PARKINSON'S PROGRESSION MARKERS INITIATIVE

Play a Part in Parkinson's Research

Variable Definitions and Score Calculations

Summary

The following tables describe the calculation of the derived variables in the PPMI study.

Study Groups

Characteristic	Variables	Dataset
Enrolled PD Subject	PATNO, APPRDX, ENROLLDT Merge SCREEN with RANDOM and count each unique PATNO with APPRDX = '1' that is not missing ENROLLDT	RANDOM, SCREEN
Enrolled Healthy Control	PATNO, APPRDX, ENROLLDT Merge SCREEN with RANDOM and count each unique PATNO with APPRDX = '2' that is not missing ENROLLDT	RANDOM, SCREEN
Enrolled SWEDD Subject	PATNO, APPRDX, ENROLLDT Merge SCREEN with RANDOM and count each unique PATNO with APPRDX = '3' that is not missing ENROLLDT	RANDOM, SCREEN
Enrolled Prodromal Subject	PATNO, APPRDX, ENROLLDT Merge SCREEN with RANDOM and count each unique PATNO with APPRDX = '4' that is not missing ENROLLDT	RANDOM, SCREEN
Enrolled Genetic Cohort Subject	PATNO, APPRDX, ENROLLDT Merge SCREEN with RANDOM and count each unique PATNO with APPRDX = '5' or '6' that is not missing ENROLLDT APPRDX = '5' are PD subjects APPRDX = '6' are Unaffected subjects	RANDOM, SCREEN
Enrolled Genetic Registry Subject	PATNO, APPRDX, ENROLLDT Merge SCREEN with RANDOM and count each unique PATNO with APPRDX = '7' or '8' that is not	RANDOM, SCREEN

| | missing ENROLLDT | |
| | APPRDX = '7' are PD subjects
APPRDX = '8' are Unaffected subjects | |

Demographics and PD Characteristics

Age	ENROLLDT - BIRTHDT	RANDOM
Gender	GENDER = 2 is Male GENDER = 0 or 1 is Female	RANDOM
Race	RAINDALS, RAASIAN, RABLACK, RAHAWOPI, RAWHITE, RANOS Other = RAINDALS, RAHAWOPI, RANOS, or more than one race specified	SCREEN
Family History	BIOMOMPD, BIODADPD, FULSIBPD, HALFSIBPD, MAGPARPD, PAGPARPD, MATAUPD, PATAUPD, KIDSPD Subject has family history of PD if any one of these variables = '1'	FAMHXPD
Duration of Disease	PDDXDT, ENROLLDT Duration = number of months between PDDXDT and ENROLLDT	PDFEAT, RANDOM

TD / PIGD Classification	First calculate Tremor and PIGD scores:
	  Tremor score = Mean of the following variables: NP2TRMR, NP3PTRMR, NP3PTRML, NP3KTRMR, NP3KTRML, NP3RTARU, NP3RTALU, NP3RTARL, NP3RTALL, NP3RTALJ, NP3RTCON
	  PIGD score = Mean of the following variables: NP2WALK, NP2FREZ, NP3GAIT, NP3FRZGT, NP3PSTBL
	
	Then calculate ratio = Tremor score / PIGD score.
	  If ratio >= 1.15, OR if PIGD score = 0 and Tremor score > 0, then subject is TD.
	  If ratio <= 0.9 then subject is PIGD.
	  If ratio > 0.9 and < 1.15, OR Tremor score and PIGD score = 0, then subject is Indeterminate.
		NUPDRS2P, NUPDRS3

