MIDUS DNA Methylation Age Data

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Abstract

MIDUS is releasing Methylation Age scores data derived from DNA. See associated documentation for details.

Title

MIDUS DNA Methylation Age Data

Related Materials

Other

· Readme
· Documentation

📊 DNAmAge

Title	DNAmAge
File Name	M2MR1_GEN_DNAmAge_N2118_20230822.sav
Case Quantity	2118
Variable Count	21

DNAmAge

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· M2MRID - M2 AND MR Public IDs combined in a single variable
· SAMPLMAJ - Major sample identification
· M2MRCASE - Which sample is R in? 1=M2, 2=MR1
· GENCONSENT - Did R consent to genetics 1=Yes, 2=No
· BRA6DTISSUE - Tissue sample source for DNA
· BRA6DMAVAIL - Is Methylation score data available?

Technical Variable

· BRA6DMQCCORR - Correlation between the sample DNAm profile and the gold standard reference profile
· BRA6DMQCDIF - Difference the sample DNAm profile from the gold standard reference profile
· BRA6DMQCFEMALE - Participant sex as inferred from X chromosome methylation abundance
· BRA6DMXCHR - X chromosome methylation
· BRA6DMARRAYID - Individual microarray used to assay samples
· BRA6DMPLATE - Individual 96-well plate storing samples for assay
· BRA6DMWELL - Individual well within the 96-well plate

Epigenetic Age Score

· BRA6DMAGEHORVATH - DNA methylation age - Horvath
· BRA6DMAGEHORVATH2 - DNA methylation age - Horvath2 (Skin)
· BRA6DMAGEHANNUM - DNA methylation age - Hannum
· BRA6DMAGEPHENOAGE - DNA methylation age - PhenoAge
· BRA6DMAGEGRIMAGE - DNA methylation age - GrimAge
· BRA6DMAGEDUNEDINPACE - DNA methylation age - DunedinPACE
· BRA6DMAGEGRIMAGE2 - DNA methylation age - GrimAge2
· BRA6DMAGEGRIMAGE1V2 - DNA methylation age - GrimAge1v2

DNAmAge

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M2MRID - M2 AND MR Public IDs combined in a single variable

Type	Numeric (Integer)
Display Values	2
Stats	1

Valid	Invalid	Minimum	Maximum	Mean	StdDev
2118	0	10002	39977	23028.720…	10360.625…

SAMPLMAJ - Major sample identification

Type	Code
Display Values	1
Stats	1

			Frequency	% of total	% of valid
Valid	1	CORE MAIN RDD	640	30.22%	30.22%
	2	CORE SIBLING	6	0.28%	0.28%
	3	CORE TWIN	388	18.32%	18.32%
	4	CORE CITY OVERSAMPLE	20	0.94%	0.94%
	13	CORE MILWAUKEE	201	9.49%	9.49%
	20	REFRESHER MAIN	746	35.22%	35.22%
	21	REFRESHER MILWAUKEE	117	5.52%	5.52%
		Total	2,118	100%	100%

Valid	Invalid	Minimum	Maximum
2118	0	1	21

M2MRCASE - Which sample is R in? 1=M2, 2=MR1

Type	Code
Display Values	1
Stats	1

			Frequency	% of total	% of valid
Valid	1	M2	1,255	59.25%	59.25%
	2	MR1	863	40.75%	40.75%
	3	M3 NEWTWIN		0%	0%
		Total	2,118	100%	100%

Valid	Invalid	Minimum	Maximum
2118	0	1	2

GENCONSENT - Did R consent to genetics 1=Yes, 2=No

Type	Code
Display Values	1
Stats	1

			Frequency	% of total	% of valid
Valid	1	YES	2,009	94.85%	94.85%
	2	NO	109	5.15%	5.15%
		Total	2,118	100%	100%
Missing	9	INAPP-M3NEWTWIN		0%	
		Total	0	0%	

Valid	Invalid	Minimum	Maximum
2118	0	1	2

BRA6DTISSUE - Tissue sample source for DNA

Type	Code
Display Values	1
Stats	1

			Frequency	% of total	% of valid
Valid	0	NONE	229	10.81%	10.81%
	1	BLOOD	1,418	66.95%	66.95%
	2	SALIVA	471	22.24%	22.24%
		Total	2,118	100%	100%
Missing	9	INAPP-M3NEWTWIN		0%	
		Total	0	0%	

Valid	Invalid	Minimum	Maximum
2118	0	0	2

BRA6DMAVAIL - Is Methylation score data available?

Type	Code
ForwardSkip	IF BRA6DMAVAIL = 2, SKIP BRA6DMQCCORR TO BRA6DMAGEDUNEDINPACE
Display Values	1
Stats	1

			Frequency	% of total	% of valid
Valid	1	YES	1,310	61.85%	61.85%
	2	NO	808	38.15%	38.15%
		Total	2,118	100%	100%
Missing	9	INAPP-M3NEWTWIN		0%	
		Total	0	0%	

Valid	Invalid	Minimum	Maximum
2118	0	1	2

Technical Variable

BRA6DMQCCORR - Correlation between the sample DNAm profile and the gold standard reference profile

Type	Numeric (Double)

Numeric Details	Decimals: 4
BackwardSkip	(BRA6DMAVAIL = 2)
Display Values	2
Stats	2

			Frequency	% of total	% of valid
Missing	9.0000	INAPP	808	38.15%	
		Total	808	38.15%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
1310	808	0.9306	0.9744	0.9698843...	0.0027901...

