Qualification Report for the {gsm} R Package

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Contents

1 Introduction

Risk-Based Quality Monitoring (RBQM) is a proactive approach to clinical trial monitoring that focuses on identifying and addressing the most critical risks to the integrity of study data and patient safety. This approach aims to ensure that study data are accurate, reliable, and credible while optimizing the use of resources and minimizing the burden on study sites.

The `{gsm}` R package supports RBQM by performing risk assessments primarily focused on detecting differences in quality at the site level. This approach is intended to detect potential issues related to critical data or process(es) across the major risk categories of safety, efficacy, disposition, treatment, and general quality. Each category consists of one or more risk assessment(s). Each risk assessment analyzes the data to flag sites with potential outliers and provides a visualization to help the user understand the issue.

2 Scope

Qualification testing ensures that core functions execute as expected on a system-wide scale. Qualification includes executing various functional, performance, and usability testing. Qualification tests are designed to provide developers with a repeatable process that is easy to update and document. This document summarizes the qualification testing performed on `{gsm}` functions essential to the analytics workflow.

3 Process Overview

Each essential `{gsm}` workflow function is independently qualified using specifications and test cases compiled in this report. Details are provided below.

3.1 Specifications

Specifications capture the most critical use cases for a given function. Each function must have at least one (1) specification, and each specification must have at least one (1) associated test case. Multiple specifications may exist for a function, and multiple test cases may exist for a specification.

Each specification includes the following components:

- **Description:** outlines the use case for the specification
- **Risk Assessment**
    - **Risk Level:** assigned a value of "Low", "Medium", or "High", corresponding to the risk associated with the specification failing
    - **Risk Impact:** assigned a value of "Low", "Medium", or "High", corresponding to the severity of the impact associated with the specification failing
- **Test Cases:** lists measurable test cases associated with the specification

3.2 Test Cases

Test cases translate specifications into testable scripts to confirm that the package functions meet the established requirements. Test cases represent how a user may utilize the function to help identify code gaps and support testing automation.

Test cases for `{gsm}` are written using the standard `testthat` workflow. A single test script is saved for each test case and is named following the convention `test_qual_{TestID}.R`, where `TestID` is the test case number. Test code within these scripts is written clearly and concisely to facilitate quick execution and interpretability. Note that a single test case may be associated with multiple specifications.

4 Test Results: Overview

Function Name	Number of Tests	Number Passed	Number Failed	Number Skipped
AE_Assess	12	12	0	0
AE_Map_Raw	4	4	0	0
Consent_Assess	3	3	0	0
DataChg_Assess	12	12	0	0
DataChg_Map_Raw	4	4	0	0
DataEntry_Assess	12	12	0	0
DataEntry_Map_Raw	4	4	0	0
Disp_Assess	12	12	0	0
Disp_Map_Raw	8	8	0	0
FilterDomain	2	2	0	0
Get_Enrolled	3	3	0	0
IE_Assess	3	3	0	0
LB_Assess	12	12	0	0
LB_Map_Raw	4	4	0	0
MergeSubjects	1	1	0	0
PD_Assess_Binary	12	12	0	0
PD_Assess_Rate	12	12	0	0
PD_Map_Raw_Binary	4	4	0	0
PD_Map_Raw_Rate	4	4	0	0
QueryAge_Assess	12	12	0	0
QueryAge_Map_Raw	4	4	0	0
QueryRate_Assess	12	12	0	0
QueryRate_Map_Raw	6	6	0	0
is_mapping_valid	9	9	0	0

5 Test Results: Detailed

5.1 One Row Per Specification

Spec ID	Spec Description	Risk	Impact	Associated Test IDs
S1_1	Given appropriate input data, an Adverse Event Assessment can be done using the Poisson method.	High	High	T1_1, T1_2, T1_3, T1_10
S1_2	Given appropriate input data, an Adverse Event Assessment can be done using the Identity method.	High	High	T1_4, T1_5, T1_6, T1_11
S1_3	Given appropriate input data, an Adverse Event Assessment can be done using the Normal Approximation method.	High	High	T1_7, T1_8, T1_9, T1_12
S1_4	Adverse Event Assessments can be done correctly using a grouping variable, such as Site or Country for KRIs, and Study for QTLs, when applicable.	Low	High	T1_1, T1_2, T1_3, T1_4, T1_5, T1_6, T1_7, T1_8, T1_9, T1_10, T1_11, T1_12
S1_5	Given appropriate input data, flag values can be correctly assigned to records that meet flagging criteria, including custom thresholding.	Medium	High	T1_1, T1_2, T1_3, T1_4, T1_5, T1_6, T1_7, T1_8, T1_9, T1_10, T1_11, T1_12
S1_6	Given an appropriate subset of input data, an Adverse Event Assessment can be done.	Medium	Medium	T1_1, T1_2, T1_4, T1_5, T1_7, T1_8

Spec ID	Spec Description	Risk	Impact	Associated Test IDs
S1_7	Given appropriate input data, flag values are correctly assigned as NA for sites with low enrollment.			T1_10, T1_11, T1_12
S2_1	Given appropriate input data, a Protocol Deviation Assessment can be done using the Poisson method.	High	High	T2_1, T2_2, T2_3, T2_10
S2_2	Given appropriate input data, a Protocol Deviation Assessment can be done using the Identity method.	High	High	T2_4, T2_5, T2_6, T2_11
S2_3	Given appropriate input data, a Protocol Deviation Assessment can be done using the Normal Approximation method.	High	High	T2_7, T2_8, T2_9, T2_12
S2_4	Protocol Deviation Assessments can be done correctly using a grouping variable, such as Site or Country for KRIs, and Study for QTLs, when applicable.	Low	High	T2_1, T2_2, T2_3, T2_4, T2_5, T2_6, T2_7, T2_8, T2_9, T2_10, T2_11, T2_12
S2_5	Given appropriate input data, flag values can be correctly assigned to records that meet flagging criteria, including custom thresholding.	Medium	High	T2_1, T2_2, T2_3, T2_4, T2_5, T2_6, T2_7, T2_8, T2_9, T2_10, T2_11, T2_12
S2_6	Given an appropriate subset of input data, a Protocol Deviation Assessment can be done.	Medium	Medium	T2_1, T2_2, T2_4, T2_5, T2_7, T2_8
S2_7	Given appropriate input data, flag values are correctly assigned as NA for sites with low enrollment.			T2_10, T2_11, T2_12
S3_1	Given appropriate input data, an Inclusion/Exclusion Criteria Assessment can be done using the Identity method.	High	High	T3_1, T3_2, T3_3
S3_2	Inclusion/Exclusion Criteria Assessments can be done correctly using a grouping variable, such as Site or Country for KRIs, and Study for QTLs, when applicable.	Low	High	T3_1, T3_2, T3_3
S3_3	Given appropriate input data, flag values can be correctly assigned to records that meet flagging criteria, including custom thresholding.	Medium	High	T3_1, T3_2, T3_3
S3_4	Given an appropriate subset of input data, an Inclusion/Exclusion Criteria Assessment can be done.	Medium	Medium	T3_2
S4_1	Given appropriate input data, a Consent Assessment can be done using the Identity method.	High	High	T4_1, T4_2, T4_3
S4_2	Consent Assessments can be done correctly using a grouping variable, such as Site or Country for KRIs, and Study for QTLs, when applicable.	Low	High	T4_1, T4_2, T4_3
S4_3	Given appropriate input data, flag values can be correctly assigned to records that meet flagging criteria, including custom thresholding.	Medium	High	T4_1, T4_2, T4_3
S4_4	Given an appropriate subset of input data, a Consent Assessment can be done.	Medium	Medium	T4_1, T4_2

Spec ID	Spec Description	Risk	Impact	Associated Test IDs
S5_1	Given appropriate input data, a Disposition Assessment can be done using the Fisher method.	High	High	T5_1, T5_2, T5_3, T5_10
S5_2	Given appropriate input data, a Disposition Assessment can be done using the Identity method.	High	High	T5_4, T5_5, T5_6, T5_11
S5_3	Given appropriate input data, a Dispositon Assessment can be done using the Normal Approximation method.	High	High	T5_7, T5_8, T5_9, T5_12
S5_4	Disposition Assessments can be done correctly using a grouping variable, such as Site or Country for KRIs, and Study for QTLs, when applicable.	Low	High	T5_1, T5_2, T5_3, T5_4, T5_5, T5_6, T5_7, T5_8, T5_9, T5_10, T5_11, T5_12
S5_5	Given appropriate input data, flag values can be correctly assigned to records that meet flagging criteria, including custom thresholding.	Medium	High	T5_1, T5_2, T5_3, T5_4, T5_5, T5_6, T5_7, T5_8, T5_9, T5_10, T5_11, T5_12
S5_6	Given an appropriate subset of input data, a Disposition Assessment can be done.	Medium	Medium	T5_1, T5_2, T5_4, T5_5, T5_7, T5_8
S5_7	Given appropriate input data, flag values are correctly assigned as NA for sites with low enrollment.			T5_10, T5_11, T5_12
S6_1	Given appropriate input data, a Labs Assessment can be done using the Fisher method.	High	High	T6_1, T6_2, T6_3, T6_9
S6_2	Given appropriate input data, a Labs Assessment can be done using the Identity method.	High	High	T6_4, T6_5, T6_6, T6_10
S6_3	Given appropriate input data, a Labs Assessment can be done using the Normal Approximation method.	High	High	T6_7, T6_8, T6_9, T6_11
S6_4	Labs Assessments can be done correctly using a grouping variable, such as Site or Country for KRIs, and Study for QTLs, when applicable.	Low	High	T6_1, T6_2, T6_3, T6_4, T6_5, T6_6, T6_7, T6_8, T6_9, T6_10, T6_11, T6_12
S6_5	Given appropriate input data, flag values can be correctly assigned to records that meet flagging criteria, including custom thresholding.	Medium	High	T6_1, T6_2, T6_3, T6_4, T6_5, T6_6, T6_7, T6_8, T6_9, T6_10, T6_11, T6_12
S6_6	Given an appropriate subset of input data, a Labs Assessment can be done.	Medium	Medium	T6_1, T6_2, T6_4, T6_5, T6_7, T6_8
S6_7	Given appropriate input data, flag values are correctly assigned as NA for sites with low enrollment.			T6_10, T6_11, T6_12
S7_1	Given appropriate input data, a Data Change Rate Assessment can be done using the Identity method.	High	High	T7_4, T7_5, T7_6, T7_11
S7_2	Given appropriate input data, a Data Change Rate Assessment can be done using the Fisher method.	High	High	T7_1, T7_2, T7_3, T7_10
S7_3	Given appropriate input data, a Data Change Rate Assessment can be done using the Normal Approximation method.	High	High	T7_7, T7_8, T7_9, T7_12

