Adolescent Pairs Data

Title

Adolescent Pairs Data

Abstract

Information that links and describes the sibling pairs identified at the Wave I in-home interview.

Variables: 11

Observations: 3,139

Variables

🚯 Adolescent Pairs Data

- PAIR UNIQUE PAIR IDENTIFICATION NUMBER
- AID_1 ADOLESCENT 1 IDENTIFICATION NUMBER
- AID_2 ADOLESCENT 2 IDENTIFICATION NUMBER
- FAMID FAMILY IDENTIFICATION NUMBER
- DNA TWIN ZYGOSITY, BASED ON DNA ANALYSIS
- SIBCL1 PAIR TYPE-ORIGINAL
- SIBCL2 PAIR TYPE-MOST DIFFERENTIATED
- SIBCL3 PAIR TYPE-WITH COUSINS, SOME DELETED
- SIBCL4 PAIR TYPE-WITH COUSINS, MORE DELETED
- SIMILAR SIMILARITY COMPOSITE FROM COMBINED TWIN
- SZYGOS ZYGOSITY BASED ON AVG.TWIN SELF REPORT

SPAIR - UNIQUE PAIR IDENTIFICATION NUMBER

Туре	Text
Constraints	Maximum Length: 7
Description	FSFFxxx, full sibling: female/female, FSMFxxx, full sibling: male/female,
	FSMMxxx, full sibling: male/male, HSFFxxx, half sibling: female/female,
	HSMFxxx, half sibling: male/female, HSMMxxx, half sibling: male/male,
	NRFFxxx, not related: female/female, NRMFxxx, not related: male/female,
	NRMMxxx, not related: male/male, TWFFxxx, twin: female/female, TWMFxxx,
	twin: male/female, TWMMxxx, twin: male/male
PAIR	Unique Pair Identification Nnumber for Each Pair

AID_1 - ADOLESCENT 1 IDENTIFICATION NUMBER

Туре

Text

Constraints	Maximum Length: 8		
AID_1	Identification Number of the First Adolescent		
SAID_2 - ADOLESCENT 2 IDENTIFICATION NUMBER			
Туре	Text		
Constraints	Maximum Length: 8		

SAMID - FAMILY IDENTIFICATION NUMBER	
Туре	Numeric (Double)
FAMID	Household Identification Number (Some households have more than 1 pair of adolescents - this number is the same for all the pairs within a single household.)

🌃 DNA - TWIN ZYGOSITY, BASED ON DNA ANALYSIS			
Туре		Code	
DNA Zygosity as Determined by Genotypes		pes	
DZ	dizygotic		
MZ monozygotic			

SIBCL1 - PAIR TYPE-ORIGINAL			
Туре		Code	
SIBCL1		Original Sibling Classification Variat	ble
DZ	dizygotic twins		
FS	full sibling		
HS	half-sibling		
MZ	monozygotic twi	ns	
NR	not related		
UD	twin pairs, uncertain zygosity		

	SIBCL2 - PAIR TYPE-MOST DIFFERENTIATED			
	Туре		Code	
SIBCL2 Second and Most Differentiated Sibling Classification Variable. (Assigns relationships to the pairs in the not related group, as well as the twin, for and half-sib pairs based on dummy variables.)		t related group, as well as the twin, full sib,		
	AA	adopted/adopte	d; both kids adopted	

AB	adopted/bio; one kid adopted, the other kid biological
AU	a pair of aunt/uncle and nephew/niece
CO	cousin pairs
DZ	DZ (fraternal) twins
FO	foster children (either one or both respondents are foster children)
FS	full sibling pairs
GH	not related pairs living in a group home
HS	half-sibling pairs
IL	pairs who are in-laws (i.e., living with a sister/brother's spouse or boy/girlfriend)
MZ	MZ (identical) twins
NR	not related pairs who are NOT step sibs, adopted sibs, cousins, etc.
SP	spousal (or boy/girlfriend) pairs
SS	step sibling pairs (includes blended families whose parents are not married, but are living together)
UD	twin pairs, uncertain zygosity

SIBCL3 - PAIR TYPE-WITH COUSINS,SOME DELETED

Туре		Code	
into		Third Pair Classification Variable (Collapses most of the unrelated pair types into the NR group, but does separate out the cousins. Codes the aunt/uncle, niece/nephew pairs and the group home pairs as missing.)	
CO	cousin pairs		
DZ	DZ (fraternal) twins		
FS	full sibling pairs		
HS	half-sibling pairs		
MZ	MZ (identical) tw	vins	
NR	not related pairs who are NOT aunt/uncle, niece/nephew pairs		
UD	twin pairs, uncer	tain zygosity	

