Gen2Siblings')
table(gen2Siblings$R) #Create a table of the Relatedness coefficients for the Gen2 sibs.
```

---

Links79PairExpanded	<i>Kinship linking file for pairs of relatives. It builds upon the <a href="#">Links79Pair</a> dataset.</i>
---------------------	---

---

## Description

Please first read the documentation for [Links79Pair](#). That dataset contains the same pairs/rows, but only a subset of the variables/columns.

NOTE: In Nov 2013, the variable naming scheme changed in order to be more consistent across variables. For variables that are measured separately for both subjects (eg, Gender), the subjects' variable name will have an \_S1 or \_S2 appended to it. For instance, the variables LastSurvey\_S1 and LastSurvey\_S2 correspond to the last surveys completed by the pair's first and second subject, respectively. Similarly, the functions CreatePairLinksDoubleEntered and CreatePairLinksSingleEntered now by default append \_S1 and \_S2, instead of \_1 and \_2. However this can be modified using the 'subject1Qualifier' and 'subject2Qualifier' parameters.

## Format

A data frame with 11,075 observations on the following 22 variables. There is one row per unique pair of subjects, irrespective of order.

**ExtendedID** see the variable of the same name in [Links79Pair](#)

**SubjectTag\_S1** see the variable of the same name in [Links79Pair](#)

**SubjectTag\_S2** see the variable of the same name in [Links79Pair](#)

**R** see the variable of the same name in [Links79Pair](#)

**RFull** This is a superset of R. This includes all the R values we estimated, while R (i.e., the variable above) excludes values like  $R=0$  for Gen1Housemates, and the associated relationships based on this R value (i.e., Gen2Cousins and AuntNieces).

**RelationshipPath** see the variable of the same name in [Links79Pair](#)

- EverSharedHouse** Indicate if the pair likely live in the same house. This is TRUE for Gen1Housemates, Gen2Siblings, and ParentChild. This is FALSE for AuntNiece and Gen2Cousins
- IsMz** Indicates if the pair is from the same zygote (ie, they are identical twins/triplets). This variable is a factor, with levels No=0, Yes=1, DoNotKnow=255.
- LastSurvey\_S1** The year of Subject1's most recently completed survey. This may be different than the survey's administration date.
- LastSurvey\_S2** The year of Subject2's most recently completed survey. This may be different than the survey's administration date.
- RImplicitPass1** The pair's  $R$  coefficient, using only implicit information. Interpolation was NOT used.
- RImplicit** The pair's  $R$  coefficient, using only implicit information. Interpolation was used.
- RImplicit2004** The pair's  $R$  coefficient released in our previous projects (\*\*need reference\*\*). This variable is provided primarily for previous users wishing to replicate previous analyses.
- RExplicitPass1** The pair's  $R$  coefficient, using only explicit information. Interpolation was NOT used.
- RExplicit** The pair's  $R$  coefficient, using only explicit information. Interpolation was used.
- RExplicitOlderSibVersion** The pair's  $R$  coefficient, according to the explicit item responses of the older sibling.
- RExplicitYoungerSibVersion** The pair's  $R$  coefficient, according to the explicit item responses of the younger sibling.
- RPass1** The pair's estimated  $R$  coefficient, using both implicit and explicit information. Interpolation was NOT used. The variable  $R$  is identically constructed, but it did use interpolation.
- Generation\_S1** The generation of the first subject. Values for Gen1 and Gen2 are 1 and 2, respectively.
- Generation\_S2** The generation of the second subject. Values for Gen1 and Gen2 are 1 and 2, respectively.
- SubjectID\_S1** The ID value assigned by NLS to the first subject. For Gen1 Subjects, this is their "CaseID" (ie, R00001.00). For Gen2 subjects, this is their "CID" (ie, C00001.00).
- SubjectID\_S2** The ID value assigned by NLS to the second subject.
- MathStandardized\_S1** The PIAT-Math score for Subject1. See [ExtraOutcomes79](#) for more information about its source.
- MathStandardized\_S2** The PIAT-Math score for Subject2.
- HeightZGenderAge\_S1** The early adult height for Subject1. See [ExtraOutcomes79](#) for more information about its source.
- HeightZGenderAge\_S2** The early adult height for Subject2.

## Details

Specifies the relatedness coefficient (ie, ' $R$ ') between subjects in the same extended family. Each row represents a unique relationship pair. An extended family with  $k$  subjects will have  $k(k-1)/2$  rows. Typically, Subject1 is older while Subject2 is younger.

RelationshipPath variable. Code written using this dataset should NOT assume it contains only Gen2 sibling pairs. See an example of filtering the relationship category in the [Links79Pair](#) documentation.

Please first read the documentation for [Links79Pair](#). That dataset contains the same pairs/rows, but only a subset of the variables/columns.

The specific steps to determine the  $R$  coefficient will be described in an upcoming publication. The following information may influence the decisions of an applied researcher.

A distinction is made between ‘Explicit’ and ‘Implicit’ information. Explicit information comes from survey items that directly address the subject’s relationships. For instance in 2006, surveys asked if the sibling pair share the same biological father (eg, Y19940.00 and T00020.00). Implicit information comes from items where the subject typically isn’t aware that their responses may be used to determine genetic relatedness. For instance, if two siblings have biological fathers with the same month of death (eg, R37722.00 and R37723.00), it may be reasonable to assume they share the same biological father.

‘Interpolation’ is our lingo when other siblings are used to leverage insight into the current pair. For example, assume Subject 101, 102, and 103 have the same mother. Further assume 101 and 102 report they share a biological father, and that 101 and 103 share one too. Finally, assume that we don’t have information about the relationship between 102 and 103. If we are comfortable with our level of uncertainty of these determinations, then we can interpolate/infer that 102 and 103 are full-siblings as well.

The math and height scores are duplicated from [ExtraOutcomes79](#), but are included here to make some examples more concise and accessible.

### Author(s)

Will Beasley

### Source

See [Links79Pair](#).

### Examples