Spec ID	Spec Description	Risk	Impact	Associated Test IDs
S7_4	Data Change Rate Assessments can be done correctly using a grouping variable, such as Site, Country, or Study, when applicable.	Low	High	T7_1, T7_2, T7_3, T7_4, T7_5, T7_6, T7_7, T7_8, T7_9, T7_10, T7_11, T7_12
S7_5	Given appropriate input data, flag values can be correctly assigned to records that meet flagging criteria, including custom thresholding.	Medium	High	T7_1, T7_2, T7_3, T7_4, T7_5, T7_6, T7_7, T7_8, T7_9, T7_10, T7_11, T7_12
S7_6	Given an appropriate subset of input data, a Data Change Rate Assessment can be done.	Medium	Medium	T7_1, T7_2, T7_4, T7_5, T7_7, T7_8
S7_7	Given appropriate input data, flag values are correctly assigned as NA for sites with low enrollment.			T7_10, T7_11, T7_12
S8_1	Given appropriate input data, a Data Entry Lag Assessment can be done using the Fisher method.	High	High	T8_1, T8_2, T8_3, T8_10
S8_2	Given appropriate input data, a Data Entry Lag Assessment can be done using the Identity method.	High	High	T8_4, T8_5, T8_6, T8_11
S8_3	Given appropriate input data, a Data Entry Lag Assessment can be done using the Normal Approximation method.	High	High	T8_7, T8_8, T8_9, T8_12
S8_4	Data Entry Lag Assessments can be done correctly using a grouping variable, such as Site, Country, or Study, when applicable.	Low	High	T8_1, T8_2, T8_3, T8_4, T8_5, T8_6, T8_7, T8_8, T8_9, T8_10, T8_11, T8_12
S8_5	Given appropriate input data, flag values can be correctly assigned to records that meet flagging criteria, including custom thresholding.	Medium	High	T8_1, T8_2, T8_3, T8_4, T8_5, T8_6, T8_7, T8_8, T8_9, T8_10, T8_11, T8_12
S8_6	Given an appropriate subset of input data, a Data Entry Lag Assessment can be done.	Medium	Medium	T8_1, T8_2, T8_4, T8_5, T8_7, T8_8
S8_7	Given appropriate input data, flag values are correctly assigned as NA for sites with low enrollment.			T8_10, T8_11, T8_12
S9_1	Given appropriate input data, a Query Age Assessment can be done using the Fisher method.	High	High	T9_1, T9_2, T9_3, T9_10
S9_2	Given appropriate input data, a Query Age Assessment can be done using the Identity method.	High	High	T9_4, T9_5, T9_6, T9_11
S9_3	Given appropriate input data, a Query Age Assessment can be done using the Normal Approximation method.	High	High	T9_7, T9_8, T9_9, T9_12
S9_4	Query Age Assessments can be done correctly using a grouping variable, such as Site, Country, or Study, when applicable.	Low	High	T9_1, T9_2, T9_3, T9_4, T9_5, T9_6, T9_7, T9_8, T9_9, T9_10, T9_11, T9_12
S9_5	Given appropriate input data, flag values can be correctly assigned to records that meet flagging criteria, including custom thresholding.	Medium	High	T9_1, T9_2, T9_3, T9_4, T9_5, T9_6, T9_7, T9_8, T9_9, T9_10, T9_11, T9_12
S9_6	Given an appropriate subset of input data, a Query Age Assessment can be done.	Medium	Medium	T9_1, T9_2, T9_4, T9_5, T9_7, T9_8

Spec ID	Spec Description	Risk	Impact	Associated Test IDs
S9_7	Given appropriate input data, flag values are correctly assigned as NA for sites with low enrollment.			T9_10, T9_11, T9_12
S10_1	Given appropriate input data, a Query Rate Assessment can be done using the Poisson method.	High	High	T10_1, T10_2, T10_3, T10_10
S10_2	Given appropriate input data, a Query Rate Assessment can be done using the Identity method.	High	High	T10_4, T10_5, T10_6, T10_11
S10_3	Given appropriate input data, a Query Rate Assessment can be done using the Normal Approximation method.	High	High	T10_7, T10_8, T10_9, T10_12
S10_4	Query Rate Assessments can be done correctly using a grouping variable, such as Site, Country, or Study, when applicable.	Low	High	T10_1, T10_2, T10_3, T10_4, T10_5, T10_6, T10_7, T10_8, T10_9, T10_10, T10_11, T10_12
S10_5	Given appropriate input data, flag values can be correctly assigned to records that meet flagging criteria, including custom thresholding.	Medium	High	T10_1, T10_2, T10_3, T10_4, T10_5, T10_6, T10_7, T10_8, T10_9, T10_10, T10_11, T10_12
S10_6	Given an appropriate subset of input data, a Query Rate Assessment can be done.	Medium	Medium	T10_1, T10_2, T10_4, T10_5, T10_7, T10_8
S10_7	Given appropriate input data, flag values are correctly assigned as NA for sites with low enrollment.			T10_10, T10_11, T10_12
S11_1	Given appropriate metadata, the raw data for an Adverse Event Assessment can be correctly mapped to an analysis-ready input dataset.	Medium	High	T11_1, T11_2, T11_3, T11_4
S12_1	Given appropriate metadata, the raw data for a Data Change Rate Assessment can be correctly mapped to an analysis-ready input dataset.	Medium	High	T12_1, T12_2, T12_3, T12_4
S13_1	Given appropriate metadata, the raw data for a Data Entry Lag Assessment can be correctly mapped to an analysis-ready input dataset.	Medium	High	T13_1, T13_2, T13_3, T13_4
S14_1	Given appropriate metadata, the raw data for a Disposition Assessment can be correctly mapped to an analysis-ready input dataset.	Medium	High	T14_1, T14_2, T14_3, T14_4, T14_5, T14_6, T14_7, T14_8
S15_1	Given appropriate metadata, the raw data for a Labs Assessment can be correctly mapped to an analysis-ready input dataset.	Medium	High	T15_1, T15_2, T15_3, T15_4
S16_1	Given appropriate metadata, the raw data for a Protocol Deviation Assessment can be correctly mapped to an analysis-ready input dataset.	Medium	High	T16_1, T16_2, T16_3, T16_4
S17_1	Given appropriate metadata, the raw data for a Query Age Assessment can be correctly mapped to an analysis-ready input dataset.	Medium	High	T17_1, T17_2, T17_3, T17_4

Spec ID	Spec Description	Risk	Impact	Associated Test IDs
S18_1	Given appropriate metadata, the raw data for a Query Rate Assessment can be correctly mapped to an analysis-ready input dataset.	Medium	High	T18_1, T18_2, T18_3, T18_4, T18_5, T18_6
S19_1	Input data can be correctly filtered on a specified key variable and key variable value.	Low	Medium	T19_1, T19_2
S20_1	Given appropriate input data and metadata, the correct number of enrolled participants per study can be derived.	Low	High	T20_1
S20_2	Given appropriate input data and metadata, the correct number of sites per study can be derived.	Low	High	T20_2
S20_3	Given appropriate input data and metadata, the correct number of enrolled participants per site can be derived.	Low	High	T20_3
S21_1	Given appropriate input data and key variable, domain-level data can be correctly merged with subject-level data.	Low	High	T21_1
S22_1	The structure of the input data can be correctly evaluated for validity of use in downstream assessment and workflow functions.	Low	Medium	T22_1, T22_2
S22_2	The structure of the mapping(s) can be correctly evaluated for validity of use in downstream assessment and workflow functions.	Low	Medium	T22_3, T22_4, T22_5
S22_3	The structure of the parameter specifications can be correctly evaluated for validity of use in downstream assessment and workflow functions.	Low	Medium	T22_5, T22_6, T22_7, T22_8, T22_9
S23_1	Given appropriate input data, a Protocol Deviation Assessment can be done using the Poisson method.	High	High	T23_1, T23_2, T23_3, T23_10
S23_2	Given appropriate input data, a Protocol Deviation Assessment can be done using the Identity method.	High	High	T23_4, T23_5, T23_6, T23_11
S23_3	Given appropriate input data, a Protocol Deviation Assessment can be done using the Normal Approximation method.	High	High	T23_7, T23_8, T23_9, T23_12
S23_4	Protocol Deviation Assessments can be done correctly using a grouping variable, such as Site or Country for KRIs, and Study for QTLs, when applicable.	Low	High	T23_1, T23_2, T23_3, T23_4, T23_5, T23_6, T23_7, T23_8, T23_9, T23_10, T23_11, T23_12
S23_5	Given appropriate input data, flag values can be correctly assigned to records that meet flagging criteria, including custom thresholding.	Medium	High	T23_1, T23_2, T23_3, T23_4, T23_5, T23_6, T23_7, T23_8, T23_9, T23_10, T23_11, T23_12
S23_6	Given an appropriate subset of input data, a Protocol Deviation Assessment can be done.	Medium	Medium	T23_1, T23_2, T23_4, T23_5, T23_7, T23_8
S23_7	Given appropriate input data, flag values are correctly assigned as NA for sites with low enrollment.			T23_10, T23_11, T23_12

(continued)

Spec ID	Spec Description	Risk	Impact	Associated Test IDs
S24_1	Given appropriate metadata, the raw data for a Protocol Deviation Assessment can be correctly mapped to an analysis-ready input dataset.	Medium	High	T24_1, T24_2, T24_3, T24_4

5.2 One Row Per Test

Function	Spec ID	Test ID	Test Description	Test Result
AE_Assess	S1_1, S1_4, S1_5, S1_6	T1_1	Given an appropriate subset of Adverse Event data, the assessment function correctly performs an Adverse Event Assessment grouped by the Site variable using the Poisson method and correctly assigns Flag variable values when given a custom threshold.	Pass
AE_Assess	S1_1, S1_4, S1_5, S1_6	T1_2	Given an appropriate subset of Adverse Event data, the assessment function correctly performs an Adverse Event Assessment grouped by the Study variable using the Poisson method and correctly assigns Flag variable values.	Pass
AE_Assess	S1_1, S1_4, S1_5	T1_3	Given appropriate Adverse Event data, the assessment function correctly performs an Adverse Event Assessment grouped by a custom variable using the Poisson method and correctly assigns Flag variable values.	Pass
AE_Assess	S1_2, S1_4, S1_5, S1_6	T1_4	Given an appropriate subset of Adverse Event data, the assessment function correctly performs an Adverse Event Assessment grouped by the Site variable using the Identity method and correctly assigns Flag variable values when given a custom threshold.	Pass
AE_Assess	S1_2, S1_4, S1_5, S1_6	T1_5	Given an appropriate subset of Adverse Event data, the assessment function correctly performs an Adverse Event Assessment grouped by the Study variable using the Identity method and correctly assigns Flag variable values.	Pass
AE_Assess	S1_2, S1_4, S1_5	T1_6	Given appropriate Adverse Event data, the assessment function correctly performs an Adverse Event Assessment grouped by a custom variable using the Identity method and correctly assigns Flag variable values.	Pass
AE_Assess	S1_3, S1_4, S1_5, S1_6	T1_7	Given an appropriate subset of Adverse Event data, the assessment function correctly performs an Adverse Event Assessment grouped by the Site variable using the Normal Approximation method and correctly assigns Flag variable values when given a custom threshold.	Pass
AE_Assess	S1_3, S1_4, S1_5, S1_6	T1_8	Given an appropriate subset of Adverse Event data, the assessment function correctly performs an Adverse Event Assessment grouped by the Study variable using the Normal Approximation method and correctly assigns Flag variable values.	Pass
AE_Assess	S1_3, S1_4, S1_5	T1_9	Given appropriate Adverse Event data, the assessment function correctly performs an Adverse Event Assessment grouped by a custom variable using the Normal Approximation method and correctly assigns Flag variable values.	Pass

Function	Spec ID	Test ID	Test Description	Test Result
AE_Assess	S1_1, S1_4, S1_5, S1_7	T1_10	Given appropriate Adverse Event data, the assessment function correctly performs an Adverse Event Assessment grouped by the Site variable using the Poisson method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass
AE_Assess	S1_2, S1_4, S1_5, S1_7	T1_11	Given appropriate Adverse Event data, the assessment function correctly performs an Adverse Event Assessment grouped by the Site variable using the Identity method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass
AE_Assess	S1_3, S1_4, S1_5, S1_7	T1_12	Given appropriate Adverse Event data, the assessment function correctly performs an Adverse Event Assessment grouped by the Site variable using the Normal Approximation method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass
PD_Assess_Rate	S2_1, S2_4, S2_5, S2_6	T2_1	Given an appropriate subset of Protocol Deviation data, the assessment function correctly performs a Protocol Deviation Assessment grouped by the Site variable using the Poisson method and correctly assigns Flag variable values when given a custom threshold.	Pass
PD_Assess_Rate	S2_1, S2_4, S2_5, S2_6	T2_2	Given an appropriate subset of Protocol Deviation data, the assessment function correctly performs a Protocol Deviation Assessment grouped by the Study variable using the Poisson method and correctly assigns Flag variable values.	Pass
PD_Assess_Rate	S2_1, S2_4, S2_5	T2_3	Given appropriate Protocol Deviation data, the assessment function correctly performs a Protocol Deviation Assessment grouped by a custom variable using the Poisson method and correctly assigns Flag variable values.	Pass
PD_Assess_Rate	S2_2, S2_4, S2_5, S2_6	T2_4	Given an appropriate subset of Protocol Deviation data, the assessment function correctly performs a Protocol Deviation Assessment grouped by the Site variable using the Identity method and correctly assigns Flag variable values when given a custom threshold.	Pass

