Parkinson's Progression Markers Initiative

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 Participants	ENROLL_DATE Find each unique PATNO that is not missing ENROLL_DATE	STATUS
Study Cohort	COHORT, CONCOHORT See ***PPMI Analytic Dataset Guide*** for more information on Consensus Cohorts (CONCOHORT).	STATUS

Demographics and PD Characteristics

Age at Enrollment	ENROLL_DATE - BIRTHDT	STATUS, SCREEN
Sex	SEX = 1 is Male SEX = 0 is Female	SCREEN
Race	RAINDALS, RAASIAN, RABLACK, RAHAWOPI, RAWHITE, RANOS Other = RAINDALS, RAHAWOPI, RANOS, or more than one race specified	SCREEN
Family History of PD	BIOMOMPD, BIODADPD, FULSIBPD, HAFSIBPD, MAGPARPD, PAGPARPD, MATAUPD, PATAUPD, KIDSPD, DISFAMPD, MATCOUSPD, PATCOUSPD Participant has <u>any</u> family history of PD if any one or more of the above variables = '1' Participant has <u>1st-degree</u> family history of PD if any one or more of the following variables = '1': BIOMOMPD, BIODADPD, FULSIBPD, HAFSIBPD, KIDSPD	FAMHXPD

Parkinson's Progression Markers Initiative

PD Duration	ENROLL_DATE - PDDXDT	STATUS, PDDXHIST
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 participant is TD. If ratio ≤ 0.9 then participant is PIGD. If ratio > 0.9 and < 1.15, OR if Tremor score and PIGD score = 0, then participant 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, NP3RIGRL, NP3RIGLL, NP3FTAPR, NP3FTAPL, NP3HMOVR, NP3HMOVL, NP3PRSPR, NP3PRSPL, NP3TTAPR, NP3TTAPL, NP3LGAGR, NP3LGAGL, NP3RISNG, NP3GAIT, NP3FRZGT, NP3PSTBL, NP3POSTR, NP3BRADY, NP3PTRMR, NP3PTRML,	NUPDRS3

Parkinson's Progression Markers Initiative

	NP3KTRMR, NP3KTRML, NP3RTARU, NP3RTALU, NP3RTARL, NP3RTALL, NP3RTALJ, NP3RTCON Part III Score = sum of these 33 variables	
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 (ESS)	Sum of ESS1 - ESS8 Participants with ESS < 10 are "Not Sleepy" Participants with ESS ≥ 10 are "Sleepy"	EPWORTH
Geriatric Depression Scale (GDS)	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 Participants with GDS ≥ 5 are "Depressed" Participants with GDS < 5 are "Not Depressed"	GDSSHORT
HVLT Immediate/Total Recall	Sum of HVLTRT1 - HVLTRT3	HVLT

Parkinson's Progression Markers Initiative

HVLT Recognition Discrimination	HVLTREC - (HVLTFPRL + HVLTFPUN)	HVLT
HVLT Retention	HVLTRDLY / max(HVLTRT2, HVLTRT3)	HVLT
Letter Number Sequencing (LNS)	Sum of LNS1A – LNS7C	LNSPD
MOCA Total Score (Education-adjusted)	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, add 1 point to score. If EDUCYRS > 12 or Unadjusted Score = 30, do not add any points to score.	MOCA, SOCIOECO
Questionnaire for Impulsive-Compulsive Disorders (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 Screening Questionnaire (RBDSQ)	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, RNINFM, CNSOTH	REMSLEEP

	If any of the previous variables are missing, then RBDSQ score is missing.	
SCOPA-AUT Total and Subscores	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. Subscores: Gastrointestinal = questions 1-7 Urinary = questions 8-13 Cardiovascular = questions 14-16 Thermoregulatory = questions 17, 18, 20, 21 Pupillomotor = question 19 Sexual dysfunction = questions 22, 23, 24, 25	SCOPAAUT
Semantic Fluency (SFT)	Sum of VLTANIM, VLTVEG, VLTFRUIT	SFT
State-Trait Anxiety Index (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 (e.g., if response = 1, add 4 points to score; if response = 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	STAI

	Use reverse scoring for the values of the remaining questions and add to the first value.	
UPSIT	Raw Score = Sum of SCENT_01_CORRECT – SCENT_40_CORRECT	UPSIT