SIBCL4 - PAIR TYPE-WITH COUSINS, MORE DELETED

Туре	Code		
SIBCL4		Fourth Pair Classification Variable (Collapses most of the unrelated pair types into the NR group, but does separate out the cousins. Codes the aunt/uncle, niece/nephew pairs, the group home pairs, the spouse pairs, and the in-law pairs as missing.)	
CO	cousin pairs		
DZ	DZ (fraternal) twins		
FS	full sibling pairs		
HS	half-sibling pairs		-
MZ	MZ (identical) twins		
NR	not related pairs who are NOT aunt/uncle, niece/nephew pairs, the group home pairs, the spouse pairs, and the in-law pairs		
UD	twin pairs, uncertain zygosity		

SIMILAR - SIMILARITY COMPOSITE FROM COMBINED TWIN

Туре	Numeric (Double)
SIMILAR	Continuous Score of Twins' Self-Report of Confusability of Appearance (In
	most cases used to estimate twin zygosity - see Appendix B for SAS code.)

Туре		Code	
Measurement Unit numeric		numeric	
SZYGOS Twins' Self-Report of Zygosity			
0	both twins report DZ		
0.5	twins disagree		
1	both twins report MZ		

SZYGOS - ZYGOSITY BASED ON AVG.TWIN SELF REPORT

Logical Products

📠 Adolescent Pairs Data

Data Layouts

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Adolescent Pairs Data

Adolescent Pairs Data

A PAIR - UNIQUE PAIR IDENTIFICATION NUMBER	
Туре	Text
Constraints	Maximum Length: 7
Description	FSFFxxx, full sibling: female/female, FSMFxxx, full sibling: male/female, FSMMxxx, full sibling: male/male, HSFFxxx, half sibling: female/female, HSMFxxx, half sibling: male/female, HSMMxxx, half sibling: male/male, NRFFxxx, not related: female/female, NRMFxxx, not related: male/female, NRMMxxx, not related: male/male, TWFFxxx, twin: female/female, TWMFxxx, twin: male/female, TWMMxxx, twin: male/male
PAIR	Unique Pair Identification Nnumber for Each Pair

AID_1 - ADOLESCENT 1 IDENTIFICATION NUMBER	
Туре	Text
Constraints	Maximum Length: 8
AID_1	Identification Number of the First Adolescent

M& AID_2 - ADOLESCENT 2 IDENTIFICATION NUMBER	
Туре	Text
Constraints	Maximum Length: 8
AID_2 Identification Number of the Second Adolescent	

SAMID - FAMILY IDENTIFICATION NUMBER	
Туре	Numeric (Double)
FAMID	Household Identification Number (Some households have more than 1 pair of adolescents - this number is the same for all the pairs within a single household.)

🌃 DNA - TWIN ZYGOSITY, BASED ON DNA ANALYSIS	
Туре	Code
DNA	Zygosity as Determined by Genotypes

DZ	dizygotic
MZ	monozygotic

SIBCL1 - PAIR TYPE-ORIGINAL

Туре		Code	
SIBCL1		Original Sibling Classification Varia	ble
DZ	dizygotic twins		
FS	full sibling		
HS	half-sibling		
MZ	monozygotic twi	ns	
NR	not related		
UD	twin pairs, uncer	tain zygosity	

-			
Туре		Code	
SIBCL2 Second and Most Differentiated Sibling Classification Variable. (As relationships to the pairs in the not related group, as well as the t and half-sib pairs based on dummy variables.)		t related group, as well as the twin, full sib	
AA	adopted/adopted	d; both kids adopted	
AB	adopted/bio; one biological	e kid adopted, the other kid	
AU	a pair of aunt/un	cle and nephew/niece	
CO	cousin pairs		_
DZ	DZ (fraternal) twins		
FO	foster children (either one or both respondents are foster children)		
FS	full sibling pairs		
GH	not related pairs	living in a group home	
HS	half-sibling pairs		
IL	pairs who are in-laws (i.e., living with a sister/brother's spouse or boy/girlfriend)		
MZ	MZ (identical) twins		
NR	not related pairs who are NOT step sibs, adopted sibs, cousins, etc.		