BRA6DMQCDIF - Difference the sample DNAm profile from the gold standard reference profile

Type	Numeric (Double)
Numeric Details	Decimals: 4
BackwardSkip	(BRA6DMAVAIL = 2)
Display Values	2
Stats	2

			Frequency	% of total	% of valid
Missing	9.0000	INAPP	808	38.15%	
		Total	808	38.15%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
1310	808	0.051	0.0795	0.0546251...	0.0022431...

BRA6DMQCFEMALE - Participant sex as inferred from X chromosome methylation abundance

Type	Numeric (Integer)
BackwardSkip	(BRA6DMAVAIL = 2)
Display Values	1
Stats	1

			Frequency	% of total	% of valid
Missing	.		1	0.05%	
	9	INAPP	808	38.15%	
		Total	809	38.2%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
1309	809	0	1	0.5576776...	0.4968519...

BRA6DMXCHR - X chromosome methylation

Type	Numeric (Double)
Numeric Details	Decimals: 4
BackwardSkip	(BRA6DMAVAIL = 2)
Display Values	2

Stats	2

			Frequency	% of total	% of valid
Missing	9.0000	INAPP	808	38.15%	
		Total	808	38.15%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
1310	808	0.3065	0.5435	0.4092324...	0.0755935...

BRA6DMARRAYID - Individual microarray used to assay samples

Type	Text
BackwardSkip	(BRA6DMAVAIL = 2)
Display Values	3
Stats	3

Valid	Invalid
2118	0

BRA6DMPLATE - Individual 96-well plate storing samples for assay

Type	Numeric (Integer)
BackwardSkip	(BRA6DMAVAIL = 2)
Display Values	2
Stats	1

			Frequency	% of total	% of valid
Missing	99	INAPP	808	38.15%	
		Total	808	38.15%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
1310	808	1	14	7.4923664...	4.0205187...

BRA6DMWELL - Individual well within the 96-well plate

Type	Text
BackwardSkip	(BRA6DMAVAIL = 2)
Display Values	3
Stats	3

Valid	Invalid
2118	0

Epigenetic Age Score

BRA6DMAGEHORVATH - DNA methylation age - Horvath

Type	Numeric (Double)
Numeric Details	Decimals: 4
BackwardSkip	(BRA6DMAVAIL = 2)
Display Values	2
Stats	2

			Frequency	% of total	% of valid
Missing	999.0000	INAPP	808	38.15%	
		Total	808	38.15%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
1310	808	25.3443	107.2746	55.460805...	11.118578...

BRA6DMAGEHORVATH2 - DNA methylation age - Horvath2 (Skin)

Type	Numeric (Double)
Numeric Details	Decimals: 4
BackwardSkip	(BRA6DMAVAIL = 2)
Display Values	2
Stats	2

			Frequency	% of total	% of valid
Missing	999.0000	INAPP	808	38.15%	
		Total	808	38.15%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
1310	808	18.8184	98.3801	51.906437...	12.444525...

BRA6DMAGEHANNUM - DNA methylation age - Hannum

Type	Numeric (Double)
Numeric Details	Decimals: 4
BackwardSkip	(BRA6DMAVAIL = 2)
Display Values	2
Stats	2

			Frequency	% of total	% of valid
Missing	999.0000	INAPP	808	38.15%	
		Total	808	38.15%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
1310	808	14.0105	110.4416	42.441519...	11.456398...

BRA6DMAGEPHENOAGE - DNA methylation age - PhenoAge

Type	Numeric (Double)
Numeric Details	Decimals: 4
BackwardSkip	(BRA6DMAVAIL = 2)
Display Values	2
Stats	2

			Frequency	% of total	% of valid
Missing	999.0000	INAPP	808	38.15%	
		Total	808	38.15%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev

| 1310 | 808 | 10.2689 | 85.0056 | 43.636760... | 12.994821... |

BRA6DMAGEGRIMAGE - DNA methylation age - GrimAge

Type	Numeric (Double)
Numeric Details	Decimals: 4
BackwardSkip	(BRA6DMAVAIL = 2)
Display Values	2
Stats	2

			Frequency	% of total	% of valid
Missing	999.0000	INAPP	808	38.15%	
		Total	808	38.15%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
1310	808	22.497	104.5895	52.649525...	11.125769...

BRA6DMAGEDUNEDINPACE - DNA methylation age - DunedinPACE

Type	Numeric (Double)
Numeric Details	Decimals: 4
BackwardSkip	(BRA6DMAVAIL = 2)
Display Values	2
Stats	2

			Frequency	% of total	% of valid
Missing	9.0000	INAPP	808	38.15%	
		Total	808	38.15%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
1310	808	0.5336	1.4541	0.9909680...	0.1374513...

BRA6DMAGEGRIMAGE2 - DNA methylation age - GrimAge2

Type	Numeric (Double)
Numeric Details	Decimals: 8
BackwardSkip	(BRA6DMAVAIL = 2)
Display Values	2
Stats	2

			Frequency	% of total	% of valid
Missing	998.0000	MISSING	1	0.05%	
	999.0000	INAPP	808	38.15%	
		Total	809	38.2%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
1309	809	33.0146	94.1379	62.675860...	10.738242...

BRA6DMAGEGRIMAGE1V2 - DNA methylation age - GrimAge1v2

Type	Numeric (Double)

Numeric Details	Decimals: 8
BackwardSkip	(BRA6DMAVAIL = 2)
Display Values	2
Stats	2

			Frequency	% of total	% of valid
Missing	998.0000	MISSING	1	0.05%	
	999.0000	INAPP	808	38.15%	
		Total	809	38.2%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
1309	809	29.7417	90.0149	57.099401...	10.936758...