Motor Assessments

MDS-UPDRS Part I	NP1COG, NP1HALL, NP1DPRS, NP1ANXS, NP1APAT,NP1DDS, NP1SLPN, NP1SLPD, NP1PAIN, NP1URIN, NP1CNST, NP1LTHD, NP1FATG Part I Score = sum of these 13 variables	NUPDRS1, NUPDRS1P
MDS-UPDRS Part II	NP2SPCH, NP2SALV, NP2SWAL, NP2EAT, NP2DRES, NP2HYGN, NP2HWRT, NP2HOBB, NP2TURN, NP2TRMR, NP2RISE, NP2WALK, NP2FREZ Part II Score = sum of these 13 variables	NUPDRS2P
MDS-UPDRS Part III	NP3SPCH, NP3FACXP, NP3RIGN, NP3RIGRU, NP3RIGLU, PN3RIGRL, NP3RIGLL, NP3FTAPR, NP3FTAPL, NP3HMOVR, NP3HMOVL, NP3PRSPR, NP3PRSPL, NP3TTAPR, NP3TTAPL, NP3LGAGR, NP3LGAGL, NP3RISNG, NP3GAIT, NP3FRZGT, NP3PSTBL, NP3POSTR, NP3BRADY, NP3PTRMR, NP3PTRML, NP3KTRMR, NP3KTRML, NP3RTARU, NP3RTALU, NP3RTARL, NP3RTALL, NP3RTALJ, NP3RTCON Part III Score = sum of these 33 variables	NUPDRS3
MDS-UPDRS Part IV	NP4WDYSK, NP4DYSKI, NP4OFF, NP4FLCTI, NP4FLCTX, NP4DYSTN Part IV Score = sum of these 6 variables	NUPDRS4
MDS-UPDRS Total Score	Sum of MDS-UPDRS Parts I, II, III	NUPDRS1, NUPDRS1P, NUPDRS2P, NUPDRS3

Non-Motor Assessments

Benton Judgment of Line Orientation Score	Sum of BJLOT1 – BJLOT30	LINEORNT
Epworth Sleepiness Scale	Sum of ESS1 - ESS8 Subjects with ESS < 10 are "Not Sleepy" Subjects with ESS ≥ 10 are "Sleepy"	EPWORTH

GDS Raw Score	Add 1 point for each response of "No" (0) to any of the following variables:
	   GDSSATIS, GDSGSPIR, GDSHAPPY,
	   GDSALIVE, GDSENRGY
	
	Add 1 point for each response of "Yes" (1) to any of the following variables:
	   GDSDROPD, GDSEMPTY, GDSBORED,
	   GDSAFRAD, GDSHLPLS, GDSHOME,
	   GDSMEMRY, GDSWRTLS, GDSHOPLS,
	   GDSBETER
	Subjects with GDS ≥ 5 are "Depressed"
	Subject with GDS < 5 are "Not Depressed"
		GDSSHORT

HVLT Immediate Recall	Sum of HVLTRT1 - HVLTRT3	HVLT
HVLT Discrimination Recognition	HVLTREC - (HVLTFPRL + HVLTFPUN)	HVLT
HVLT Retention	HVLTRDLY / max(HVLTRT2, HVLTRT3)	HVLT
Letter Number Sequencing (LNS)	Sum of LNS1A – LNS7C	LNSPD
MOCA Total Score	Unadjusted Score = sum of MCAALTTM, MCACUBE, MCACLCKC, MCACLCKN, MCACLCKH, MCALION, MCARHINO, MCACAMEL, MCAFDS, MCABDS, MCAVIGIL, MCASER7, MCASNTNC, MCAVF, MCAABSTR, MCAREC1, MCAREC2, MCAREC3, MCAREC4, MCAREC5, MCADATE, MCAMONTH, MCAYR, MCADAY, MCAPLACE, MCACITY If EDUCYRS ≤ 12 and Unadjusted Score < 30,	MOCA, SOCIOECO

	add 1 more point to score. If EDUCYRS > 12, do not add any more points to score.	

QUIP	For Sections A - D, add 1 point if <u>either</u> question has a response of "Yes" (1):
	   Section A: CNTRLGMB, TMGAMBLE
	   Section B: CNTRLSEX, TMSEX
	   Section C: CNTRLBUY, TMBUY
	   Section D: CNTRLEAT, TMEAT
	
	For Section E, add 1 point for <u>each</u> response of "Yes" (1):
	   TMTORACT, TMTMTACT, TMTRWD
		QUIPCS

REM Sleep Behavior Disorder (RBD)	Add 1 point for <u>each</u> response of "Yes" (1) to any of the following variables:
	   DRMVIVID, DRMAGRAC, DRMNOCTB,
	   SLPLMBMV, SLPINJUR, DRMVERBL,
	   DRMFIGHT, DRMUMV, DRMOBJFL,
	   MVAWAKEN, DRMREMEM, SLPDSTRB
	
	Add 1 point if <u>any</u> of the following variables has a response of "Yes" (1):
	   STROKE, HETRA, PARKISM, RLS,
	   NARCLPSY, DEPRS, EPILEPSY, BRNINFM,
	   CNSOTH
	
	If any of the previous variables are missing, then RBD score is missing.
	
