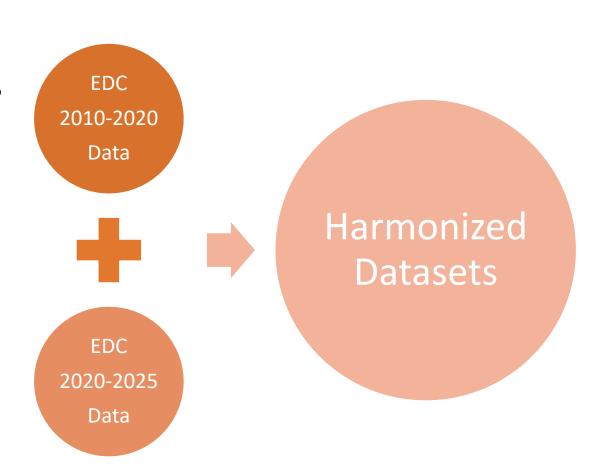
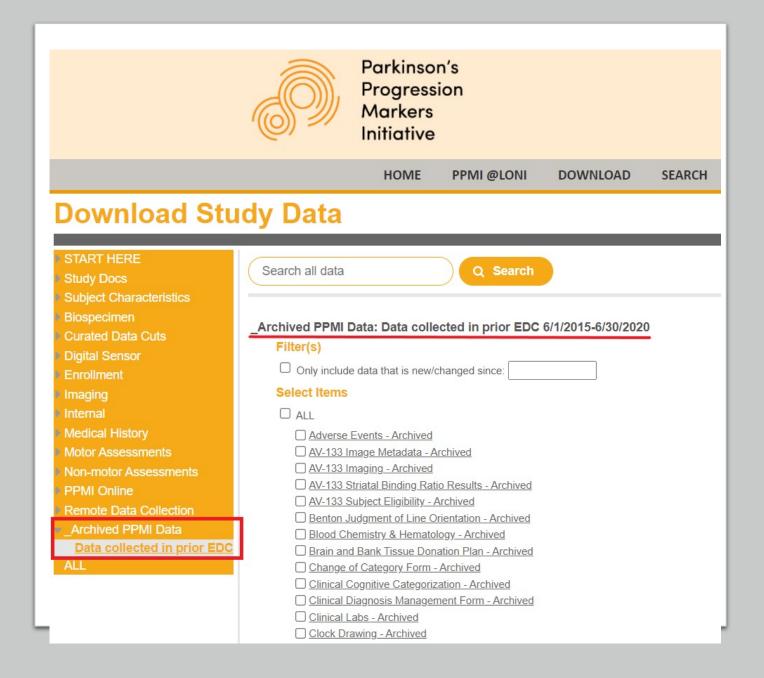
PPMI Expansion Introduction

- Data from the 2010-2020 and the current (2020+) Clinical EDCs have been harmonized
- These harmonized datasets are currently available to approved PPMI investigators
- An archival copy of the 2010— 2020 datasets have been moved to an Archived PPMI Data section



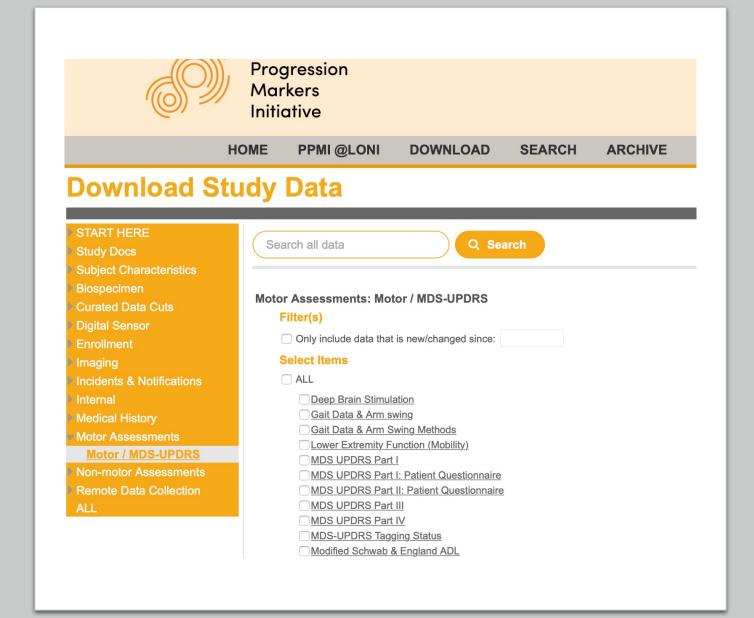
2010-2020 Data

- All 2010-2020 datasets were moved from their current locations and into a new section called 'Archived PPMI Data'
 - Static
 - Deprecated



2020+ Data

- The harmonized datasets inclusive of all data 2010 to current resides in the appropriate sections
 - Updated nightly/weekly
 - Aligned with harmonized data dictionary



Important Changes -Cohorts

- Genetic Cohort Unaffected participants have been transitioned to the Prodromal cohort
- Genetic Cohort PD participants have been transitioned into the PD cohort
- Records from Genetic Registry Unaffected and Genetic Registry PD cohorts are not part of the harmonized datasets

Important Changes -Variables and Codes

- Some variables from the 2010-2020 data have been renamed to be consistent with the new clinical EDC
- Some coded values from the 2010-2020 data have been mapped into new codes to be consistent with the new clinical EDC
- An annotated data dictionary and an annotated code book are available containing:
 - Previous variable name
 - Previous code
 - Mapping notes
- The annotated data dictionary and codebook should be consulted when transitioning existing analysis processes from old to current data

Quick Start

- If your processes relied on the APPRDX variable from the Screening dataset for identifying cohort, please use the COHORT variable in the Patient Status dataset instead
 - NOTE: COHORT coded values are consistent with previous APPRDX values
- The COHORT value represents the enrollment cohort for each participant and is the basis for the SOA
- An Analytic Dataset has been created that contains the consensus diagnosis for each participant
- It is recommended that the Analytic Dataset cohort be used for all analyses