Function	Spec ID	Test ID	Test Description	Test Result
PD_Assess_Rate	S2_2, S2_4, S2_5, S2_6	T2_5	Given an appropriate subset of Protocol Deviation data, the assessment function correctly performs a Protocol Deviation Assessment grouped by a custom variable using the Identity method and correctly assigns Flag variable values.	Pass
PD_Assess_Rate	S2_2, S2_4, S2_5	T2_6	Given appropriate Protocol Deviation data, the assessment function correctly performs a Protocol Deviation Assessment grouped by the Site variable using the Identity method and correctly assigns Flag variable values.	Pass
PD_Assess_Rate	S2_3, S2_4, S2_5, S2_6	T2_7	Given an appropriate subset of Protocol Deviation data, the assessment function correctly performs a Protocol Deviation Assessment grouped by the Site variable using the Normal Approximation method and correctly assigns Flag variable values when given a custom threshold.	Pass
PD_Assess_Rate	S2_3, S2_4, S2_5, S2_6	T2_8	Given an appropriate subset of Protocol Deviation data, the assessment function correctly performs a Protocol Deviation Assessment grouped by the Study variable using the Normal Approximation method and correctly assigns Flag variable values.	Pass
PD_Assess_Rate	S2_3, S2_4, S2_5	T2_9	Given appropriate Protocol Deviation data, the assessment function correctly performs a Protocol Deviation Assessment grouped by a custom variable using the Normal Approximation method and correctly assigns Flag variable values.	Pass
PD_Assess_Rate	S2_1, S2_4, S2_5, S2_7	T2_10	Given appropriate Protocol Deviation data, the assessment function correctly performs a Protocol Deviation Assessment grouped by the Site variable using the Poisson method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass
PD_Assess_Rate	S2_2, S2_4, S2_5, S2_7	T2_11	Given appropriate Protocol Deviation data, the assessment function correctly performs a Protocol Deviation Assessment grouped by the Site variable using the Identity method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass
PD_Assess_Rate	S2_3, S2_4, S2_5, S2_7	T2_12	Given appropriate Protocol Deviation data, the assessment function correctly performs a Protocol Deviation Assessment grouped by the Site variable using the Normal Approximation method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass

Function	Spec ID	Test ID	Test Description	Test Result
IE_Assess	S3_1, S3_2, S3_3	T3_1	Given appropriate Inclusion/Exclusion data, the assessment function correctly performs an Inclusion/Exclusion Assessment grouped by the Site variable using the Identity method and correctly assigns Flag variable values.	Pass
IE_Assess	S3_1, S3_2, S3_3, S3_4	T3_2	Given an appropriate subset of Inclusion/Exclusion data, the assessment function correctly performs an Inclusion/Exclusion Assessment grouped by the Study variable using the Identity method and correctly assigns Flag variable values when given a custom threshold.	Pass
IE_Assess	S3_1, S3_2, S3_3	T3_3	Given appropriate Inclusion/Exclusion data, the assessment function correctly performs an Inclusion/Exclusion Assessment grouped by a custom variable using the Identity method and correctly assigns Flag variable values.	Pass
Consent_Assess	S4_1, S4_2, S4_3, S4_4	T4_1	Given an appropriate subset of Consent data, the assessment function correctly performs a Consent Assessment grouped by the Site variable using the Identity method and correctly assigns Flag variable values.	Pass
Consent_Assess	S4_1, S4_2, S4_3, S4_4	T4_2	Given an appropriate subset of Consent data, the assessment function correctly performs a Consent Assessment grouped by the Study variable using the Identity method and correctly assigns Flag variable values when given a custom threshold.	Pass
Consent_Assess	S4_1, S4_2, S4_3	T4_3	Given appropriate Consent data, the assessment function correctly performs a Consent Assessment grouped by a custom variable using the Identity method and correctly assigns Flag variable values.	Pass
Disp_Assess	S5_1, S5_4, S5_5, S5_6	T5_1	Given an appropriate subset of Disposition data, the assessment function correctly performs a Disposition Assessment grouped by the Site variable using the Fisher method and correctly assigns Flag variable values when given a custom threshold.	Pass
Disp_Assess	S5_1, S5_4, S5_5, S5_6	T5_2	Given an appropriate subset of Disposition data, the assessment function correctly performs a Disposition Assessment grouped by the Country variable using the Fisher method and correctly assigns Flag variable values.	Pass
Disp_Assess	S5_1, S5_4, S5_5	T5_3	Given appropriate Disposition data, the assessment function correctly performs a Disposition Assessment grouped by a custom variable using the Fisher method and correctly assigns Flag variable values.	Pass

Function	Spec ID	Test ID	Test Description	Test Result
Disp_Assess	S5_2, S5_4, S5_5, S5_6	T5_4	Given an appropriate subset of Disposition data, the assessment function correctly performs a Disposition Assessment grouped by the Site variable using the Identity method and correctly assigns Flag variable values when given a custom threshold.	Pass
Disp_Assess	S5_2, S5_4, S5_5, S5_6	T5_5	Given an appropriate subset of Disposition data, the assessment function correctly performs a Disposition Assessment grouped by the Study variable using the Identity method and correctly assigns Flag variable values.	Pass
Disp_Assess	S5_2, S5_4, S5_5	T5_6	Given appropriate Disposition data, the assessment function correctly performs a Disposition Assessment grouped by a custom variable using the Identity method and correctly assigns Flag variable values.	Pass
Disp_Assess	S5_3, S5_4, S5_5, S5_6	T5_7	Given an appropriate subset of Disposition data, the assessment function correctly performs a Disposition Assessment grouped by the Site variable using the Normal Approximation method and correctly assigns Flag variable values when given a custom threshold.	Pass
Disp_Assess	S5_3, S5_4, S5_5, S5_6	T5_8	Given an appropriate subset of Disposition data, the assessment function correctly performs a Disposition Assessment grouped by the Study variable using the Normal Approximation method and correctly assigns Flag variable values.	Pass
Disp_Assess	S5_3, S5_4, S5_5	T5_9	Given appropriate Disposition data, the assessment function correctly performs a Disposition Assessment grouped by a custom variable using the Normal Approximation method and correctly assigns Flag variable values.	Pass
Disp_Assess	S5_1, S5_4, S5_5, S5_7	T5_10	Given appropriate Disposition data, the assessment function correctly performs a Disposition Assessment grouped by the Site variable using the Fisher method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass
Disp_Assess	S5_2, S5_4, S5_5, S5_7	T5_11	Given appropriate Disposition data, the assessment function correctly performs a Disposition Assessment grouped by the Site variable using the Identity method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass

(continued)

Function	Spec ID	Test ID	Test Description	Test Result
Disp_Assess	S5_3, S5_4, S5_5, S5_7	T5_12	Given appropriate Disposition data, the assessment function correctly performs a Disposition Assessment grouped by the Site variable using the Normal Approximation method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass
LB_Assess	S6_1, S6_4, S6_5, S6_6	T6_1	Given an appropriate subset of Labs data, the assessment function correctly performs a Labs Assessment grouped by the Site variable using the Fisher method and correctly assigns Flag variable values when given a custom threshold.	Pass
LB_Assess	S6_1, S6_4, S6_5, S6_6	T6_2	Given an appropriate subset of Labs data, the assessment function correctly performs a Labs Assessment grouped by the Country variable using the Fisher method and correctly assigns Flag variable values.	Pass
LB_Assess	S6_1, S6_4, S6_5	T6_3	Given appropriate Labs data, the assessment function correctly performs a Labs Assessment grouped by a custom variable using the Fisher method and correctly assigns Flag variable values.	Pass
LB_Assess	S6_2, S6_4, S6_5, S6_6	T6_4	Given an appropriate subset of Labs data, the assessment function correctly performs a Labs Assessment grouped by the Site variable using the Identity method and correctly assigns Flag variable values when given a custom threshold.	Pass
LB_Assess	S6_2, S6_4, S6_5, S6_6	T6_5	Given an appropriate subset of Labs data, the assessment function correctly performs a Labs Assessment grouped by the Study variable using the Identity method and correctly assigns Flag variable values.	Pass
LB_Assess	S6_2, S6_4, S6_5	T6_6	Given appropriate Labs data, the assessment function correctly performs a Labs Assessment grouped by a custom variable using the Identity method and correctly assigns Flag variable values.	Pass
LB_Assess	S6_3, S6_4, S6_5, S6_6	T6_7	Given an appropriate subset of Labs data, the assessment function correctly performs a Labs Assessment grouped by the Site variable using the Normal Approximation method and correctly assigns Flag variable values when given a custom threshold.	Pass
LB_Assess	S6_3, S6_4, S6_5, S6_6	T6_8	Given an appropriate subset of Labs data, the assessment function correctly performs a Labs Assessment grouped by the Study variable using the Normal Approximation method and correctly assigns Flag variable values.	Pass

(continued)

Function	Spec ID	Test ID	Test Description	Test Result
LB_Assess	S6_1, S6_3, S6_4, S6_5	T6_9	Given appropriate Labs data, the assessment function correctly performs a Labs Assessment grouped by a custom variable using the Normal Approximation method and correctly assigns Flag variable values.	Pass
LB_Assess	S6_2, S6_4, S6_5, S6_7	T6_10	Given appropriate Labs data, the assessment function correctly performs a Labs Assessment grouped by the Site variable using the Fisher method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass
LB_Assess	S6_3, S6_4, S6_5, S6_7	T6_11	Given appropriate Labs data, the assessment function correctly performs a Labs Assessment grouped by the Site variable using the Identity method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass
LB_Assess	S6_4, S6_5, S6_7	T6_12	Given appropriate Labs data, the assessment function correctly performs a Labs Assessment grouped by the Site variable using the Normal Approximation method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass
DataChg_Assess	S7_2, S7_4, S7_5, S7_6	T7_1	Given an appropriate subset of Data Change Rate data, the assessment function correctly performs a Data Change Rate Assessment grouped by the Site variable using the Fisher method and correctly assigns Flag variable values when given a custom threshold.	Pass
DataChg_Assess	S7_2, S7_4, S7_5, S7_6	T7_2	Given an appropriate subset of Data Change Rate data, the assessment function correctly performs a Data Change Rate Assessment grouped by the Country variable using the Fisher method and correctly assigns Flag variable values.	Pass
DataChg_Assess	S7_2, S7_4, S7_5	T7_3	Given appropriate Data Change Rate data, the assessment function correctly performs a Data Change Rate Assessment grouped by a custom variable using the Fisher method and correctly assigns Flag variable values.	Pass

Function	Spec ID	Test ID	Test Description	Test Result
DataChg_Assess	S7_1, S7_4, S7_5, S7_6	T7_4	Given an appropriate subset of Data Change Rate data, the assessment function correctly performs a Data Change Rate Assessment grouped by the Site variable using the Identity method and correctly assigns Flag variable values when given a custom threshold.	Pass
DataChg_Assess	S7_1, S7_4, S7_5, S7_6	T7_5	Given an appropriate subset of Data Change Rate data, the assessment function correctly performs a Data Change Rate Assessment grouped by the Study variable using the Identity method and correctly assigns Flag variable values.	Pass
DataChg_Assess	S7_1, S7_4, S7_5	T7_6	Given appropriate Data Change Rate data, the assessment function correctly performs a Data Change Rate Assessment grouped by a custom variable using the Identity method and correctly assigns Flag variable values.	Pass
DataChg_Assess	S7_3, S7_4, S7_5, S7_6	T7_7	Given an appropriate subset of Data Change Rate data, the assessment function correctly performs a Data Change Rate Assessment grouped by the Site variable using the Normal Approximation method and correctly assigns Flag variable values when given a custom threshold.	Pass
DataChg_Assess	S7_3, S7_4, S7_5, S7_6	T7_8	Given an appropriate subset of Data Change Rate data, the assessment function correctly performs a Data Change Rate Assessment grouped by the Study variable using the Normal Approximation method and correctly assigns Flag variable values.	Pass
DataChg_Assess	S7_3, S7_4, S7_5	T7_9	Given appropriate Data Change Rate data, the assessment function correctly performs a Data Change Rate Assessment grouped by a custom variable using the Normal Approximation method and correctly assigns Flag variable values.	Pass
DataChg_Assess	S7_2, S7_4, S7_5, S7_7	T7_10	Given appropriate Data Change Rate data, the assessment function correctly performs a Data Change Rate Assessment grouped by the Site variable using the Fisher method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass
DataChg_Assess	S7_1, S7_4, S7_5, S7_7	T7_11	Given appropriate Data Change Rate data, the assessment function correctly performs a Data Change Rate Assessment grouped by the Site variable using the Identity method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass

Function	Spec ID	Test ID	Test Description	Test Result
DataChg_Assess	S7_3, S7_4, S7_5, S7_7	T7_12	Given appropriate Data Change Rate data, the assessment function correctly performs a Data Change Rate Assessment grouped by the Site variable using the Normal Approximation method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass
DataEntry_Assess	S8_1, S8_4, S8_5, S8_6	T8_1	Given an appropriate subset of Data Entry Lag data, the assessment function correctly performs a Data Entry Lag Assessment grouped by the Site variable using the Fisher method and correctly assigns Flag variable values when given a custom threshold.	Pass
DataEntry_Assess	S8_1, S8_4, S8_5, S8_6	T8_2	Given an appropriate subset of Data Entry Lag data, the assessment function correctly performs a Data Entry Lag Assessment grouped by the Country variable using the Fisher method and correctly assigns Flag variable values.	Pass
DataEntry_Assess	S8_1, S8_4, S8_5	T8_3	Given appropriate Data Entry Lag data, the assessment function correctly performs a Data Entry Lag Assessment grouped by a custom variable using the Fisher method and correctly assigns Flag variable values.	Pass
DataEntry_Assess	S8_2, S8_4, S8_5, S8_6	T8_4	Given an appropriate subset of Data Entry Lag data, the assessment function correctly performs a Data Entry Lag Assessment grouped by the Site variable using the Identity method and correctly assigns Flag variable values when given a custom threshold.	Pass
DataEntry_Assess	S8_2, S8_4, S8_5, S8_6	T8_5	Given an appropriate subset of Data Entry Lag data, the assessment function correctly performs a Data Entry Lag Assessment grouped by the Study variable using the Identity method and correctly assigns Flag variable values.	Pass
DataEntry_Assess	S8_2, S8_4, S8_5	T8_6	Given appropriate Data Entry Lag data, the assessment function correctly performs a Data Entry Lag Assessment grouped by a custom variable using the Identity method and correctly assigns Flag variable values.	Pass
DataEntry_Assess	S8_3, S8_4, S8_5, S8_6	T8_7	Given an appropriate subset of Data Entry Lag data, the assessment function correctly performs a Data Entry Lag Assessment grouped by the Site variable using the Normal Approximation method and correctly assigns Flag variable values when given a custom threshold.	Pass

Function	Spec ID	Test ID	Test Description	Test Result
DataEntry_Assess	S8_3, S8_4, S8_5, S8_6	T8_8	Given an appropriate subset of Data Entry Lag data, the assessment function correctly performs a Data Entry Lag Assessment grouped by the Study variable using the Normal Approximation method and correctly assigns Flag variable values.	Pass
DataEntry_Assess	S8_3, S8_4, S8_5	T8_9	Given appropriate Data Entry Lag data, the assessment function correctly performs a Data Entry Lag Assessment grouped by a custom variable using the Normal Approximation method and correctly assigns Flag variable values.	Pass
DataEntry_Assess	S8_1, S8_4, S8_5, S8_7	T8_10	Given appropriate Data Entry Lag data, the assessment function correctly performs a Data Entry Lag Assessment grouped by the Site variable using the Fisher method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass
DataEntry_Assess	S8_2, S8_4, S8_5, S8_7	T8_11	Given appropriate Data Entry Lag data, the assessment function correctly performs a Data Entry Lag Assessment grouped by the Site variable using the Identity method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass
DataEntry_Assess	S8_3, S8_4, S8_5, S8_7	T8_12	Given appropriate Data Entry Lag data, the assessment function correctly performs a Data Entry Lag Assessment grouped by the Site variable using the Normal Approximation method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass
QueryAge_Assess	S9_1, S9_4, S9_5, S9_6	T9_1	Given an appropriate subset of Query Age data, the assessment function correctly performs a Query Age Assessment grouped by the Site variable using the Fisher method and correctly assigns Flag variable values when given a custom threshold.	Pass
QueryAge_Assess	S9_1, S9_4, S9_5, S9_6	T9_2	Given an appropriate subset of Query Age data, the assessment function correctly performs a Query Age Assessment grouped by the Country variable using the Fisher method and correctly assigns Flag variable values.	Pass
QueryAge_Assess	S9_1, S9_4, S9_5	T9_3	Given appropriate Query Age data, the assessment function correctly performs a Query Age Assessment grouped by a custom variable using the Fisher method and correctly assigns Flag variable values.	Pass

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Function	Spec ID	Test ID	Test Description	Test Result
QueryAge_Assess	S9_2, S9_4, S9_5, S9_6	T9_4	Given an appropriate subset of Query Age data, the assessment function correctly performs a Query Age Assessment grouped by the Site variable using the Identity method and correctly assigns Flag variable values when given a custom threshold.	Pass
QueryAge_Assess	S9_2, S9_4, S9_5, S9_6	T9_5	Given an appropriate subset of Query Age data, the assessment function correctly performs a Query Age Assessment grouped by the Study variable using the Identity method and correctly assigns Flag variable values.	Pass
QueryAge_Assess	S9_2, S9_4, S9_5	T9_6	Given appropriate Query Age data, the assessment function correctly performs a Query Age Assessment grouped by a custom variable using the Identity method and correctly assigns Flag variable values.	Pass
QueryAge_Assess	S9_3, S9_4, S9_5, S9_6	T9_7	Given an appropriate subset of Query Age data, the assessment function correctly performs a Query Age Assessment grouped by the Site variable using the Normal Approximation method and correctly assigns Flag variable values when given a custom threshold.	Pass
QueryAge_Assess	S9_3, S9_4, S9_5, S9_6	T9_8	Given an appropriate subset of Query Age data, the assessment function correctly performs a Query Age Assessment grouped by the Study variable using the Normal Approximation method and correctly assigns Flag variable values.	Pass
QueryAge_Assess	S9_3, S9_4, S9_5	T9_9	Given appropriate Query Age data, the assessment function correctly performs a Query Age Assessment grouped by a custom variable using the Normal Approximation method and correctly assigns Flag variable values.	Pass
QueryAge_Assess	S9_1, S9_4, S9_5, S9_7	T9_10	Given appropriate Query Age data, the assessment function correctly performs a Query Age Assessment grouped by the Site variable using the Fisher method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass
QueryAge_Assess	S9_2, S9_4, S9_5, S9_7	T9_11	Given appropriate Query Age data, the assessment function correctly performs a Query Age Assessment grouped by the Site variable using the Identity method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass

Function	Spec ID	Test ID	Test Description	Test Result
QueryAge_Assess	S9_3, S9_4, S9_5, S9_7	T9_12	Given appropriate Query Age data, the assessment function correctly performs a Query Age Assessment grouped by the Site variable using the Normal Approximation method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass
QueryRate_Assess	S10_1, S10_4, S10_5, S10_6	T10_1	Given an appropriate subset of Query Rate data, the assessment function correctly performs a Query Rate Assessment grouped by the Site variable using the Poisson method and correctly assigns Flag variable values when given a custom threshold.	Pass
QueryRate_Assess	S10_1, S10_4, S10_5, S10_6	T10_2	Given an appropriate subset of Query Rate data, the assessment function correctly performs a Query Rate Assessment grouped by the Study variable using the Poisson method and correctly assigns Flag variable values.	Pass
QueryRate_Assess	S10_1, S10_4, S10_5	T10_3	Given appropriate Query Rate data, the assessment function correctly performs a Query Rate Assessment grouped by a custom variable using the Poisson method and correctly assigns Flag variable values.	Pass
QueryRate_Assess	S10_2, S10_4, S10_5, S10_6	T10_4	Given an appropriate subset of Query Rate data, the assessment function correctly performs a Query Rate Assessment grouped by the Site variable using the Identity method and correctly assigns Flag variable values when given a custom threshold.	Pass
QueryRate_Assess	S10_2, S10_4, S10_5, S10_6	T10_5	Given an appropriate subset of Query Rate data, the assessment function correctly performs a Query Rate Assessment grouped by the Study variable using the Identity method and correctly assigns Flag variable values.	Pass
QueryRate_Assess	S10_2, S10_4, S10_5	T10_6	Given appropriate Query Rate data, the assessment function correctly performs a Query Rate Assessment grouped by a custom variable using the Identity method and correctly assigns Flag variable values.	Pass
QueryRate_Assess	S10_3, S10_4, S10_5, S10_6	T10_7	Given an appropriate subset of Query Rate data, the assessment function correctly performs a Query Rate Assessment grouped by the Site variable using the Normal Approximation method and correctly assigns Flag variable values when given a custom threshold.	Pass

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Function	Spec ID	Test ID	Test Description	Test Result
QueryRate_Assess	S10_3, S10_4, S10_5, S10_6	T10_8	Given an appropriate subset of Query Rate data, the assessment function correctly performs a Query Rate Assessment grouped by the Study variable using the Normal Approximation method and correctly assigns Flag variable values.	Pass
QueryRate_Assess	S10_3, S10_4, S10_5	T10_9	Given appropriate Query Rate data, the assessment function correctly performs a Query Rate Assessment grouped by a custom variable using the Normal Approximation method and correctly assigns Flag variable values.	Pass
QueryRate_Assess	S10_1, S10_4, S10_5, S10_7	T10_10	Given appropriate Query Rate data, the assessment function correctly performs a Query Rate Assessment grouped by the Site variable using the Poisson method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass
QueryRate_Assess	S10_2, S10_4, S10_5, S10_7	T10_11	Given appropriate Query Rate data, the assessment function correctly performs a Query Rate Assessment grouped by the Site variable using the Identity method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass
QueryRate_Assess	S10_3, S10_4, S10_5, S10_7	T10_12	Given appropriate Query Rate data, the assessment function correctly performs a Query Rate Assessment grouped by the Site variable using the Normal Approximation method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass
AE_Map_Raw	S11_1	T11_1	Raw+ Adverse Event data can be mapped correctly to create an analysis-ready input dataset that has properly merged demographics and Adverse Event data with one record per subject, omitting subjects with zero days of treatment exposure.	Pass
AE_Map_Raw	S11_1	T11_2	Raw+ Adverse Event data can be mapped correctly to create an analysis-ready input dataset that has all required columns in the default Raw+ mapping specifications.	Pass
AE_Map_Raw	S11_1	T11_3	Raw+ Adverse Event data can be mapped correctly to create an analysis-ready input dataset which accurately calculates the number of Adverse Events and days of treatment exposure per subject.	Pass
AE_Map_Raw	S11_1	T11_4	A subset of Raw+ Adverse Event data can be mapped correctly to create an analysis-ready input dataset.	Pass

Function	Spec ID	Test ID	Test Description	Test Result
DataChg_Map_Raw	S12_1	T12_1	Raw data entry data can be mapped correctly to create an analysis-ready input dataset that has properly merged demographics and data point change counts with one record per subject, omitting subjects with no reported data points.	Pass
DataChg_Map_Raw	S12_1	T12_2	Raw data entry data can be mapped correctly to create an analysis-ready input dataset that has all required columns in the default EDC mapping specifications.	Pass
DataChg_Map_Raw	S12_1	T12_3	Raw data entry data can be mapped correctly to create an analysis-ready input dataset which accurately calculates the number of times any data point changed for a given data page and the total number of data points reported per subject.	Pass
DataChg_Map_Raw	S12_1	T12_4	A subset of raw data entry data can be mapped correctly to create an analysis-ready input dataset.	Pass
DataEntry_Map_Raw	S13_1	T13_1	Raw data entry data can be mapped correctly to create an analysis-ready input dataset that has properly merged demographics and data entry lag counts with one record per subject, omitting subjects with no reported data pages.	Pass
DataEntry_Map_Raw	S13_1	T13_2	Raw data entry data can be mapped correctly to create an analysis-ready input dataset that has all required columns in the default EDC mapping specifications.	Pass
DataEntry_Map_Raw	S13_1	T13_3	Raw data entry data can be mapped correctly to create an analysis-ready input dataset which accurately calculates the number of data entry lag counts and total number of data pages reported per subject.	Pass
DataEntry_Map_Raw	S13_1	T13_4	A subset of raw data entry data can be mapped correctly to create an analysis-ready input dataset.	Pass
Disp_Map_Raw	S14_1	T14_1	Raw+ Study Disposition data can be mapped correctly to create an analysis-ready input dataset that has properly merged demographics and Study Disposition data with one record per subject.	Pass
Disp_Map_Raw	S14_1	T14_2	Raw+ Study Treatment Disposition data can be mapped correctly to create an analysis-ready input dataset that has properly merged demographics and Study Treatment Disposition data with one record per subject.	Pass
Disp_Map_Raw	S14_1	T14_3	Raw+ Study Disposition data can be mapped correctly to create an analysis-ready input dataset that has all required columns in the default Raw+ mapping specifications.	Pass