```
library(NlsyLinks) #Load the package into the current R session.
olderR <- Links79PairExpanded$RExplicitOlderSibVersion #Declare a concise variable name.
youngerR <- Links79PairExpanded$RExplicitYoungerSibVersion #Declare a concise variable name.

plot(jitter(olderR), jitter(youngerR)) #Scatterplot the siblings' responses.
table(youngerR, olderR) #Table of the relationship between the siblings' responses.
ftable(youngerR, olderR, dnn=c("Younger's Version", "Older's Version")) #A formatted table.

#write.csv(Links79PairExpanded, file='~/NlsyLinksStaging/Links79PairExpanded.csv',
# row.names=FALSE)
```

---

ReadCsvNlsy79

*Read a CSV file downloaded from the NLS Investigator*

---

### Description

The function accepts a (file path to) CSV file and creates a data.frame. The data.frame is modified and augmented with columns to assist later routines.

### Usage

```
ReadCsvNlsy79Gen1(filePath, dsExtract=read.csv(filePath))
```

```
ReadCsvNlsy79Gen2(filePath, dsExtract=read.csv(filePath))
```

**Arguments**

<code>filePath</code>	A path to the CSV file. Remember to use double back-slashes in Windows, or forward-slashes in Windows or Linux.
<code>dsExtract</code>	A 'data.frame' (containing the extract) can be passed instead of the file path if the data has already been read into R's memory.

**Details**

The function does seven things.

1. Reads the CSV into a `data.frame`.
2. Checks that the NLSY variables `C00001.00` and `C00002.00` exist in the `data.frame`.
3. The NLSY variable `C00001.00` is renamed `SubjectID`.
4. A variable named `Generation` is given a value of 2 for all subjects.
5. The `SubjectTag` variable is created.
6. The NLSY variable `C00002.00` is multiplied by 100 and renamed `SubjectTagOfMother`.
7. The NLSY variable `R00001.49` (ie, their Mother's HHID is attached to each Gen2 record).

**Value**

A `data.frame` to facilitate biometric analysis.

**Author(s)**

Will Beasley

**Examples**

```
## Not run:
filePathGen2 <- "~/Nlsy/Datasets/Gen2Birth.csv"
ds <- ReadCsvNlsy79Gen2(filePath=filePathGen2)

## End(Not run)
```

---

<code>RGroupSummary</code>	<i>Calculates summary statistics for each Relatedness Group in the sample.</i>
----------------------------	--

---

**Description**

Before and after running ACE Models, it is important to examine the characteristics of the different groups. When the ACE is estimated with an SEM using multiple groups, it is even even more important. Groups may contain too few subjects to have a well-behaved covariance matrix.

If a group's covariance matrix is not Positive Definite (or it's misbehaving in some other way), it's typically recommended to exclude that group from the SEM.

**Usage**