Cognition

Test-based Mild Cognitive Impairment (MCI)	DVT_TOTAL_RECALL, DVT_RECOG_DISC_INDEX, DVS_JLO_MSSAE, DVS_LNS, DVT_SFTANIM, DVT_SDM Participant has MCI if 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)	HVLT, LINEORNT, LNSPD, SFT, SDM

DaTSCAN

Contralateral side	For Healthy Controls and Prodromal participants, no contralateral side is identified. Instead, the average of the left and right values is calculated. For PD and SWEDD participants: 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)	DaTScan Analysis, PDDXHIST
Ipsilateral side	For Healthy Controls and Prodromal participants, no ipsilateral side is identified. Instead, the average of the left and right values is calculated. For PD and SWEDD participants: Use Right value if DOMSIDE = '2' (Right) Use Left value if DOMSIDE = '1' (Left)	DaTScan Analysis, PDDXHIST

	Use the average of the left and right values if DOMSIDE = '3' (Symmetric)	
Mean Caudate	(DATSCAN_CAUDATE_R + DATSCAN_CAUDATE_L) / 2	DaTScan Analysis
Mean Putamen	(DATSCAN_PUTAMEN_R + DATSCAN_PUTAMEN_L) / 2	DaTScan Analysis
Mean Striatum	(DATSCAN_CAUDATE_R + DATSCAN_CAUDATE_L + DATSCAN_PUTAMEN_R + DATSCAN_PUTAMEN_L) / 4	DaTScan Analysis
Count Density Ratio	Caudate / Putamen	DaTScan Analysis, PDDXHIST
Asymmetry Index	$\left\lvert \frac{left-right}{mean(left+right)} \times 100 \right\rvert$	DaTScan Analysis, PDDXHIST

CSF Biomarkers

ABeta 1-42	PROJECTID, TESTNAME, TESTVALUE Create a subset of observations that have: PROJECTID = "159" and TESTNAME = "ABeta" PROJECTID = "125" and TESTNAME = "ABeta 1-42" The value of ABeta is the variable TESTVALUE. Any values at or below 200 should be treated as below the limit of detection. Any values at or above 1475.4 should be treated as above the limit of detection. In cases where both Project IDs have values for the same visit, use the mean of the two values.	Current Biospecimen Analysis Results
t-tau	PROJECTID, TESTNAME, TESTVALUE Create a subset of observations that have: PROJECTID = "159" and TESTNAME = "tTau" PROJECTID = "125" and TESTNAME = "tTau"	Current Biospecimen Analysis Results

	The value of t-tau is the variable TESTVALUE. Any values at or below 80 should be treated as below the limit of detection. In cases where both Project IDs have values for the same visit, use the mean of the two values.	
p-tau	PROJECTID, TESTNAME, TESTVALUE Create a subset of observations that have: PROJECTID = "159" and TESTNAME = "pTau" PROJECTID = "125" and TESTNAME = "pTau" The value of p-tau is the variable TESTVALUE. Any values at or below 8 should be treated as below the limit of detection. In cases where both Project IDs have values for the same visit, use the mean of the two values.	Current Biospecimen Analysis Results
Alpha-synuclein	PROJECTID, TESTNAME, TESTVALUE, RUNDATE Create a subset of observations that have PROJECTID = "124" and TESTNAME = "CSF Alpha-synuclein". The value of CSF Alpha-synuclein is the variable TESTVALUE. In cases where multiple results are available for the same visit, use the results with the most recent RUNDATE.	Current Biospecimen Analysis Results
Hemoglobin	PROJECTID, TESTNAME, TESTVALUE, RUNDATE Create a subset of observations that have PROJECTID = "134" and TESTNAME = "CSF Hemoglobin". The value of Hemoglobin is the variable TESTVALUE. In cases where multiple results are available for the same visit, use the results with the most recent RUNDATE.	Current Biospecimen Analysis Results

Biospecimens

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

Parkinson's Progression Markers Initiative

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 Total LEDD calculation 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 Levodopa only, then multiply that value by either 0.5 or 0.33 as instructed.	LEDDLOG

About the Authors

This document was prepared by Chelsea J. Caspell-Garcia, University of Iowa, Department of Biostatistics Clinical Trials Statistical and Data Management Center. For more information, please contact Chelsea J. Caspell-Garcia by e-mail at chelsea-caspell@uiowa.edu.