SP	spousal (or boy/girlfriend) pairs
SS	step sibling pairs (includes blended families whose parents are not married, but are living together)
UD	twin pairs, uncertain zygosity

SIBCL3 - PAIR TYPE-WITH COUSINS, SOME DELETED			
Туре		Code	
SIBCL3		Third Pair Classification Variable (Collapses most of the unrelated pair types into the NR group, but does separate out the cousins. Codes the aunt/uncle, niece/nephew pairs and the group home pairs as missing.)	
CO	cousin pairs		
DZ	DZ (fraternal) twins		
FS	full sibling pairs		
HS	half-sibling pairs		
MZ	MZ (identical) twins		
NR	not related pairs who are NOT aunt/uncle, niece/nephew pairs		
UD	twin pairs, uncertain zygosity		

🐝 SIBCL4 - PAIR	TYPE-WITH COUSI	NS,MORE DELETED	
Туре		Code	
SIBCL4		Fourth Pair Classification Variable (Collapses most of the unrelated pair types into the NR group, but does separate out the cousins. Codes the aunt/uncle, niece/nephew pairs, the group home pairs, the spouse pairs, and the in-law pairs as missing.)	
CO	cousin pairs		
DZ	DZ (fraternal) tw	ins	
FS	full sibling pairs		
HS	half-sibling pairs		
MZ	MZ (identical) twins		
NR	not related pairs who are NOT aunt/uncle, niece/nephew pairs, the group home pairs, the spouse pairs, and the in-law pairs		
UD	twin pairs, uncertain zygosity		

🖗 SIMILAR - SIMILARITY COMPOSITE FROM COMBINED TWIN

Туре	Numeric (Double)	
SIMILAR	Continuous Score of Twins' Self-Report of Confusability of Appearance (In	
	most cases used to estimate twin zygosity - see Appendix B for SAS code.)	

🌾 SZYGOS - ZYGOSITY BASED ON AVG.TWIN SELF REPORT

Туре		Code	
Measurement Ur	nit	numeric	
SZYGOS		Twins' Self-Report of Zygosity	
0	both twins repor	t DZ	
0.5	twins disagree	twins disagree	
1	both twins repor	t MZ	

Physical Instances

🐱 Adolescent Pairs Data				
Title	Adolescent Pairs Data			
File Name	pairs.sas7bdat			
Case Quantity	3139			
Variable Count	11			
⁴ PAIR - UNIQUE PAIR IDENT	IFICATION NUMBER			
Туре	Text			
Constraints	Maximum Length: 7			
Description	FSFFxxx, full sibling: female/female, FSMFxxx, full sibling: male/female, FSMMxxx, full sibling: male/male, HSFFxxx, half sibling: female/female, HSMFxxx, half sibling: male/female, HSMMxxx, half sibling: male/male, NRFFxxx, not related: female/female, NRMFxxx, not related: male/female, NRMMxxx, not related: male/male, TWFFxxx, twin: female/female, TWMFxxx, twin: male/female, TWMMxxx, twin: male/male			
PAIR	Unique Pair Identification Nnumber for Each Pair			
Valid Invalid 3139 O				
AID_1 - ADOLESCENT 1 IDI	ENTIFICATION NUMBER			
Туре	Text			
Constraints	Maximum Length: 8			

