ACE Models with the NLSY

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Abstract

We describe how to use the NlsyLinks package to examine various biometric models, using the NLSY79.

Contents

//Note to team: *Not only am I hoping to capitalize on all researchers initially interested in NLSY BG studies, I'm also hoping to attract a small slice of those that aren't initially interested in BG. If the vignette or articles are good, they should rank well among search engines for terms like "NLSY and R". Maybe some researchers using those terms (and not initially interested in BG) could stumble on the vignettes. If the examples are clear and are easy to run quickly, they may get interested in BG. Therefore, I'd like at least a few paragraphs explaining what BG is. This section is tentatively located in the appendix.*

1 Terminology

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 offspring of the Gen1 females -*i.e.*, those in the NLSY79 Children and Young Adults sample (http://www.bls.gov/nls/nlsy79ch.htm). The NLSY97 is a third dataset that can be used for behavior genetic research (http://www.bls.gov/nls/nlsy97.htm), although this vignette focuses on the two generations in the NLSY79.

Standard terminology is to refer Gen2 subjects as 'children' when they are younger than age 15 (NSLY79-C), and as 'young adults' when they are 15 and older (NLSY79-YA); though they are the same respon-

dents, different funding mechanisms and different survey items necessitate the distinction. This cohort is sometimes abbreviated as 'NLSY79-C', 'NLSY79C', 'NLSY-C' or 'NLSYC'.

The **SubjectTag** variable uniquely identify NLSY79 subjects when a dataset contains both generations. For Gen2 subjects, the `SubjectTag` is identical to their CID (*i.e.*, C00001.00 -the ID assigned in the NLSY79-Children files). However for Gen1 subjects, the `SubjectTag` is their CaseID (*i.e.*, 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 `SubjectTag`s of her four children remain 4301, 4302, 4303, and 4304.

The **expected coefficient of relatedness** of a pair of subjects is typically represented by the variable `R`. Examples are: Monozygotic twins have `R`=1; dizygotic twins have `R`=0.5; full siblings (*i.e.*, those who share both biological parents) have `R`=0.5; half-siblings (*i.e.*, those who share exactly one biological parent) have `R`=0.25; adopted siblings have `R`=0.0. Other possibilities exist too. The font (and hopefully their context) should distinguish the variable `R` from the software R.

A subject's `ExtendedID` indicates their extended family. Two 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 (*i.e.*, 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|uncle) and (niece|nephew) (in Gen1 and Gen2, respectively).

An **outcome variable** is directly relevant to the applied researcher; these might represent constructs like height, IQ, and income. A **plumbing variable** is necessary to manage BG datasets; examples are `R`, a subject's ID, and the date of a subject's last survey.

An ACE model is the basic biometrical model used by Behavior Genetic researchers, where the genetic and environmental effects are assumed to be additive. The three primary variance components are (1) the proportion of variability due to a shared genetic influence (typically represented as a^2, or sometimes h^2), (2) the proportion of variability due to shared common environmental influence (typically c^2), and (3) the proportion of variability due to unexplained/residual/error influence (typically e^2).

The variables are scaled so that they account for all observed variability in the outcome variable; specifically: $a^2+c^2+e^2 = 1$. Using appropriate designs that can logically distinguish these different components (under carefully specified assumptions), the basic biometrical modeling strategy is to estimate the magnitude of a^2, c^2, and e^2 within the context of a particular model. For gentle introductions to Behavior Genetic research, we recommend Plomin (1990) and Carey (2003). For more in-depth ACE model-fitting strategies, we recommend Neale & Cardon (1992). //This paragraph may get moved to the yet-to-be-written introduction that precedes the Terminology section.

The **NLS Investigator** (http://www.nlsinfo.org/investigator/) is the best way to obtain the NLSY79 and NLSY97 datasets. See our vignette dedicated to the NLS Investigator by typing `vignette("NlsInvestigator")` or by visiting http://cran.r-project.org/web/packages/NlsyLinks/.