```
RGroupSummary(ds, oName_S1, oName_S2, rName,
  determinantThreshold=1e-5)
```

**Arguments**

<code>ds</code>	The <code>data.frame</code> containing the following variables:
<code>oName_S1</code>	The name of the outcome variable corresponding to the first subject in the pair.
<code>oName_S2</code>	The name of the outcome variable corresponding to the first subject in the pair.
<code>rName</code>	The name of the variable specifying the pair's Relatedness coefficient.
<code>determinantThreshold</code>	The minimum value the covariance matrix's determinant (for the group) should exceed to be considered Positive Definite.

**Details**

This function isn't specific to an ACE model and groups defined by R. It could be applied to any multiple-group SEM with two manifest/outcome variables. In the future, we may generalize it beyond two manifest variables.

To get summary stats for the entire sample, create a dummy indicator variable that assigns everyone to the same group. See the second example below.

The default `determinantThreshold` value is nonzero, in order to forgive slight numerical inaccuracies caused by fixed-precision arithmetic.

**Value**

A `data.frame` with one row per group. The `data.frame` contains the following variables:

<code>R</code>	The group's R value. Note the name of this variable can be changed by the user, by specifying a non-default value to the <code>rName</code> argument.
<code>Included</code>	Indicates if the group should be included in a multiple-group SEM.
<code>PairCount</code>	The number of pairs in the group with <i>complete</i> data for R and the two outcome/manifest variables.
<code>O1Mean</code>	The mean (of the outcome variable) among the group's first members, excluding the missing values.
<code>O2Mean</code>	The mean (of the outcome variable) among the group's second members, excluding the missing values.
<code>O1Variance</code>	The variance (of the outcome variable) among the group's first members.
<code>O2Variance</code>	The variance (of the outcome variable) among the group's second members.
<code>O1O2Covariance</code>	The covariance (of the outcome variable) across the group's first and second members.
<code>Correlation</code>	The correlation (of the outcome variable) across the group's first and second members.
<code>Determinant</code>	The determinant of the group's covariance matrix.
<code>PosDefinite</code>	Indicates if the group's covariance matrix is positive definite.

**Author(s)**

Will Beasley and David Bard

**References**

Please see [Neale & Maes](#) for more information about SEM with multiple groups.

## Examples

```
library(NlsyLinks) #Load the package into the current R session.
dsLinks <- Links79PairExpanded #Load the dataset from the NlsyLinks package.
dsLinks <- dsLinks[dsLinks$RelationshipPath=='Gen2Siblings', ]
oName_S1 <- "MathStandardized_S1" #Stands for Outcome1
oName_S2 <- "MathStandardized_S2" #Stands for Outcome2
dsGroupSummary <- RGroupSummary(dsLinks, oName_S1, oName_S2)
dsGroupSummary

#Should return:
#      R Included PairCount   O1Mean   O2Mean O1Variance O2Variance O1O2Covariance Correlation
#1 0.250    TRUE      2718  94.6439  95.5990   169.650   207.842      41.0783    0.218761
#2 0.375    TRUE      139  92.6043  93.1655   172.531   187.081      40.4790    0.225311
#3 0.500    TRUE     5511  99.8940 100.1789   230.504   232.971     107.3707    0.463336
#4 0.750   FALSE       2 108.5000 106.0000   220.500    18.000      63.0000    1.000000
#5 1.000    TRUE       22  98.6364  95.5455   319.195   343.117     277.5887    0.838789
# Determinant PosDefinite
#1      33573.0      TRUE
#2      30638.7      TRUE
#3      42172.2      TRUE
#4         0.0     FALSE
#5      32465.6      TRUE

#To get summary stats for the whole sample, create one large inclusive group.
dsLinks$Dummy <- 1
(dsSampleSummary <- RGroupSummary(dsLinks, oName_S1, oName_S2, rName="Dummy"))

#Should return:
# Dummy Included PairCount   O1Mean   O2Mean O1Variance O2Variance O1O2Covariance
#1      1      TRUE      8392  98.07162  98.56864   216.466   229.2988      90.90266
# Correlation Determinant PosDefinite
#1  0.4080195   41372.1      TRUE
###
### ReadCsvNlsy79
###
## Not run:
filePathGen2 <- "~/Nlsy/Datasets/Gen2Birth.csv"
ds <- ReadCsvNlsy79Gen2(filePath=filePathGen2)