AID_1			Identification N	lumber o	of the First	Adol	escent		
Valid 3139	Inval 0	id	Minimum 10316654	Maxim 99886					
\delta AID_2 - 1	ADOLES	CENT 2 ID	ENTIFICATION	NUMB	ER				
Туре			Text						
Constraints			Maximum Leng	gth: 8					
AID_2			Identification N	lumber o	of the Seco	nd A	dolescent		
Valid	Inva	id	Minimum	Maxim	านm				
3139	0		21316754	99886	999				
🍄 FAMID -	- FAMILY	IDENTIFIC	CATION NUMB	BER					
Туре			Numeric (Doub	ole)					
FAMID			Household Ider adolescents - th household.)			-			-
Valid			Minimum Maximum Mean						
Valid	Inva	id	Minimum	Maxim	num	Mea	in	StdDev	
3139	Inval 0	id	Minimum 1001	Maxim 3785	-		in 7.9467	StdDev 809.87454	
3139	0			3785					1
3139	0		1001	3785					
3139 🐔 DNA - T	0		1001 SED ON DNA /	3785 ANALYS	ilS	238			
3139 DNA - T Type	0		1001 SED ON DNA A	3785 ANALYS	ilS	2387 7pes			
3139 🔧 DNA - T\ Type	0		1001 SED ON DNA A	3785 ANALYS	IS by Genoty Frequen	2387 7pes	7.9467	809.87454	
3139 S DNA - T Type DNA	0 WIN ZYC	OSITY, BA	1001 SED ON DNA / Code Zygosity as Det	3785 ANALYS	SIS by Genoty Frequen	238 pes cy 47 42	7.9467 % of total 1.5% 1.34%	809.87454 % of valid 52.81% 47.19%	
3139 S DNA - T Type DNA	0 WIN ZYG	iOSITY, BA	1001 SED ON DNA / Code Zygosity as Det	3785 ANALYS	SIS by Genoty Frequen	2387 7pes cy 47	7.9467 % of total 1.5%	809.87454 % of valid 52.81%	
3139 S DNA - T Type DNA	0 WIN ZYG	dizygotic monozygo Total	1001 SED ON DNA / Code Zygosity as Det	3785 ANALYS	SIS by Genoty Frequen	238 ppes cy 47 42 89	7.9467 % of total 1.5% 1.34%	809.87454 % of valid 52.81% 47.19%	
3139 S DNA - T Type DNA Valid	0 WIN ZYG	dizygotic monozygo Total	1001 SED ON DNA A Code Zygosity as Det	3785 ANALYS	SIS by Genoty Frequen	238 rpes cy 47 42 89	7.9467 % of total 1.5% 1.34% 2.84%	809.87454 % of valid 52.81% 47.19%	
3139 S DNA - T Type DNA Valid	0 WIN ZYG	dizygotic monozygo Total zygosity r Total	1001 SED ON DNA A Code Zygosity as Det	3785 ANALYS	by Genoty Frequen	238 rpes cy 47 42 89	7.9467 % of total 1.5% 1.34% 2.84% 97.16%	809.87454 % of valid 52.81% 47.19%	
3139 SDNA - TV Type DNA Valid Missing	0 WIN ZYG DZ MZ	dizygotic monozygo Total zygosity r Total	1001 SED ON DNA A Code Zygosity as Det	3785 ANALYS	by Genoty Frequen	238 rpes cy 47 42 89	7.9467 % of total 1.5% 1.34% 2.84% 97.16%	809.87454 % of valid 52.81% 47.19%	
3139 DNA - TV Type DNA Valid Missing Valid	DZ MZ MZ Inval 3050	dizygotic monozygo Total zygosity r Total	1001 SED ON DNA / Code Zygosity as Det otic	3785 ANALYS	by Genoty Frequen	238 rpes cy 47 42 89	7.9467 % of total 1.5% 1.34% 2.84% 97.16%	809.87454 % of valid 52.81% 47.19%	
3139 SDNA - TV Type DNA Valid Missing Valid 89	DZ MZ MZ Inval 3050	dizygotic monozygo Total zygosity r Total	1001 SED ON DNA / Code Zygosity as Det otic	3785 ANALYS	by Genoty Frequen	238 rpes cy 47 42 89	7.9467 % of total 1.5% 1.34% 2.84% 97.16%	809.87454 % of valid 52.81% 47.19%	
3139 SIBCL1 -	DZ MZ MZ Inval 3050	dizygotic monozygo Total zygosity r Total	1001 SED ON DNA A Code Zygosity as Det otic not measured	3785 ANALYS rermined	SIS by Genoty Frequen 2 309 3,09	238 ypes cy 47 42 39 50 50 50	7.9467 % of total 1.5% 1.34% 2.84% 97.16%	809.87454 % of valid 52.81% 47.19%	

Valid	d DZ	dizygotic twins	452	14.4%	14.4%
	FS	full sibling	1251	39.85%	39.85%
	HS	half-sibling	442	14.08%	14.08%
	MZ	monozygotic twins	289	9.21%	9.21%
	NR	not related	662	21.09%	21.09%
	UD	twin pairs, uncertain zygosity	43	1.37%	1.37%
		Total	3,139	100%	100%

Valid	Invalid	
3139	0	
% SIBCL2 -	PAIR TYPE-MOST	DIFFERENTIATED
Туре		Code
SIBCL2		Second and Most Differentiated Sibling Classification Variable. (Assigns relationships to the pairs in the not related group, as well as the twin, full sib, and half-sib pairs based on dummy variables.)
		Frequency % of total % of valid