Function	Spec ID	Test ID	Test Description	Test Result
Disp_Map_Raw	S14_1	T14_4	Raw+ Study Treatment Disposition data can be mapped correctly to create an analysis-ready input dataset that has all required columns in the default Raw+ mapping specifications.	Pass
Disp_Map_Raw	S14_1	T14_5	Raw+ Study Disposition data can be mapped correctly to create an analysis-ready input dataset which accurately calculates the number of subjects who discontinued from the study.	Pass
Disp_Map_Raw	S14_1	T14_6	Raw+ Study Treatment Disposition data can be mapped correctly to create an analysis-ready input dataset which accurately calculates the number of subjects who discontinued use of study treatment.	Pass
Disp_Map_Raw	S14_1	T14_7	A subset of Raw+ Study Disposition data can be mapped correctly to create an analysis-ready input dataset.	Pass
Disp_Map_Raw	S14_1	T14_8	A subset of Raw+ Study Treatment Disposition data can be mapped correctly to create an analysis-ready input dataset.	Pass
LB_Map_Raw	S15_1	T15_1	Raw+ Labs data can be mapped correctly to create an analysis-ready input dataset that has properly merged demographics and abnormal lab data with one record per subject, omitting subjects with no reported lab values.	Pass
LB_Map_Raw	S15_1	T15_2	Raw+ Labs data can be mapped correctly to create an analysis-ready input dataset that has all required columns in the default Raw+ mapping specifications.	Pass
LB_Map_Raw	S15_1	T15_3	Raw+ Labs data can be mapped correctly to create an analysis-ready input dataset which accurately calculates the number of abnormal lab values and total number of lab values reported per subject.	Pass
LB_Map_Raw	S15_1	T15_4	A subset of Raw+ Labs data can be mapped correctly to create an analysis-ready input dataset.	Pass
PD_Map_Raw_Rate	S16_1	T16_1	Raw+ Protocol Deviation data can be mapped correctly to create an analysis-ready input dataset that has properly merged demographics and Protocol Deviation data with one record per subject, omitting subjects with zero days on study.	Pass
PD_Map_Raw_Rate	S16_1	T16_2	Raw+ Protocol Deviation data can be mapped correctly to create an analysis-ready input dataset that has all required columns in the default Raw+ mapping specifications.	Pass

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Function	Spec ID	Test ID	Test Description	Test Result
PD_Map_Raw_Rate	S16_1	T16_3	Raw+ Protocol Deviation data can be mapped correctly to create an analysis-ready input dataset which accurately calculates the number of Protocol Deviations and days on study per subject.	Pass
PD_Map_Raw_Rate	S16_1	T16_4	A subset of Raw+ Protocol Deviation data can be mapped correctly to create an analysis-ready input dataset.	Pass
QueryAge_Map_Raw	S17_1	T17_1	Raw data query data can be mapped correctly to create an analysis-ready input dataset that has properly merged demographics and data query age counts with one record per subject, omitting subjects with no reported data queries.	Pass
QueryAge_Map_Raw	S17_1	T17_2	Raw data query data can be mapped correctly to create an analysis-ready input dataset that has all required columns in the default EDC mapping specifications.	Pass
QueryAge_Map_Raw	S17_1	T17_3	Raw data query data can be mapped correctly to create an analysis-ready input dataset which accurately calculates the number of data query age counts and total number of data queries reported per subject.	Pass
QueryAge_Map_Raw	S17_1	T17_4	A subset of raw data query data can be mapped correctly to create an analysis-ready input dataset.	Pass
QueryRate_Map_Raw	S18_1	T18_1	Raw data query data can be mapped correctly to create an analysis-ready input dataset that has properly merged demographics, data query rates, and data point counts with one record per subject, omitting subjects with no reported data points.	Pass
QueryRate_Map_Raw	S18_1	T18_2	Raw data query data can be mapped correctly to create an analysis-ready input dataset that has all required columns in the default EDC mapping specifications.	Pass
QueryRate_Map_Raw	S18_1	T18_3	Raw data query data can be mapped correctly to create an analysis-ready input dataset which accurately calculates the query rate (i.e., the number of data queries over the total number of data points) per subject.	Pass
QueryRate_Map_Raw	S18_1	T18_4	A subset of raw data query data can be mapped correctly to create an analysis-ready input dataset.	Pass
QueryRate_Map_Raw	S18_1	T18_5	Raw data query data can be mapped correctly to create an analysis-ready input dataset where the sum of the variable Count is equivalent to the number of rows in the source 'edc_queries' dataset.	Pass

Function	Spec ID	Test ID	Test Description	Test Result
QueryRate_Map_Raw	S18_1	T18_6	Raw data query data can be mapped correctly to create an analysis-ready input dataset where the sum of Count/Rate is equivalent to the number of rows in the original 'edc_data_points' dataset.	Pass
FilterDomain	S19_1	T19_1	Given pre-specified mapping, input data can be filtered to produce a data frame with the correct number of rows.	Pass
FilterDomain	S19_1	T19_2	Given pre-specified mapping, input data can be filtered to produce a data frame which retains all original source columns.	Pass
Get_Enrolled	S20_1	T20_1	Given correct input data and metadata, the correct number of enrolled participants per study can be derived.	Pass
Get_Enrolled	S20_2	T20_2	Given correct input data and metadata, the correct number of sites per study can be derived.	Pass
Get_Enrolled	S20_3	T20_3	Given correct input data and metadata, the correct number of enrolled participants per site can be derived.	Pass
MergeSubjects	S21_1	T21_1	Domain-level data can be correctly merged into subject-level data using subject ID as the key variable.	Pass
is_mapping_valid	S22_1	T22_1	The utility function can correctly evaluate that the input data is or is not a data frame.	Pass
is_mapping_valid	S22_1	T22_2	The utility function can correctly evaluate that the input data frame has or does not have the expected columns.	Pass
is_mapping_valid	S22_2	T22_3	The utility function can correctly evaluate that the input mapping(s) is(are) or is(are) not a list.	Pass
is_mapping_valid	S22_2	T22_4	The utility function can correctly evaluate that the elements of the input mapping(s) are or are not of character class.	Pass
is_mapping_valid	S22_2, S22_3	T22_5	The utility function can correctly evaluate that the input mapping(s) have or do not have all required parameters.	Pass
is_mapping_valid	S22_3	T22_6	The utility function can correctly evaluate that the input parameter specifications are or are not a list.	Pass
is_mapping_valid	S22_3	T22_7	The utility function can correctly evaluate if NA values are or are not acceptable in given columns depending on the vNACols component of the input parameter specifications.	Pass
is_mapping_valid	S22_3	T22_8	The utility function can correctly evaluate if empty string values are or are not acceptable in given columns depending on the vNACols component of the input parameter specifications.	Pass

Function	Spec ID	Test ID	Test Description	Test Result
is_mapping_valid	S22_3	T22_9	The utility function can correctly evaluate if duplicate values are or are not acceptable in given columns depending on the vUniqueCols component of the input parameter specifications.	Pass
PD_Assess_Binary	S23_1, S23_4, S23_5, S23_6	T23_1	Given an appropriate subset of Protocol Deviation data, the assessment function correctly performs a Protocol Deviation Assessment grouped by the Site variable using the Poisson method and correctly assigns Flag variable values when given a custom threshold.	Pass
PD_Assess_Binary	S23_1, S23_4, S23_5, S23_6	T23_2	Given an appropriate subset of Protocol Deviation data, the assessment function correctly performs a Protocol Deviation Assessment grouped by the Study variable using the Poisson method and correctly assigns Flag variable values.	Pass
PD_Assess_Binary	S23_1, S23_4, S23_5	T23_3	Given appropriate Protocol Deviation data, the assessment function correctly performs a Protocol Deviation Assessment grouped by a custom variable using the Poisson method and correctly assigns Flag variable values.	Pass
PD_Assess_Binary	S23_2, S23_4, S23_5, S23_6	T23_4	Given an appropriate subset of Protocol Deviation data, the assessment function correctly performs a Protocol Deviation Assessment grouped by the Site variable using the Identity method and correctly assigns Flag variable values when given a custom threshold.	Pass
PD_Assess_Binary	S23_2, S23_4, S23_5, S23_6	T23_5	Given an appropriate subset of Protocol Deviation data, the assessment function correctly performs a Protocol Deviation Assessment grouped by a custom variable using the Identity method and correctly assigns Flag variable values.	Pass
PD_Assess_Binary	S23_2, S23_4, S23_5	T23_6	Given appropriate Protocol Deviation data, the assessment function correctly performs a Protocol Deviation Assessment grouped by the Site variable using the Identity method and correctly assigns Flag variable values.	Pass
PD_Assess_Binary	S23_3, S23_4, S23_5, S23_6	T23_7	Given an appropriate subset of Protocol Deviation data, the assessment function correctly performs a Protocol Deviation Assessment grouped by the Site variable using the Normal Approximation method and correctly assigns Flag variable values when given a custom threshold.	Pass

Function	Spec ID	Test ID	Test Description	Test Result
PD_Assess_Binary	S23_3, S23_4, S23_5, S23_6	T23_8	Given an appropriate subset of Protocol Deviation data, the assessment function correctly performs a Protocol Deviation Assessment grouped by the Study variable using the Normal Approximation method and correctly assigns Flag variable values.	Pass
PD_Assess_Binary	S23_3, S23_4, S23_5	T23_9	Given appropriate Protocol Deviation data, the assessment function correctly performs a Protocol Deviation Assessment grouped by a custom variable using the Normal Approximation method and correctly assigns Flag variable values.	Pass
PD_Assess_Binary	S23_1, S23_4, S23_5, S23_7	T23_10	Given appropriate Protocol Deviation data, the assessment function correctly performs a Protocol Deviation Assessment grouped by the Site variable using the Poisson method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass
PD_Assess_Binary	S23_2, S23_4, S23_5, S23_7	T23_11	Given appropriate Protocol Deviation data, the assessment function correctly performs a Protocol Deviation Assessment grouped by the Site variable using the Identity method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass
PD_Assess_Binary	S23_3, S23_4, S23_5, S23_7	T23_12	Given appropriate Protocol Deviation data, the assessment function correctly performs a Protocol Deviation Assessment grouped by the Site variable using the Normal Approximation method and correctly assigns Flag variable values when given a custom threshold, and Flag variable values are set to NA for sites with low enrollment.	Pass
PD_Map_Raw_Binary	S24_1	T24_1	Raw+ Protocol Deviation data can be mapped correctly to create an analysis-ready input dataset that has properly merged demographics and Protocol Deviation data with one record per subject, omitting subjects with zero days on study.	Pass
PD_Map_Raw_Binary	S24_1	T24_2	Raw+ Protocol Deviation data can be mapped correctly to create an analysis-ready input dataset that has all required columns in the default Raw+ mapping specifications.	Pass
PD_Map_Raw_Binary	S24_1	T24_3	Raw+ Protocol Deviation data can be mapped correctly to create an analysis-ready input dataset, which accurately indicates if there are Protocol Deviations associated with each subject (0 = no associated Protocol Deviations, 1 = associated Protocol Deviations).	Pass

(continued)

Function	Spec ID	Test ID	Test Description	Test Result
PD_Map_Raw_Binary	S24_1	T24_4	A subset of Raw+ Protocol Deviation data can be mapped correctly to create an analysis-ready input dataset.	Pass

6 Unit Tests

6.1 Unit Testing Overview

Unit testing was performed in addition to qualification testing to help ensure that individual pieces of code within the R package function correctly and produce the expected results. By testing individual units of code in isolation, developers can identify and fix issues early in the development process before more significant and scaled problems arise.

6.2 Unit Test Coverage

The table below summarizes unit test coverage of each {gsm} function. This metric quantifies the extent of unit testing. The closer this measure is to 100%, the more unit testing that function has.