## End(Not run)
```

---

SubjectDetails79

*Dataset containing further details of the Gen1 and Gen2 subjects.*


---

## Description

These variables are useful to many types of analyses (not just behavior genetics), and are provided to save users time.

## Format

A data frame with 24,181 observations on the following 12 variables.

**SubjectTag** see the variable of the same name in [Links79Pair](#)

**ExtendedID** see the variable of the same name in [Links79Pair](#)

**Generation** Indicates if the subject is in generation 1 or 2.

**Gender** Indicates if the subject is Male or Female.

**RaceCohort** Indicates if the race cohort is Hispanic, Black or Nbnh (*ie*, Non-black, non-hispanic). This comes from the Gen1 variable R02147.00 and Gen2 variable C00053.00.

**SiblingCountInNls** The number of the subject's siblings, including himself/herself (a singleton has a value of one). This considers only the siblings in the NLSY. For Gen1, this can exclude anyone outside the age range. For Gen2, this excludes anyone who doesn't share the same mother.

**BirthOrderInNls** Indicates the subject's birth order among the NLSY siblings.

**SimilarAgeCount** The number of children who were born within roughly 30 days of the subject's birthday, including the subject (for instance, even an only child will have a value of 1). For Gen2 subjects, this should reflect how many children the Gen1 mother gave birth to at the same time (1: singleton; 2: twins; 3: triplets). For Gen1 subjects, this is less certain, because the individual might have been living with a similarly-aged housemate, born to a different mother.

**HasMzPossibly** Indicates if the subject *might* be a member of an MZ twin/triplet. This will be true if there is a sibling with a DOB within a month, and they are the same gender.

**IsMz** Indicates if the subject has been identified as a member of an MZ twin/triplet.

**KidCountBio** The number of biological children known to the NLSY (but not necessarily interviewed by the NLSY).

**KidCountInNls** The number of children who belong to the NLSY. This is nonnull for only Gen1 subjects.

**Mob** The subject's month of birth. The exact day is not available to the public. By default, we set their birthday to the 15th day of the month.

**LastSurveyYearCompleted** The year of the most recently completed survey.

**AgeAtLastSurvey** The subject's age at the most recently completed survey.

**IsDead** ##This variable is not available yet## Indicates if the subject was alive for the last attempted survey.

**DeathDate** ##This variable is not available yet## The subject's month of death. The exact day is not available to the public. By default, we set their birthday to the 15th day of the month.

## Author(s)

Will Beasley

## Source

Gen1 information comes from the Summer 2013 release of the [NLSY79 sample](#). Gen2 information comes from the Summer 2013 release of the [NLSY79 Children and Young Adults sample](#). Data were extracted with the NLS Investigator (<https://www.nlsinfo.org/investigator/>).

## Examples

```
library(NlsyLinks) #Load the package into the current R session.

summary(SubjectDetails79)

oldPar <- par(mfrow=c(3,2), mar=c(2,2,1,.5), tcl=0, mgp=c(1,0,0))
```



```

hist(SubjectDetails79$SiblingCountInNls, main="",
     breaks=seq(from=0, to=max(SubjectDetails79$SiblingCountInNls, na.rm=TRUE), by=1)
)
hist(SubjectDetails79$BirthOrderInNls, main="",
     breaks=seq(from=0, to=max(SubjectDetails79$BirthOrderInNls, na.rm=TRUE), by=1)
)
hist(SubjectDetails79$SimilarAgeCount, main="",
     breaks=seq(from=0, to=max(SubjectDetails79$SimilarAgeCount, na.rm=TRUE), by=1)
)
hist(SubjectDetails79$KidCountBio, main="",
     breaks=seq(from=0, to=max(SubjectDetails79$KidCountBio, na.rm=TRUE), by=1)
)
hist(SubjectDetails79$KidCountInNls, main="",
     breaks=seq(from=0, to=max(SubjectDetails79$KidCountInNls, na.rm=TRUE), by=1)
)
#hist(SubjectDetails79$Mob, main="",
#     breaks=seq.Date(
#         from=min(SubjectDetails79$Mob, na.rm=TRUE),
#         to=max(SubjectDetails79$Mob, na.rm=TRUE),
#         by="year")
#)
par(oldPar)

```

---

ValidateOutcomeDataset

*Validates the schema of datasets containing outcome variables.*


---

## Description

The **NlsyLinks** handles a lot of the plumbing code needed to transform extracted NLSY datasets into a format that statistical routines can interpret. In some cases, a dataset of measured variables is needed, with one row per subject. This function validates the measured/outcome dataset, to ensure it posses an interpretable schema. For a specific list of the requirements, see Details below.

## Usage

```
ValidateOutcomeDataset(dsOutcome, outcomeNames)
```

## Arguments

dsOutcome	A data.frame with the measured variables
outcomeNames	The column names of the measure variables that eventually will be used by a statistical procedure.

## Details

The dsOutcome parameter must:

1. Have a non-missing value.
2. Contain at least one row.
3. Contain a column called 'SubjectTag' (case sensitive).
4. Have the SubjectTag column containing only positive numbers.

5. Have the SubjectTag column where all values are unique (ie, two rows/subjects cannot have the same value).

The outcomeNames parameter must:

1. Have a non-missing value
2. Contain only column names that are present in the dsOutcome data frame.

### Value

Returns TRUE if the validation passes. Returns an error (and associated descriptive message) if it false.

### Author(s)

Will Beasley

### Examples