	Subjects with score ≥ 5 are RBD Positive
	Subjects with score < 5 are RBD Negative
		REMSLEEP

SCOPA-AUT Total Score	SCAU1 - SCAU25 For questions 1-21 (SCAU1 - SCAU21), add 3 points for each response of "9." Otherwise, add the number of points in response. For questions 22-25 (SCAU22 - SCAU25), add 0 points for each response of "9." Otherwise, add the number of points in response.	SCOPA
Semantic Fluency (SFT)	Sum of VLTANIM, VLTVEG, VLTFRUIT	SFT

State Trait Anxiety Total Score (STAI)	STAIAD1 - STAIAD40 Add values for the following questions: 3, 4, 6, 7, 9, 12, 13, 14, 17, 18, 22, 24, 25, 28, 29, 31, 32, 35, 37, 38, 40 Use reverse scoring for the remaining questions and add to the first score (eg, if value = 1, add 4 points to score; if value = 2, add 3 points to score, etc).	STAI
STAI - State Subscore	STAIAD1 - STAIAD20 Add values for the following questions: 3, 4, 6, 7, 9, 12, 13, 14, 17, 18 Use reverse scoring for the values of the remaining questions through question 20 and add to the first value.	STAI
STAI - Trait Subscore	STAIAD21 - STAIAD40 Add values for the following questions: 22, 24, 25, 28, 29, 31, 32, 35, 37, 38, 40 Use reverse scoring for the values of the remaining questions and add to the first value.	STAI
UPSIT Raw Score	Sum of UPSITBK1 - UPSITBK4	UPSIT

Cognitive

Mild Cognitive Impairment (MCI)	COGDECLN, FNCDTCOG, DVT_TOTAL_RECALL, DVT_RECOG_DISC_INDEX, DVS_JLO_MSSAE, DVS_LNS, DVT_SFTANIM, DVT_SDM Subject has MCI if the following 3 criteria are met: 1) Cognitive decline marked as 'Yes' (COGDECLN = '1') 2) Any 2 or more of the following cognitive tests are >1.5 SD below the standardized mean: • HVLT Total Recall (DVT_TOTAL_RECALL <= 35) • HVLT Recognition Discrimination (DVT_RECOG_DISC_INDEX <= 35) • Benton Judgment of Line Orientation (DVS_JLO_MSSAE <= 6) • Letter Number Sequencing (DVS_LNS <= 6) • Semantic Fluency Test (DVT_SFTANIM <= 35) • Symbol Digit Modalities (DVT_SDM <= 35) 3) Functional impairment marked as 'No' (FNCDTCOG = '0').	COGCATG, HVLT, LINEORNT, LNSPD, SFT, SDM

DaTSCAN

Contralateral	For Healthy Controls, no contralateral side is identified. Instead, the average of the left and right values is calculated.
	
	For PD and SWEDD subjects:
	  Use Left value if DOMSIDE = '2' (Right)
	  Use Right value if DOMSIDE = '1' (Left)
	  Use the average of the left and right values if DOMSIDE = '3' (Symmetric)
		SBR, PDFEAT

Ipsilateral	For Healthy Controls, no ipsilateral side is identified. Instead, the average of the left and right values is calculated.
	