Valid	AA	adopted/adopted; both kids adopted	31	0.99%	0.99%
	AB	adopted/bio; one kid adopted, the other kid biological	49	1.56%	1.56%
	AU	a pair of aunt/uncle and nephew/niece	18	0.57%	0.57%
	СО	cousin pairs	201	6.4%	6.4%
	DZ	DZ (fraternal) twins	452	14.4%	14.4%
	FO	foster children (either one or both respondents are foster children)	27	0.86%	0.86%
	FS	full sibling pairs	1251	39.85%	39.85%
GH	GH	not related pairs living in a group home	7	0.22%	0.22%
	HS	half-sibling pairs	442	14.08%	14.08%
IL	IL	pairs who are in-laws (i.e., living with a sister/brother's spouse or boy/girlfriend)	12	0.38%	0.38%
	MZ	MZ (identical) twins	289	9.21%	9.21%
	NR	not related pairs who are NOT step sibs, adopted sibs, cousins, etc.	151	4.81%	4.81%
	SP	spousal (or boy/girlfriend) pairs	16	0.51%	0.51%
	SS	step sibling pairs (includes blended families whose parents are not married, but are living together)	150	4.78%	4.78%
	UD	twin pairs, uncertain zygosity	43	1.37%	1.37%
		Total	3,139	100%	100%

Valid	Invalid	
3139	0	
% SIBCL3 - PA	AIR TYPE-WITH (COUSINS,SOME DELETED
Туре		Code
SIBCL3		Third Pair Classification Variable (Collapses most of the unrelated pair types into the NR group, but does separate out the cousins. Codes the aunt/uncle, niece/nephew pairs and the group home pairs as missing.)
		Frequency % of total % of valid

Valid	СО	cousin pairs	201	6.4%	6.45%
	DZ	DZ (fraternal) twins	452	14.4%	14.52%
	FS	full sibling pairs	1251	39.85%	40.17%
	HS	half-sibling pairs	442	14.08%	14.19%
	MZ	MZ (identical) twins	289	9.21%	9.28%
	NR	not related pairs who are NOT	436	13.89%	14%
		aunt/uncle, niece/nephew pairs			
	UD	twin pairs, uncertain zygosity	43	1.37%	1.38%
		Total	3,114	99.2%	100%
Missing		not related pairs who are aunt/uncle, niece/nephew pairs	25	0.8%	
		Total	25	0.8%	

Valid Invalid 3114 25

SIBCL4 - PAIR TYPE-WITH COUSINS, MORE DELETED Type Code SIBCL4 Fourth Pair Classification Variable (Collapses most of the unrelated pair types into the NR group, but does separate out the cousins. Codes the aunt/uncle, niece/nephew pairs, the group home pairs, the spouse pairs, and the in-law pairs as missing.)

			Frequency	% of total	% of valid
Valid	со	cousin pairs	201	6.4%	6.51%
valiu	DZ	DZ (fraternal) twins	452	14.4%	14.65%
	FS	full sibling pairs	1251	39.85%	40.54%
	HS	half-sibling pairs	442	14.08%	14.32%
	MZ	MZ (identical) twins	289	9.21%	9.36%
	NR	not related pairs who are NOT aunt/uncle, niece/nephew pairs, the group home pairs, the spouse pairs, and the in-law pairs	408	13%	13.22%
	UD	twin pairs, uncertain zygosity	43	1.37%	1.39%
		Total	3,086	98.31%	100%
Missing		not related pairs who are aunt/uncle, niece/nephew pairs, the group home pairs, the spouse pairs, and the in-law pairs	53	1.69%	
		Total	53	1.69%	

Valid	Invalid	
3086	53	
% SIMILA	R - SIMILARITY CON	/POSITE FROM COMBINED TWIN
-		
Туре		Numeric (Double)

		Frequency	% of total	% of valid
Missing	missing	2405	76.62%	
	Total	2,405	76.62%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
734	2405	0	100	45.111934	40.676256

SZYGOS - ZYGOSITY BASED ON AVG.TWIN SELF REPORT

Туре	Code
Measurement Unit	numeric
SZYGOS	Twins' Self-Report of Zygosity

			Frequency	% of total	% of valid
Valid	0	both twins report DZ	472	15.04%	64.39%
	0.5	twins disagree	23	0.73%	3.14%
	1	both twins report MZ	238	7.58%	32.47%
		Total	733	23.35%	100%
Missing		missing	2406	76.65%	
		Total	2,406	76.65%	

Valid	Invalid	Minimum	Maximum
733	2406	0	1