Function	File Coverage
R/AE_Assess.R	99.19 %
R/AE_Map_Adam.R	97.73 %
R/AE_Map_Raw.R	100.00 %
R/Analyze_Fisher.R	100.00 %
R/Analyze_Identity.R	100.00 %
R/Analyze_NormalApprox_PredictBounds.R	94.64 %
R/Analyze_NormalApprox.R	100.00 %
R/Analyze_Poisson_PredictBounds.R	89.80 %
R/Analyze_Poisson.R	100.00 %
R/Analyze_QTL.R	100.00 %
R/barChart.R	84.00 %
R/CheckSnapshotInputs.R	100.00 %
R/Consent_Assess.R	98.46 %
R/Consent_Map_Raw.R	88.89 %
R/DataChg_Assess.R	97.37 %
R/DataChg_Map_Raw.R	100.00 %
R/DataEntry_Assess.R	97.37 %
R/DataEntry_Map_Raw.R	100.00 %
R/Disp_Assess.R	96.77 %
R/Disp_Map_Raw.R	100.00 %
R/ExportCode.R	89.72 %
R/Flag_Fisher.R	100.00 %
R/Flag_NormalApprox.R	100.00 %
R/Flag_Poisson.R	100.00 %
R/Flag_QTL.R	100.00 %
R/Flag.R	100.00 %
R/Get_Enrolled.R	100.00 %
R/IE_Assess.R	98.46 %
R/IE_Map_Raw.R	100.00 %
R/is_workflow_valid.R	100.00 %
R/LB_Assess.R	97.37 %
R/LB_Map_Raw.R	100.00 %
R/Make_Snapshot.R	98.90 %
R/Overview_Table.R	100.00 %
R/PD_Assess_Binary.R	96.00 %
R/PD_Assess_Rate.R	95.20 %
R/PD_Map_Raw_Binary.R	100.00 %
R/PD_Map_Raw_Rate.R	100.00 %
R/QueryAge_Assess.R	97.37 %

(continued)

Function	File Coverage
R/QueryAge__Map__Raw.R	100.00 %
R/QueryRate__Assess.R	91.13 %
R/QueryRate__Map__Raw.R	100.00 %
R/RunQTL.R	100.00 %
R/SaveQTL.R	90.48 %
R/scatterPlot.R	84.00 %
R/Screening__Assess.R	93.55 %
R/Screening__Map__Raw.R	100.00 %
R/Study__Assess.R	92.16 %
R/Study__AssessmentReport.R	100.00 %
R/Study__Report.R	0.00 %
R/Summarize.R	100.00 %
R/tests-assess__helpers.R	68.75 %
R/tests-map__raw__helpers.R	85.19 %
R/Transform__Count.R	100.00 %
R/Transform__Rate.R	100.00 %
R/UpdateParams.R	100.00 %
R/util-build__markdown.R	0.00 %
R/util-CheckClindataMeta.R	100.00 %
R/util-CheckInputs.R	100.00 %
R/util-ConsolidateStrata.R	100.00 %
R/util-FilterData.R	96.67 %
R/util-FilterDomain.R	100.00 %
R/util-generate__md__table.R	0.00 %
R/util-is__mapping__valid.R	100.00 %
R/util-kri__directionality__logo.R	84.62 %
R/util-MakeDfConfig.R	100.00 %
R/util-MakeStratifiedAssessment.R	92.86 %
R/util-MakeWorkflowList.R	100.00 %
R/util-MergeSubjects.R	97.73 %
R/util-parse__data__mapping.R	0.00 %
R/util-parse__data__spec.R	0.00 %
R/util-ParseWarnings.R	100.00 %
R/util-rank__chg.R	100.00 %
R/util-RunStep.R	100.00 %
R/util-RunStratifiedWorkflow.R	90.91 %
R/util-RunWorkflow.R	90.24 %
R/util-UpdateGSMVersion.R	0.00 %
R/Visualize__Scatter.R	100.00 %
R/Visualize__Score.R	100.00 %
R/Visualize__Workflow.R	98.44 %
Total Coverage	92.93 %

7 Qualification Testing Environment

7.1 Session Information

R version 4.2.0 (2022-04-22)

Platform: x86_64-pc-linux-gnu (64-bit)

locale: *LC_CTYPE=C.UTF-8, LC_NUMERIC=C, LC_TIME=C.UTF-8, LC_COLLATE=C.UTF-8, LC_MONETARY=C.UTF-8, LC_MESSAGES=C.UTF-8, LC_PAPER=C.UTF-8, LC_NAME=C, LC_ADDRESS=C, LC_TELEPHONE=C, LC_MEASUREMENT=C.UTF-8* and *LC_IDENTIFICATION=C*

attached base packages: *stats*, *graphics*, *grDevices*, *utils*, *datasets*, *methods* and *base*

other attached packages: *gsm(v.1.5.0)*, *riskmetric(v.0.2.0)*, *gh(v.1.4.0)*, *pander(v.0.6.5)*, *knitr(v.1.42)*, *lubridate(v.1.9.2)*, *forcats(v.1.0.0)*, *stringr(v.1.5.0)*, *dplyr(v.1.1.0)*, *purrr(v.1.0.1)*, *readr(v.2.1.4)*, *tidyr(v.1.3.0)*, *tibble(v.3.2.0)*, *ggplot2(v.3.4.1)*, *tidyverse(v.2.0.0)*, *rvest(v.1.0.3)* and *testthat(v.3.1.6)*

loaded via a namespace (and not attached): *colorspace(v.2.1-0)*, *selectr(v.0.4-2)*, *ellipsis(v.0.3.2)*, *rprojroot(v.2.0.3)*, *fs(v.1.6.1)*, *rstudioapi(v.0.14)*, *waldo(v.0.4.0)*, *urltools(v.1.7.3)*, *remotes(v.2.4.2)*, *DT(v.0.27)*, *bit64(v.4.0.5)*, *fansi(v.1.0.4)*, *xml2(v.1.3.3)*, *R.methodsS3(v.1.8.2)*, *cachem(v.1.0.7)*, *pkgload(v.1.3.2)*, *jsonlite(v.1.8.4)*, *gt(v.0.8.0)*, *broom(v.1.0.3)*, *R.oo(v.1.25.0)*, *shiny(v.1.7.4.9001)*, *BiocManager(v.1.30.20)*, *DiagrammeR(v.1.0.9)*, *compiler(v.4.2.0)*, *httr(v.1.4.5)*, *tictoc(v.1.1)*, *backports(v.1.4.1)*, *lazyeval(v.0.2.2)*, *assertthat(v.0.2.1)*, *fastmap(v.1.1.1)*, *cli(v.3.6.0)*, *later(v.1.3.0)*, *visNetwork(v.2.1.2)*, *htmltools(v.0.5.4.9000)*, *prettyunits(v.1.1.1)*, *tools(v.4.2.0)*, *gtable(v.0.3.1)*, *glue(v.1.6.2)*, *Rcpp(v.1.0.10)*, *jquerylib(v.0.1.4)*, *styler(v.1.9.1)*, *vctrs(v.0.6.0)*, *lamW(v.2.1.2)*, *svglite(v.2.1.1)*, *clindata(v.0.14.1)*, *xfun(v.0.37)*, *ps(v.1.7.2)*, *brio(v.1.1.3)*, *timechange(v.0.2.0)*, *mime(v.0.12)*, *miniUI(v.0.1.1.1)*, *lifecycle(v.1.0.3)*, *devtools(v.2.4.5)*, *scales(v.1.2.1)*, *hms(v.1.1.2)*, *promises(v.1.2.0.1)*, *rex(v.1.2.1)*, *RColorBrewer(v.1.1-3)*, *yaml(v.2.3.7)*, *curl(v.5.0.0)*, *memoise(v.2.0.1)*, *sass(v.0.4.5)*, *triebeard(v.0.4.1)*, *stringi(v.1.7.12)*, *desc(v.1.4.2)*, *pkgbuild(v.1.4.0)*, *systemfonts(v.1.0.4)*, *rlang(v.1.1.0)*, *pkgconfig(v.2.0.3)*, *prompt(v.1.0.1)*, *evaluate(v.0.20)*, *datapasta(v.3.1.0)*, *fontawesome(v.0.5.0)*, *htmlwidgets(v.1.6.1)*, *bit(v.4.0.5)*, *processx(v.3.8.0)*, *tidyselect(v.1.2.0)*, *here(v.1.0.1)*, *magrittr(v.2.0.3)*, *R6(v.2.5.1)*, *generics(v.0.1.3)*, *profvis(v.0.3.7)*, *pillar(v.1.8.1)*, *withr(v.2.5.0)*, *crayon(v.1.5.2)*, *utf8(v.1.2.3)*, *tzdb(v.0.3.0)*, *rmarkdown(v.2.20)*, *urlchecker(v.1.0.1)*, *usethis(v.2.1.6)*, *grid(v.4.2.0)*, *data.table(v.1.14.8)*, *callr(v.3.7.3)*, *cranlogs(v.2.1.1)*, *webshot(v.0.5.4)*, *reprex(v.2.0.2)*, *digest(v.0.6.31)*, *xtable(v.1.8-4)*, *R.cache(v.0.16.0)*, *covr(v.3.6.1)*, *httpuv(v.1.6.9)*, *R.utils(v.2.12.2)*, *arrow(v.11.0.0.3)*, *RcppParallel(v.5.1.7)*, *munsell(v.0.5.0)*, *viridisLite(v.0.4.1)*, *kableExtra(v.1.3.4)*, *bslib(v.0.4.2)* and *sessioninfo(v.1.2.2)*

7.2 Package List

The table below utilizes the `riskmetric` package, which quantifies the robustness of an R package. The `pkg_score` column captures the risk involved with using a package. The risk level ranges from 0 (low risk) to 1 (high risk).

package	version	pkg_score
broom	1.0.3	0.387
cli	3.6.0	0.481
DiagrammeR	1.0.9	0.540
dplyr	1.1.0	0.451
DT	0.27	0.494
fontawesome	0.5.0	0.415
fs	1.6.1	0.411
glue	1.6.2	0.360
gt	0.8.0	0.509
ggplot2	3.4.1	0.470
htmlwidgets	1.6.1	0.379
here	1.0.1	0.354
knitr	1.42	0.570
lamW	2.1.2	0.571
lifecycle	1.0.3	0.383
magrittr	2.0.3	0.349
purrr	1.0.1	0.448
rmarkdown	2.20	0.458
rstudioapi	0.14	0.407
stringr	1.5.0	0.436
tibble	3.2.0	0.435
tidyr	1.3.0	0.460
yaml	2.3.7	0.508
rlang	1.1.0	0.464

8 Pull Request History

8.0.1 Pull Request 1121: Fix 1079 - Updated Qual Report Rmd

Merging fix-1079 into dev

https://github.com/Gilead-BioStats/gsm/pull/1121

Requester	Date Requested	Reviewers	Review Status
collleenmclaughlin	2023-03-20 21:10:50		CHANGES_REQUESTED

8.0.2 Pull Request 1119: Update protocol deviation mapping.

Merging fix-1096-pd into dev

https://github.com/Gilead-BioStats/gsm/pull/1119

Requester	Date Requested	Reviewers	Review Status
samussiah	2023-03-16 17:24:22	chelseadickens Zhongkai-Wang collleenmclaughlin	APPROVED

8.0.3 Pull Request 1117: Fix 1096 Qualification - Aligning Qual. Tests with Updates

Merging fix-1096-qualification into fix-1096

https://github.com/Gilead-BioStats/gsm/pull/1117

Requester	Date Requested	Reviewers	Review Status
collleenmclaughlin	2023-03-16 16:39:09	Zhongkai-Wang	APPROVED

8.0.4 Pull Request 1115: Fix 1086 - Add Unit Tests/Code Coverage

Merging fix-1086 into dev

https://github.com/Gilead-BioStats/gsm/pull/1115

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-03-14 22:02:17	Zhongkai-Wang	COMMENTED

8.0.5 Pull Request 1114: update qualification_analyze_normalapprox() in helper-qualification.R

Merging fix-1113 into fix-1107

https://github.com/Gilead-BioStats/gsm/pull/1114

Requester	Date Requested	Reviewers	Review Status
chelseadickens	2023-03-14 20:22:08		APPROVED

8.0.6 Pull Request 1112: Fix 1107 - Update Analyze_NormalApprox

Merging fix-1107 into dev

https://github.com/Gilead-BioStats/gsm/pull/1112

Requester	Date Requested	Reviewers	Review Status
Zhongkai-Wang	2023-03-13 14:15:05	chelseadickens collleenmclaughlin	COMMENTED

8.0.7 Pull Request 1104: Update domain and column mappings.

Merging fix-1096 into dev

https://github.com/Gilead-BioStats/gsm/pull/1104

Requester	Date Requested	Reviewers	Review Status
samussiah	2023-03-10 17:13:41	chelseadickens Zhongkai-Wang collleenmclaughlin	APPROVED