	For PD and SWEDD subjects:
	  Use Right value if DOMSIDE = '2' (Right)
	  Use Left value if DOMSIDE = '1' (Left)
	  Use the average of the left and right values if
		SBR, PDFEAT

	DOMSIDE = '3' (Symmetric)	
Mean Caudate	(CAUDATE_R + CAUDATE_L) / 2	SBR
Mean Putamen	(PUTAMEN_R + PUTAMEN_L) / 2	SBR
Mean Striatum	(CAUDATE_R + CAUDATE_L + PUTAMEN_R + PUTAMEN_L) / 4	SBR
Count Density Ratio	Caudate / Putamen	SBR, PDFEAT
Asymmetry Index	$\left\lvert \dfrac{left - right}{mean(left + right)} \times 100 \right\rvert$	SBR, PDFEAT

CSF

Note: In cases where multiple CSF results are available for the same visit, the statistical core uses the results with the earlier date (variable: RUNDATE).		
Abeta 1-42	TESTNAME, TESTVALUE Create a subset of observations that have TESTNAME = "Abeta 42". The value of Abeta 42 is the variable TESTVALUE.	BIOSPECAN
t-tau	TESTNAME, TESTVALUE Create a subset of observations that have TESTNAME = "Total tau". The value of Total Tau is the variable TESTVALUE.	BIOSPECAN
p-tau	TESTNAME, TESTVALUE Create a subset of observations that have TESTNAME = "p-Tau 181P". The value of p-Tau 181P is the variable TESTVALUE.	BIOSPECAN
Alpha-synuclein	TESTNAME, TESTVALUE Create a subset of observations that have TESTNAME = "CSF Alpha-synuclein". The value of CSF Alpha-synuclein is the variable TESTVALUE.	BIOSPECAN
t-tau/Abeta 1-42	"Total Tau" / "Abeta 42"	BIOSPECAN
p-tau/Abeta 1-42	"p-Tau 181P" / "Abeta 42"	BIOSPECAN

p-tau/t-tau	"p-Tau 191P" / "Total tau"	BIOSPECAN
CSF Hemoglobin	TESTNAME, TESTVALUE Create a subset of observations that have TESTNAME = "CSF Hemoglobin". The value of CSF Hemoglobin is the variable TESTVALUE.	BIOSPECAN

Biospecimen

Urate	LTSTNAME, LSIRES, LSIUNIT Create a subset of observations that have LTSTNAME = "Serum Uric Acid". The value of Urate is the variable LSIRES, and the units are the variable LSIUNIT.	COVANCE

Genetics

ApoE	TESTNAME, TESTVALUE Create a subset of observations that have TESTNAME = "APOE GENOTYPE" or "ApoE_Genotype". The genotype is the variable TESTVALUE.	BIOSPECAN
SNCA rs3910105	TESTNAME, TESTVALUE Create a subset of observations that have TESTNAME = "rs3910105". The genotype is the variable TESTVALUE.	BIOSPECAN
SNCA rs356181	TESTNAME, TESTVALUE Create a subset of observations that have TESTNAME = "rs356181". The genotype is the variable TESTVALUE.	BIOSPECAN
MAPT H1/H2	Extract the following 5 SNPs from the genetics data and count the number of minor alleles in each SNP: 　rs17652121, minor allele = C 　rs8070723, minor allele = G 　rs1052587, minor allele = C 　rs16940799, minor allele = C 　rs17652748, minor allele = T If the sum of minor alleles for all 5 SNPs is: • < 5, then genotype = H1/H1 • = 5, then genotype = H1/H2	NeuroX SNP Data

	• = 10, then genotype = H2/H2	

Levodopa Equivalent Daily Dose

Levodopa Equivalent Daily Dose (LEDD)	The variable LEDD shows the Levodopa equivalent daily dose for each individual PD medication. To find the total LEDD at a specific time point, add all values of the variable LEDD for each PD medication being taken at that time point. Anticholinergics and other medications that are not included in the calculation of the total LEDD will have a missing value for the variable LEDD. For COMT inhibitors, the variable LEDD will read "LD x 0.5" or "LD x 0.33". To find the LEDD for COMT inhibitors, first find the total dose of <u>Levodopa only</u>, and then multiply that value by either 0.5 or 0.33 as instructed. **Note: The variable LEDD is only updated quarterly, so this variable will not necessarily be up-to-date with the other data in the CONMED data file.**	CONMED

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