Before starting the real examples, first verify that the NlsyLinks package is installed correctly. If not, refer to Appendix B.

```
> any(.packages(all.available=TRUE) == "NlsyLinks") #Should evaluate to TRUE.
[1] TRUE
> require(NlsyLinks) #Load the package into the current session.
> ?NlsyLinks #Open the package's documentation manual.
```

2 Example: DF analysis with a Simple Outcome for Gen2 Subjects, Using a Package Variable

The vignette's first example uses a simple statistical model and all available Gen2 subjects. The `CreatePairLinksDoubleEntered` function will create a data frame where each represents one pair of siblings, respective of order (*i.e.*, there is a row for Subjects 201 and 202, and a second row for Subjects 202 and 201). This function examines the subjects' IDs and determines who is related to whom (and by how much). By default, each row it produces has at least six values/columns: (i) ID for the older member of

the kinship pair: `Subject1Tag`, (ii) ID for the younger member: `Subject2Tag`, (iii) ID for their extended family: `ExtendedID`, (iv) their estimated coefficient of genetic relatedness: `R`, (v *and beyond*) outcome values for the older member; (vi *and beyond*) outcome values for the younger member.

A DeFries-Fulker (**DF**) Analysis uses linear regression to estimate the a^2, c^2, and e^2 of a univariate biometric system. The interpretations of the DF analysis can be found in Rodgers & Kohler (2005) and Rodgers, Rowe, & Li (1999). The steps are:

1. Use the NLS Investigator to select and download a Gen2 dataset.
2. Open R and create a new script (see Appendix A) and load the NlsyLinks package. If you haven't done so, first install the NlsyLinks package (see Appendix B).
3. Within the R script, load the linking dataset. Then select only Gen2 subjects. The 'Pair' version of the linking dataset is essentially a sparse matrix.
4. Load and assign the `ExtraOutcomes79` dataset.
5. Specify the outcome variable name and filter out all subjects who have a negative value in this variable. The NLSY typically uses negative values to indicate different types of missingness (see 'Further Information' below).
6. Create a double-entered file by calling the `CreatePairLinksDoubleEntered` function. At minimum, pass the (i) outcome dataset, the (ii) linking dataset, and the (iii) name(s) of the outcome variable(s).
7. Use `DeFriesFulkerMethod3` function (i.e., general linear model) to estimate the coefficients of the DF model.

```
> ### R Code for Example DF analysis with a simple outcome and Gen2 subjects
> #Step 2: Load the package containing the linking routines.
> require(NlsyLinks)
> #
> #Step 3: Load the LINKING dataset and filter for the Gen2 subjects
> data(Links79Pair)
> dsLinking <- subset(Links79Pair, RelationshipPath=="Gen2Siblings")
> summary(dsLinking) #Notice there are 11,075 records.
```

```
   ExtendedID     Subject1Tag       Subject2Tag            R
 Min.   :    2   Min.   :    201   Min.   :    202   Min.   :  0.2500
 1st Qu.: 3159   1st Qu.: 315901   1st Qu.: 315902   1st Qu.:  0.2500
 Median : 6116   Median : 611901   Median : 611902   Median :  0.5000
 Mean   : 5937   Mean   : 593989   Mean   : 593991   Mean   :  0.4192
 3rd Qu.: 8511   3rd Qu.: 851103   3rd Qu.: 851104   3rd Qu.:  0.5000
 Max.   :12673   Max.   :1267301   Max.   :1267302   Max.   :  1.0000
                                                     NA's   :563.0000
     RelationshipPath
 Gen2Siblings:11075
```

```
> #
> #Step 4: Load the OUTCOMES dataset and the linking dataset, and then examine the summary.
> data(ExtraOutcomes79)
> dsOutcomes <- ExtraOutcomes79 #'ds' stands for 'DataSet'
> summary(dsOutcomes)
```

```
   SubjectTag        SubjectID         Generation MathStandardized
 Min.   :    201   Min.   :    201   Min.   :2    Min.   :  65.00
 1st Qu.: 310302   1st Qu.: 310302   1st Qu.:2    1st Qu.:  91.00
 Median : 604607   Median : 604607   Median :2    Median : 100.00
 Mean   : 601313   Mean   : 601313   Mean   :2    Mean   :  99.97
 3rd Qu.: 876203   3rd Qu.: 876203   3rd Qu.:2    3rd Qu.: 110.00
 Max.   :1267501   Max.   :1267501   Max.   :2    Max.   : 135.00
                                                  NA's   :2353.00
     Weight       WeightForAge19To25 WeightStandardized
```

```