8.0.8 Pull Request 1103: Fix 1099, 1100, 1102

Merging fix-1100 into dev

https://github.com/Gilead-BioStats/gsm/pull/1103

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-03-09 20:53:15		APPROVED

8.0.9 Pull Request 1093: Fix 1066 - update qualification test ordering

Merging fix-1066 into dev

https://github.com/Gilead-BioStats/gsm/pull/1093

Requester	Date Requested	Reviewers	Review Status
chelseadickens	2023-03-02 18:53:34	collleenmclaughlin	COMMENTED

8.0.10 Pull Request 1090: Fix 1080

Merging fix-1080 into dev

https://github.com/Gilead-BioStats/gsm/pull/1090

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-02-28 22:32:51		

8.0.11 Pull Request 1088: Fix 1083 - update meta_workflow

Merging fix-1083 into dev

https://github.com/Gilead-BioStats/gsm/pull/1088

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-02-24 21:17:47	Zhongkai-Wang	COMMENTED

8.0.12 Pull Request 1087: Fix 1066 - Test Script Language Update

Merging fix-1066 into dev

https://github.com/Gilead-BioStats/gsm/pull/1087

Requester	Date Requested	Reviewers	Review Status
collleenmclaughlin	2023-02-23 22:58:44		APPROVED

8.0.13 Pull Request 1075: Fix 1074 - update data

Merging fix-1074 into dev

https://github.com/Gilead-BioStats/gsm/pull/1075

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-02-21 19:34:30		APPROVED

8.0.14 Pull Request 1073: Fix 1035 - add badge to documentation

Merging fix-1035 into dev

https://github.com/Gilead-BioStats/gsm/pull/1073

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-02-20 22:08:49	collleenmclaughlin	APPROVED

8.0.15 Pull Request 1072: Fix 1052 - util-is_mapping_valid() Qual. Tests

Merging fix-1052 into dev

https://github.com/Gilead-BioStats/gsm/pull/1072

Requester	Date Requested	Reviewers	Review Status
collleenmclaughlin	2023-02-16 16:58:39		APPROVED

8.0.16 Pull Request 1071: Fix 1070 - add flag counts to report

Merging fix-1070 into dev

https://github.com/Gilead-BioStats/gsm/pull/1071

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-02-15 22:32:44	jwildfire chelseadickens collleenmclaughlin	APPROVED

8.0.17 Pull Request 1068: Fix 1061 - fix report error log

Merging fix-1061 into dev

https://github.com/Gilead-BioStats/gsm/pull/1068

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-02-14 17:58:44	chelseadickens collleenmclaughlin	APPROVED

8.0.18 Pull Request 1067: Fix 1065 - update is_mapping_valid

Merging fix-1065 into dev

https://github.com/Gilead-BioStats/gsm/pull/1067

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-02-13 21:20:52	Zhongkai-Wang	APPROVED

8.0.19 Pull Request 1064: Add input data schema to {gsm}.

Merging fix-639 into dev

https://github.com/Gilead-BioStats/gsm/pull/1064

Requester	Date Requested	Reviewers	Review Status
samussiah	2023-02-08 17:43:58	mattroumaya	

8.0.20 Pull Request 1063: Sync dev and main

Merging main into dev

https://github.com/Gilead-BioStats/gsm/pull/1063

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-02-07 21:52:21	jwildfire samussiah	APPROVED

8.0.21   Pull Request 1059: Fix 1057 - PD_Map_Raw() Qual. Tests Updates

Merging fix-1057 into dev

https://github.com/Gilead-BioStats/gsm/pull/1059

Requester	Date Requested	Reviewers	Review Status
collleenmclaughlin	2023-02-02 22:35:08		APPROVED

8.0.22   Pull Request 1056: Fix-1049: Update non-serious AE KRI to include all AEs

Merging fix-1049 into dev

https://github.com/Gilead-BioStats/gsm/pull/1056

Requester	Date Requested	Reviewers	Review Status
Zhongkai-Wang	2023-02-02 16:27:28		APPROVED

8.0.23   Pull Request 1055: Release v1.5.0

Merging release-v1.5.0 into main

https://github.com/Gilead-BioStats/gsm/pull/1055

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-02-01 22:29:19	samussiah Zhongkai-Wang	COMMENTED

8.0.24   Pull Request 1054: Fix 929 - util-FilterDomain() Qual. Tests

Merging fix-929 into dev

https://github.com/Gilead-BioStats/gsm/pull/1054

Requester	Date Requested	Reviewers	Review Status
collleenmclaughlin	2023-02-01 20:40:59		APPROVED

8.0.25   Pull Request 1051: Fix 935 - util-MergeSubjects() Qual. Test

Merging fix-935 into dev

https://github.com/Gilead-BioStats/gsm/pull/1051

Requester	Date Requested	Reviewers	Review Status
collleenmclaughlin	2023-02-01 19:40:33		APPROVED

8.0.26 Pull Request 1048: Fix 932 - Get_Enrolled() Qual. Tests

Merging fix-932 into dev

https://github.com/Gilead-BioStats/gsm/pull/1048

Requester	Date Requested	Reviewers	Review Status
collleenmclaughlin	2023-02-01 18:00:11		APPROVED

8.0.27 Pull Request 1046: qualification specs management

Merging fix-1016 into dev

https://github.com/Gilead-BioStats/gsm/pull/1046

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-01-30 23:21:19	samussiah collleenmclaughlin	APPROVED

8.0.28 Pull Request 1044: Fix 1034 - Qual Scraping Function

Merging fix-1034 into dev

https://github.com/Gilead-BioStats/gsm/pull/1044

Requester	Date Requested	Reviewers	Review Status
collleenmclaughlin	2023-01-30 21:22:42	chelseadickens Zhongkai-Wang	APPROVED

8.0.29 Pull Request 1042: tweaks

Merging fix-1003-review into fix-1003

https://github.com/Gilead-BioStats/gsm/pull/1042

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-01-26 03:19:19		APPROVED

8.0.30 Pull Request 1041: Fix 905 - Create stats vignette

Merging fix-905 into dev

https://github.com/Gilead-BioStats/gsm/pull/1041

Requester	Date Requested	Reviewers	Review Status
Zhongkai-Wang	2023-01-25 14:03:37	jwildfire mattroumaya	APPROVED

8.0.31 Pull Request 1040: Fix 1003 - Update IPD QTL

Merging fix-1003 into dev

https://github.com/Gilead-BioStats/gsm/pull/1040

Requester	Date Requested	Reviewers	Review Status
Zhongkai-Wang	2023-01-25 13:51:13	samussiah	COMMENTED

8.0.32 Pull Request 1039: Fix 967 - Check workflow list for Make_Snapshot

Merging fix-967 into dev

https://github.com/Gilead-BioStats/gsm/pull/1039

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-01-24 22:44:07	jwildfire	DISMISSED

8.0.33 Pull Request 1038: 987/1031 - resolve conflicts

Merging 987-subset-oriented-qualification-tests into 1031-qual-tests-for-nmindenominator

https://github.com/Gilead-BioStats/gsm/pull/1038

Requester	Date Requested	Reviewers	Review Status
chelseadickens	2023-01-24 21:46:39		

8.0.34 Pull Request 1037: Add `Estimate` to QTL output.

Merging fix-894 into dev

https://github.com/Gilead-BioStats/gsm/pull/1037

Requester	Date Requested	Reviewers	Review Status
samussiah	2023-01-24 14:40:21		APPROVED

8.0.35 Pull Request 1036: Fix 1031; 987; 1058 - qual tests for nMinDenominator + subset-oriented tests + PD_Assess() updates

Merging 1031-qual-tests-for-nmindenominator into dev

https://github.com/Gilead-BioStats/gsm/pull/1036

Requester	Date Requested	Reviewers	Review Status
chelseadickens	2023-01-23 20:48:23		COMMENTED

8.0.36 Pull Request 1032: Fix 987 - subset oriented qualification tests

Merging 987-subset-oriented-qualification-tests into dev

https://github.com/Gilead-BioStats/gsm/pull/1032

Requester	Date Requested	Reviewers	Review Status
chelseadickens	2023-01-20 21:43:35	samussiah Zhongkai-Wang	

8.0.37 Pull Request 1030: Update mappings to more easily integrate with safetyGraphics for gsmApp.

Merging consistent-mappings into dev

https://github.com/Gilead-BioStats/gsm/pull/1030

Requester	Date Requested	Reviewers	Review Status
samussiah	2023-01-20 18:25:31	chelseadickens collleenmclaughlin	APPROVED

8.0.38 Pull Request 1028: Fix 988 even more tweaks

Merging fix-988-tweaks-tweak into fix-988-tweaks

https://github.com/Gilead-BioStats/gsm/pull/1028

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-01-19 22:13:59		APPROVED

8.0.39 Pull Request 1027: Reposition dropdown to remain visible throughout report.

Merging fix-988-tweaks into fix-988

https://github.com/Gilead-BioStats/gsm/pull/1027

Requester	Date Requested	Reviewers	Review Status
samussiah	2023-01-19 19:15:45	mattroumaya	

8.0.40 Pull Request 1026: Fix 639; 1025 - fix barcharts + warning during rcmd check

Merging fix-639 into dev

https://github.com/Gilead-BioStats/gsm/pull/1026

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-01-18 20:42:30		COMMENTED

8.0.41 Pull Request 1023: Fix 988 - report-level site dropdown

Merging fix-988 into dev

https://github.com/Gilead-BioStats/gsm/pull/1023

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-01-17 22:43:46		APPROVED

8.0.42 Pull Request 1022: Fix 962 - clean up Make_Snapshot() merging

Merging fix-962 into dev

https://github.com/Gilead-BioStats/gsm/pull/1022

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-01-17 16:10:19	samussiah	APPROVED

8.0.43 Pull Request 1019: Fix 1018 - Minor Qual. Test Updates

Merging fix-1018 into dev

https://github.com/Gilead-BioStats/gsm/pull/1019

Requester	Date Requested	Reviewers	Review Status
collleenmclaughlin	2023-01-13 17:54:14		APPROVED

8.0.44 Pull Request 1017: Fix 941 - QueryRate_Map_Raw() Qual. Tests

Merging fix-941 into dev

https://github.com/Gilead-BioStats/gsm/pull/1017

Requester	Date Requested	Reviewers	Review Status
collleenmclaughlin	2023-01-13 16:36:17		COMMENTED

8.0.45 Pull Request 1015: Fix 1014 - update reporting functions

Merging fix-1014 into dev

https://github.com/Gilead-BioStats/gsm/pull/1015

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-01-12 22:12:52	Zhongkai-Wang	COMMENTED

8.0.46 Pull Request 1013: Fix 966 - update rbm-viz function docs

Merging fix-966 into dev

https://github.com/Gilead-BioStats/gsm/pull/1013

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-01-12 20:48:55		APPROVED

8.0.47 Pull Request 1011: Update `rbm-viz` to `v1.0.0`.

Merging fix-1010 into dev

https://github.com/Gilead-BioStats/gsm/pull/1011

Requester	Date Requested	Reviewers	Review Status
samussiah	2023-01-11 20:14:47		APPROVED

8.0.48 Pull Request 1009: Fix-1005 - Additional update to correct counting and merging logic

Merging fix-1005-more into dev

https://github.com/Gilead-BioStats/gsm/pull/1009

Requester	Date Requested	Reviewers	Review Status
Zhongkai-Wang	2023-01-11 15:30:02	collleenmclaughlin	APPROVED

8.0.49 Pull Request 1008: Fix 1006 - make flowchart optional

Merging fix-1006 into dev

https://github.com/Gilead-BioStats/gsm/pull/1008

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-01-10 22:53:52	jwildfire Zhongkai-Wang	APPROVED

8.0.50 Pull Request 1007: Fix 1005 - QueryRate_Map_Raw Grouping

Merging fix-1005 into dev

https://github.com/Gilead-BioStats/gsm/pull/1007

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-01-10 17:22:04	samussiah collleenmclaughlin	APPROVED

8.0.51 Pull Request 1004: Fix 520 - add ability to export code from workflow, lData, and lMapping

Merging fix-520 into dev

https://github.com/Gilead-BioStats/gsm/pull/1004

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-01-09 22:10:48	jwildfire	COMMENTED

8.0.52 Pull Request 1002: fix 925 - qualify DataEntry__Assess

Merging 925-qualify-dataentry_assess into dev

https://github.com/Gilead-BioStats/gsm/pull/1002

Requester	Date Requested	Reviewers	Review Status
chelseadickens	2023-01-06 15:44:35		APPROVED