```
library(NlsyLinks) #Load the package into the current R session.
ds <- ExtraOutcomes79
outcomeNames <- c("MathStandardized", "WeightZGenderAge")
ValidateOutcomeDataset(dsOutcome=ds, outcomeNames=outcomeNames) #Returns TRUE.
outcomeNamesBad <- c("MathMisspelled", "WeightZGenderAge")
#ValidateOutcomeDataset(dsOutcome=ds, outcomeNames=outcomeNamesBad) #Throws error.
```

---

ValidatePairLinks	<i>Validates the schema of a links for pairs of relatives</i>
-------------------	---

---

### Description

A helper function that verifies the linking dataset contains (A) the essential columns exist, and (B) at least one row. It is called by CreatePairLinks.

Typical use of **NlsyLinks** will not require this function, since a valid paired links are supplied for each supported sample (ie, [Links79Pair](#)).

The **NlsyLinks** uses several types of linking schemas. This function validates the type where each relative subject has their own row.

The following four columns must be present: (1) Subect1Tag, (2) Subect2Tag, (3) R, and (4) MultipleBirth. They must have a numeric mode/datatype.

### Usage

```
ValidatePairLinks(linksPair)
```

### Arguments

linksPair      The data.frame to validate.

### Value

Returns TRUE if the validation passes. Returns an error (and associated descriptive message) if it false.

**Author(s)**

Will Beasley

**See Also**[Links79Pair](#), [Links79PairExpanded](#),**Examples**

```

dsSingleLinks <- data.frame(
  ExtendedID=c(1, 1, 1, 2),
  SubjectTag_S1=c(101, 101, 102, 201),
  SubjectTag_S2=c(102, 103, 103, 202),
  R=c(.5, .25, .25, .5),
  RelationshipPath=rep("Gen2Siblings", 4)
)
dsSingleOutcomes <- data.frame(
  SubjectTag=c(101, 102, 103, 201, 202),
  DV1=c(11, 12, 13, 41, 42),
  DV2=c(21, 22, 23, 51, 52))
dsDouble <- CreatePairLinksDoubleEntered(
  outcomeDataset=dsSingleOutcomes,
  linksPairDataset=dsSingleLinks,
  outcomeNames=c("DV1", "DV2"),
  validateOutcomeDataset=TRUE)
dsDouble #Show the 8 rows in the double-entered pair links
summary(dsDouble) #Summarize the variables

ValidatePairLinksAreSymmetric(dsDouble) #Should return TRUE.

```

---

ValidatePairLinksAreSymmetric

*Verifies that the pair relationships are symmetric.*


---

**Description**

For certain analyses, the pairs links (which can be considered a type of sparse matrix) need to be symmetric. For instance, if there is a row for Subjects 201 and 202 with R=0.5, there should be a second row for Subjects 202 and 201 with R=0.5.

This validation function is useful to some types of DF methods and some spatially-inspired methods.

**Usage**

```
ValidatePairLinksAreSymmetric(linksPair)
```

**Arguments**

`linksPair`      The [data.frame](#) object that should be symmetric

**Value**

Returns TRUE if symmetric. Throw an error with [stop](#) if asymmetric.

**Author(s)**

Will Beasley

**See Also**

[CreatePairLinksDoubleEntered](#)

**Examples**

```
dsSingleLinks <- data.frame(  
  ExtendedID=c(1, 1, 1, 2),  
  SubjectTag_S1=c(101, 101, 102, 201),  
  SubjectTag_S2=c(102, 103, 103, 202),  
  R=c(.5, .25, .25, .5),  
  RelationshipPath=rep("Gen2Siblings", 4)  
)  
dsSingleOutcomes <- data.frame(  
  SubjectTag=c(101, 102, 103, 201, 202),  
  DV1=c(11, 12, 13, 41, 42),  
  DV2=c(21, 22, 23, 51, 52))  
dsDouble <- CreatePairLinksDoubleEntered(  
  outcomeDataset=dsSingleOutcomes,  
  linksPairDataset=dsSingleLinks,  
  outcomeNames=c("DV1", "DV2"),  
  validateOutcomeDataset=TRUE)  
dsDouble #Show the 8 rows in the double-entered pair links  
summary(dsDouble) #Summarize the variables  
  
ValidatePairLinksAreSymmetric(dsDouble) #Should return TRUE.
```

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