 Min.   :  75.0   Min.   :  75.0     Min.   :-2.768e+00
 1st Qu.: 130.0   1st Qu.: 140.0     1st Qu.:-7.059e-01
 Median : 155.0   Median : 165.0     Median :-2.207e-01
 Mean   : 161.9   Mean   : 172.1     Mean   :-4.252e-11
 3rd Qu.: 186.0   3rd Qu.: 195.0     3rd Qu.: 4.739e-01
 Max.   : 485.0   Max.   : 485.0     Max.   : 7.178e+00
 NA's   :3475.0   NA's   :6380.0     NA's   : 3.475e+03
 WeightStandardizedForAge19To25
 Min.   :-2.772e+00
 1st Qu.:-6.879e-01
 Median :-1.969e-01
 Mean   :-4.086e-11
 3rd Qu.: 4.905e-01
 Max.   : 7.489e+00
 NA's   : 6.380e+03
> #
> #Step 5: This step isn't necessary for this example, because Kelly Meredith already
> #   groomed the values.  But if not if the negative values
> #   (which represent NLSY missing or skip patterns) still exist, then:
> dsOutcomes$MathStandardized[dsOutcomes$MathStandardized < 0] <- NA
> #
> #Step 6: Create the double entered dataset.
> dsDouble <- CreatePairLinksDoubleEntered(
   outcomeDataset=dsOutcomes,
   linksPairDataset=dsLinking,
   outcomeNames=c('MathStandardized')
 )
> summary(dsDouble) #Notice there are 22,150=(2*11,075) records.
  Subject1Tag       Subject2Tag        ExtendedID          R
 Min.   :    201   Min.   :    201   Min.   :    2   Min.   :   0.2500
 1st Qu.: 315752   1st Qu.: 315752   1st Qu.: 3158   1st Qu.:   0.2500
 Median : 611901   Median : 611901   Median : 6116   Median :   0.5000
 Mean   : 593990   Mean   : 593990   Mean   : 5937   Mean   :   0.4192
 3rd Qu.: 851104   3rd Qu.: 851104   3rd Qu.: 8511   3rd Qu.:   0.5000
 Max.   :1267302   Max.   :1267302   Max.   :12673   Max.   :   1.0000
                                                     NA's   :1126.0000
     RelationshipPath MathStandardized_1 MathStandardized_2
 Gen2Siblings:22150   Min.   :  65.00    Min.   :  65.00
                      1st Qu.:  89.00    1st Qu.:  89.00
                      Median :  98.00    Median :  98.00
                      Mean   :  98.29    Mean   :  98.29
                      3rd Qu.: 108.00    3rd Qu.: 108.00
                      Max.   : 135.00    Max.   : 135.00
                      NA's   :3791.00    NA's   :3791.00
> #
> #Step 7: Estimate the ACE components with a DF Analysis
> ace <- DeFriesFulkerMethod3(
     dataSet=dsDouble,
     oName_1="MathStandardized_1",
     oName_2="MathStandardized_2")
> ace
[1] "Results of ACE estimation: [show]"
    ASquared     CSquared     ESquared    CaseCount
8.595078e-01 3.879863e-02 1.016935e-01 1.658800e+04
```

Further Information: If the different reasons of missingness are important, further work is necessary. For instance, some analyses that use item `Y19940000` might need to distinguish a response of "Don't Know"

(which is coded as -2) from "Missing" (which is coded as -7). For this vignette example, we'll assume it's safe to clump the responses together.

3 Example: DF analysis with a univariate outcome from a Gen2 Extract

The vignette's second example differs from the previous example in two ways. First, the outcome variables are read from a CSV (comma separated values file) that was downloaded from the NLS Investigator. Second, the DF analysis is called through the function `AceUnivariate`; this function is a wrapper around some simple ACE methods, and will help us smoothly transition to more techniques later in the vignette.

The steps are:

1. Use the NLS Investigator to select and download a Gen2 dataset. Select the variables 'length of gestation of child in weeks' (`C03280.00`), 'weight of child at birth in ounces' (`C03286.00`), and 'length of child at birth' (`C03288.00`), and then download the *.zip file to your local computer.
2. Open R and create a new script (see Appendix A) and load the `NlsyLinks` package.
3. Within the R script, load the linking dataset. Then select only Gen2 subjects.
4. Read the CSV into R as a `data.frame` using `ReadCsvNlsy79Gen2`.
5. Verify the desired outcome column exists, and rename it something meaningful to your project. It is important that the `data.frame` is reassigned (*i.e.*, `ds <- RenameNlsyColumn(...)`). In this example, we rename column `C0328800` to `BirthWeightInOunces`.
6. Filter out all subjects who have a negative `BirthWeightInOunces` value. See the 'Further Information' note in the previous example.
7. Create a double-entered file by calling the `CreatePairLinksDoubleEntered` function. At minimum, pass the (i) outcome dataset, the (ii) linking dataset, and the (iii) name(s) of the outcome variable(s).
8. Call the `AceUnivariate` function to estimate the coefficients.

```
> ### R Code for Example of a DF analysis with a simple outcome and Gen2 subjects
> #Step 2: Load the package containing the linking routines.
> require(NlsyLinks)
> #
> #Step 3: Load the linking dataset and filter for the Gen2 subjects
> data(Links79Pair)
> dsLinking <- subset(Links79Pair, RelationshipPath=="Gen2Siblings")
> #
> #Step 4: Load the outcomes dataset and the linking dataset, and then examine the summary.
> #   Your path might be: filePathOutcomes <- 'C:/BGResearch/NlsExtracts/Gen2Birth.csv'
> filePathOutcomes <- file.path(path.package("NlsyLinks"), "extdata", "Gen2Birth.csv")
> dsOutcomes <- ReadCsvNlsy79Gen2(filePathOutcomes)
> summary(dsOutcomes)
```

```
   SubjectTag         SubjectID          ExtendedID       Generation
 Min.   :    201   Min.   :    201   Min.   :    2   Min.   :2
 1st Qu.: 310302   1st Qu.: 310302   1st Qu.: 3103   1st Qu.:2
 Median : 604607   Median : 604607   Median : 6045   Median :2
 Mean   : 601313   Mean   : 601313   Mean   : 6008   Mean   :2
 3rd Qu.: 876203   3rd Qu.: 876203   3rd Qu.: 8757   3rd Qu.:2
 Max.   :1267501   Max.   :1267501   Max.   :12675   Max.   :2
 SubjectTagOfMother    C0005300         C0005400         C0005700
 Min.   :    200    Min.   :1.000   Min.   :-3.000   Min.   :  -3
 1st Qu.: 310300    1st Qu.:2.000   1st Qu.: 1.000   1st Qu.:1981
```

```
 Median : 604600    Median :3.000   Median : 1.000   Median :1985
 Mean   : 601311    Mean   :2.338   Mean   : 1.489   Mean   :1986
 3rd Qu.: 876200    3rd Qu.:3.000   3rd Qu.: 2.000   3rd Qu.:1990
 Max.   :1267500    Max.   :3.000   Max.   : 2.000   Max.   :2008
    C0328000        C0328600        C0328800
 Min.   :-7.00   Min.   : -7.0   Min.   :-7.00
 1st Qu.:37.00   1st Qu.: 99.0   1st Qu.:18.00
 Median :39.00   Median :115.0   Median :20.00
 Mean   :33.51   Mean   :103.9   Mean   :16.51
 3rd Qu.:39.00   3rd Qu.:128.0   3rd Qu.:21.00
 Max.   :51.00   Max.   :768.0   Max.   :48.00
> #
> #Step 5: Verify and rename an existing column.
> VerifyColumnExists(dsOutcomes,  "C0328800") #Should return '11' in this example.
[1] 11
> dsOutcomes <- RenameNlsyColumn(dsOutcomes, "C0328800", "BirthWeightInOunces")
> #
> #Step 6: For this item, a negative value indicates the parent refused, didn't know,
> #   invalidly skipped, or was missing for some other reason.
> #   For our present purposes, we'll treat these responses equivalently.
> dsOutcomes$BirthWeightInOunces[dsOutcomes$BirthWeightInOunces < 0] <- NA
> #
> #Step 7: Create the double entered dataset.
> dsDouble <- CreatePairLinksDoubleEntered(
   outcomeDataset=dsOutcomes,
   linksPairDataset=dsLinking,
   outcomeNames=c('BirthWeightInOunces')
 )
> #
> #Step 8: Estimate the ACE components with a DF Analysis
> ace <- AceUnivariate(
   method="DeFriesFulkerMethod3",
   dataSet=dsDouble,
   oName_1="BirthWeightInOunces_1",
   oName_2="BirthWeightInOunces_2"
 )
> ace
[1] "Results of ACE estimation: [show]"
    ASquared     CSquared     ESquared    CaseCount
4.822847e-01 4.685057e-02 4.708647e-01 1.482200e+04
```

4 Example: Multiple Group SEM of a Simple Outcome for Gen2 Subjects

The example differs from the first one by the statistical mechanism used to estimate the components. The first example uses multiple regression to estimate the influence of the shared genetic and environmental factors, while this example uses structural equation modeling (SEM).

The `CreatePairLinksSingleEntered` function will create a `data.frame` where each row represents one unique pair of siblings, *irrespective of order*. Other than producing half the number of rows, this function is identical to `CreatePairLinksDoubleEntered`.

The steps are:

(Steps 1-5 proceed identically to the first example.)

6. Create a *single*-entered file by calling the `CreatePairLinksSingleEntered` function. At minimum, pass the (i) outcome dataset, the (ii) linking dataset, and the (iii) name(s) of the outcome variable(s).
7. Declare the names of the manifest variables corresponding to the two members in each pair. Assuming the variable is called 'ZZZ' and the preceeding steps have been followed, the variable 'ZZZ_1' corresponds to the first members and ZZZ_2' corresponds to the second members.
8. Create a GroupSummary `data.frame`, which identifies the `R` groups that should be considered by the model. Inspect the output to see if the groups show unexpected or fishy differences.
9. Create a `data.frame` with cleaned variables to pass to the SEM function. This `data.frame` contains only the three necessary rows and columns.
10. Estimate the SEM with the `lavaan` package. The function returns an `S4` object, which shows the basic ACE information.
11. Inspect details of the SEM, beyond the ACE components. In this example, we look at the fit stats and the parameter estimates. The `lavaan` package has additional methods that may be useful for your purposes.

```
> ### R Code for Example lavaan estimation analysis with a simple outcome and Gen2 subjects
> #Steps 1-5 are explained in the vignette's first example:
> require(NlsyLinks)
> data(Links79Pair)
> dsLinking <- subset(Links79Pair, RelationshipPath=="Gen2Siblings")
> data(ExtraOutcomes79)
> dsOutcomes <- ExtraOutcomes79
> dsOutcomes$MathStandardized[dsOutcomes$MathStandardized < 0] <- NA
> #
> #Step 6: Create the single entered dataset.
> dsSingle <- CreatePairLinksSingleEntered(outcomeDataset=dsOutcomes,
   linksPairDataset=dsLinking, outcomeNames=c('MathStandardized'))
> #
> #Step 7: Declare the names for the two manifest variables.
> oName_1 <- "MathStandardized_1" #Stands for Manifest1
> oName_2 <- "MathStandardized_2" #Stands for Manifest2
> #
> #Step 8: Summarize the R groups and determine which groups can be estimated.
> dsGroupSummary <- RGroupSummary(dsSingle, oName_1, oName_2)
> dsGroupSummary

      R Included PairCount O1Variance O2Variance O1O2Covariance Correlation
1 0.250     TRUE      2719   169.1291   207.0233       40.66048   0.2172970
2 0.375     TRUE        43   187.7209   220.9302       28.66334   0.1407482
3 0.500     TRUE      5508   230.9663   233.3492      107.59822   0.4634764
4 0.750    FALSE         2   220.5000    18.0000       63.00000   1.0000000
5 1.000     TRUE        22   319.1948   343.1169      277.58874   0.8387893
  Determinant PosDefinite
1    33360.38        TRUE
2    40651.64        TRUE
3    42318.42        TRUE
4        0.00       FALSE
5    32465.62        TRUE

> #
> #Step 9: Create a cleaned dataset
> dsClean <- CleanSemAceDataset(dsDirty=dsSingle, dsGroupSummary, oName_1, oName_2)
> #
> #Step 10: Run the model
> ace <- AceLavaanGroup(dsClean)
> ace
```

```
[1] "Results of ACE estimation: [show]"
    ASquared     CSquared     ESquared    CaseCount
   0.6701032    0.1167060    0.2131907 8292.0000000
```

```
> #Notice the `CaseCount' is 8,292 instead of 16,588.
> #  This is because (a) one pair with R=.75 was excluded, and
> #  (b) the SEM uses a single-entered dataset instead of double-entered.
> #
> #Step 11: Inspect the output further
> require(lavaan) #Load the package to access methods of the lavaan class.
> GetDetails(ace)
```

```
lavaan (0.4-13) converged normally after 61 iterations
  Number of observations per group
  1                                                2719
  2                                                  43
  3                                                5508
  4                                                  22

  Estimator                                         ML
  Minimum Function Chi-square                  435.491
  Degrees of freedom                                16
  P-value                                        0.000

Chi-square for each group:

  1                                            290.182
  2                                             22.151
  3                                            118.815
  4                                              4.343
```

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

```
           chisq                 df             pvalue    baseline.chisq
         435.491             16.000              0.000          1491.127
    baseline.df   baseline.pvalue                cfi                tli
           4.000              0.000              0.718              0.929
            logl unrestricted.logl               npar                aic
     -67585.491         -67367.746              4.000         135178.982
             bic             ntotal               bic2              rmsea
      135207.074           8292.000         135194.363              0.112
  rmsea.ci.lower    rmsea.ci.upper      rmsea.pvalue               srmr
           0.103              0.122              0.000              0.126
```

```
>
> #Examine low-level details like each group's individual parameter estimates
> #  and standard errors.  Uncomment the following line to view the entire
> #  output (which is roughly four PDF pages).
> #summary(GetDetails(ace))
```

A Appendix: Creating and Saving R Scripts

TODO: write something here.

B Appendix: Installing the NlsyLinks Package

TODO: write something here.

C Appendix: References

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Plomin, Robert (1990). *Nature and nurture: an introduction to human behavioral genetics.* Brooks/Cole Publishing Company.

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Neale, Michael C., & Cardon, Lou R. (1992). *Methodology for genetic studies of twins and families.* Norwell, MA: Kluwer Academic Publishers. (Also see Neale & Maes: `http://www.vipbg.vcu.edu/OpenMxFall09/NMbook05.pdf`).

D Notes

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