8.0.53 Pull Request 1001: fix 923 - qualify DataChg__Assess

Merging 923-qualify-datachg_assess into dev

https://github.com/Gilead-BioStats/gsm/pull/1001

Requester	Date Requested	Reviewers	Review Status
chelseadickens	2023-01-06 15:23:23		APPROVED

8.0.54 Pull Request 1000: fix 938 - qualify QueryAge__Assess

Merging 938-qualify-queryage_assess into dev

https://github.com/Gilead-BioStats/gsm/pull/1000

Requester	Date Requested	Reviewers	Review Status
chelseadickens	2023-01-06 14:58:19		APPROVED

8.0.55 Pull Request 999: fix 940 - qualify QueryRate__Assess

Merging 940-qualify-queryrate_assess into dev

https://github.com/Gilead-BioStats/gsm/pull/999

Requester	Date Requested	Reviewers	Review Status
chelseadickens	2023-01-06 14:51:37		APPROVED

8.0.56 Pull Request 998: Fix 965 - add missing unit tests

Merging fix-965 into dev

https://github.com/Gilead-BioStats/gsm/pull/998

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-01-05 22:27:06		APPROVED

8.0.57 Pull Request 997: Data model fixes

Merging data-model-fixes into dev

https://github.com/Gilead-BioStats/gsm/pull/997

Requester	Date Requested	Reviewers	Review Status
samussiah	2023-01-05 22:09:30	Zhongkai-Wang collleenmclaughlin	APPROVED

8.0.58 Pull Request 996: Fix 939 - QueryAge_Map_Raw() Qual. Tests

Merging fix-939 into dev

https://github.com/Gilead-BioStats/gsm/pull/996

Requester	Date Requested	Reviewers	Review Status
collleenmclaughlin	2023-01-05 22:04:51		APPROVED

8.0.59 Pull Request 995: Fix 926 - DataEntry_Map_Raw() Qual. Tests

Merging fix-926 into dev

https://github.com/Gilead-BioStats/gsm/pull/995

Requester	Date Requested	Reviewers	Review Status
collleenmclaughlin	2023-01-05 14:58:53		APPROVED

8.0.60 Pull Request 992: Fix 924 - DataChg_Map_Raw() Qual. Tests

Merging fix-924 into dev

https://github.com/Gilead-BioStats/gsm/pull/992

Requester	Date Requested	Reviewers	Review Status
collleenmclaughlin	2023-01-04 19:57:21		APPROVED

8.0.61 Pull Request 991: Fix 924 - DataChg_Map_Raw() Qual. Tests

Merging fix-924 into dev

https://github.com/Gilead-BioStats/gsm/pull/991

Requester	Date Requested	Reviewers	Review Status
collleenmclaughlin	2023-01-04 19:20:45		

8.0.62 Pull Request 990: multiple select

Merging fix-984-multiple into dev

https://github.com/Gilead-BioStats/gsm/pull/990

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-01-03 18:30:48		

8.0.63 Pull Request 989: Fix 986 - make unit tests faster

Merging fix-986 into dev

https://github.com/Gilead-BioStats/gsm/pull/989

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2023-01-03 14:28:03	jwildfire Zhongkai-Wang	COMMENTED

8.0.64 Pull Request 985: Add dropdown to widgets to highlight sites.

Merging fix-984 into dev

https://github.com/Gilead-BioStats/gsm/pull/985

Requester	Date Requested	Reviewers	Review Status
samussiah	2022-12-22 21:34:46	MayaGans	APPROVED

8.0.65 Pull Request 983: Fix 961 - minify lData

Merging fix-961 into dev

https://github.com/Gilead-BioStats/gsm/pull/983

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2022-12-22 20:03:27		APPROVED

8.0.66 Pull Request 982: Fix 979 - remove unused functions and dependencies

Merging fix-979 into dev

https://github.com/Gilead-BioStats/gsm/pull/982

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2022-12-22 19:16:40		APPROVED

8.0.67 Pull Request 980: Fix 928 - Disp_Map_Raw() Qual. Tests

Merging fix-928 into dev

https://github.com/Gilead-BioStats/gsm/pull/980

Requester	Date Requested	Reviewers	Review Status
collleenmclaughlin	2022-12-22 17:15:53	samussiah gwu05 Zhongkai-Wang	COMMENTED

8.0.68 Pull Request 978: Fix 934 - LB_Map_Raw() Qual. Tests

Merging fix-934 into dev

https://github.com/Gilead-BioStats/gsm/pull/978

Requester	Date Requested	Reviewers	Review Status
collleenmclaughlin	2022-12-21 21:30:03	samussiah gwu05 Zhongkai-Wang	APPROVED

8.0.69 Pull Request 977: Fix 937 - PD_Map_Raw() Qual. Tests

Merging fix-937 into dev

https://github.com/Gilead-BioStats/gsm/pull/977

Requester	Date Requested	Reviewers	Review Status
collleenmclaughlin	2022-12-21 19:26:15	samussiah gwu05 Zhongkai-Wang	APPROVED

8.0.70 Pull Request 976: Fix 953 - remove qualification YAML −> csv file

Merging fix-953 into dev

https://github.com/Gilead-BioStats/gsm/pull/976

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2022-12-20 22:52:52	jwildfire chelseadickens Zhongkai-Wang collleenmclaughlin	APPROVED

8.0.71 Pull Request 975: Fix 920 - AE_Map_Raw() Qual. Tests

Merging fix-920 into dev

https://github.com/Gilead-BioStats/gsm/pull/975

Requester	Date Requested	Reviewers	Review Status
collleenmclaughlin	2022-12-20 21:44:00	samussiah gwu05 Zhongkai-Wang	APPROVED

8.0.72 Pull Request 974: Remove `nStep` argument in `QueryRate_Assess()`.

Merging fix-973 into dev

https://github.com/Gilead-BioStats/gsm/pull/974

Requester	Date Requested	Reviewers	Review Status
samussiah	2022-12-20 19:04:44		APPROVED

8.0.73 Pull Request 972: Sync `dev` and `main`

Merging main into dev

https://github.com/Gilead-BioStats/gsm/pull/972

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2022-12-20 15:17:04	samussiah	APPROVED

8.0.74 Pull Request 971: Release v1.4.1

Merging release-v1.4.1 into main

https://github.com/Gilead-BioStats/gsm/pull/971

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2022-12-19 22:03:35	samussiah gwu05	COMMENTED

8.0.75 Pull Request 970: (targeted wrong branch) Release v1.4.1

Merging release-v1.4.1 into main

https://github.com/Gilead-BioStats/gsm/pull/970

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2022-12-19 22:00:24		

8.0.76   Pull Request 968: Sync `main` and `dev` for `v1.4.0` release

Merging main into dev

https://github.com/Gilead-BioStats/gsm/pull/968

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2022-12-19 15:25:32	Zhongkai-Wang collleenmclaughlin	APPROVED

8.0.77   Pull Request 964: Fix 614 - denominator requirement and score/flag rules

Merging fix-614 into dev

https://github.com/Gilead-BioStats/gsm/pull/964

Requester	Date Requested	Reviewers	Review Status
Zhongkai-Wang	2022-12-15 15:50:53	gwu05	COMMENTED

8.0.78   Pull Request 960: fix 936 - qualify PD__Assess for normal approximation

Merging 936-qualify-pd_assess into dev

https://github.com/Gilead-BioStats/gsm/pull/960

Requester	Date Requested	Reviewers	Review Status
chelseadickens	2022-12-14 15:48:01	jwildfire gwu05	APPROVED

8.0.79   Pull Request 959: fix 933 - qualify LB__Assess for normal approximation

Merging 933-qualify-lb_assess into dev

https://github.com/Gilead-BioStats/gsm/pull/959

Requester	Date Requested	Reviewers	Review Status
chelseadickens	2022-12-14 14:50:59	jwildfire gwu05	APPROVED

8.0.80   Pull Request 958: Release v1.4.0

Merging release-v1.4.0 into main

https://github.com/Gilead-BioStats/gsm/pull/958

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2022-12-14 04:36:45	jwildfire	APPROVED

8.0.81 Pull Request 957: Add # of participants to overview table in KRI report.

Merging fix-954 into dev

https://github.com/Gilead-BioStats/gsm/pull/957

Requester	Date Requested	Reviewers	Review Status
samussiah	2022-12-13 21:30:12	Zhongkai-Wang	APPROVED

8.0.82 Pull Request 956: fix 927 - qualify Disp_Assess for normal approximation

Merging 927-qualify-disp_assess into dev

https://github.com/Gilead-BioStats/gsm/pull/956

Requester	Date Requested	Reviewers	Review Status
chelseadickens	2022-12-13 20:57:14	jwildfire gwu05	DISMISSED

8.0.83 Pull Request 955: fix 919 - qualify AE_Assess for normal approximation

Merging 919-qualify-ae_assess into dev

https://github.com/Gilead-BioStats/gsm/pull/955

Requester	Date Requested	Reviewers	Review Status
chelseadickens	2022-12-13 20:35:10	jwildfire gwu05	APPROVED

8.0.84 Pull Request 952: Report tweaks

Merging report-tweaks into fix-950

https://github.com/Gilead-BioStats/gsm/pull/952

Requester	Date Requested	Reviewers	Review Status
samussiah	2022-12-12 20:49:48	Zhongkai-Wang	APPROVED

8.0.85 Pull Request 951: Report updates

Merging fix-950 into dev

https://github.com/Gilead-BioStats/gsm/pull/951

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2022-12-12 19:10:03	samussiah gwu05	APPROVED

8.0.86   Pull Request 949: systime-based elementId

Merging fix-948 into dev

https://github.com/Gilead-BioStats/gsm/pull/949

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2022-12-09 22:44:13		APPROVED

8.0.87   Pull Request 947: Add screen fail assessment.

Merging fix-902 into dev

https://github.com/Gilead-BioStats/gsm/pull/947

Requester	Date Requested	Reviewers	Review Status
samussiah	2022-12-09 16:50:14	Zhongkai-Wang	APPROVED

8.0.88   Pull Request 946: Release changes

Merging release-changes into dev

https://github.com/Gilead-BioStats/gsm/pull/946

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2022-12-08 20:59:35		COMMENTED

8.0.89   Pull Request 945: Fix 912 - Merge/join handling in mapping

Merging fix-912 into dev

https://github.com/Gilead-BioStats/gsm/pull/945

Requester	Date Requested	Reviewers	Review Status
Zhongkai-Wang	2022-12-08 20:21:48		APPROVED

8.0.90   Pull Request 917: Fix 915 - add rbm-viz widgets to new KRIs

Merging fix-915 into dev

https://github.com/Gilead-BioStats/gsm/pull/917

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2022-12-06 19:56:59	jwildfire	APPROVED

8.0.91 Pull Request 913: Fix 837 report

Merging fix-837-report into dev

https://github.com/Gilead-BioStats/gsm/pull/913

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2022-12-03 00:04:07	jwildfire	COMMENTED

8.0.92 Pull Request 910: Filter `qtl0004` workflow on important PDs.

Merging fix-909 into dev

https://github.com/Gilead-BioStats/gsm/pull/910

Requester	Date Requested	Reviewers	Review Status
samussiah	2022-12-01 18:07:35		APPROVED

8.0.93 Pull Request 908: fix-781-update-merge: update merge

Merging fix-781-update-merge into fix-781

https://github.com/Gilead-BioStats/gsm/pull/908

Requester	Date Requested	Reviewers	Review Status
Zhongkai-Wang	2022-12-01 14:03:18	mattroumaya	COMMENTED

8.0.94 Pull Request 907: Tweak UpdateParams

Merging tweak-UpdateParams into fix-783

https://github.com/Gilead-BioStats/gsm/pull/907

Requester	Date Requested	Reviewers	Review Status
samussiah	2022-11-30 23:11:58		APPROVED

8.0.95 Pull Request 906: Fix 781 assess tests

Merging fix-781-assess-tests into fix-781

https://github.com/Gilead-BioStats/gsm/pull/906

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2022-11-30 20:11:46		COMMENTED

8.0.96   Pull Request 903: update tests + workflows

Merging fix-781-add-tests into fix-781

https://github.com/Gilead-BioStats/gsm/pull/903

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2022-11-29 22:36:06		APPROVED

8.0.97   Pull Request 899: Fix 769 - Add CheckSnapshotInputs()

Merging fix-769 into dev

https://github.com/Gilead-BioStats/gsm/pull/899

Requester	Date Requested	Reviewers	Review Status
mattroumaya	2022-11-22 20:30:31	jwildfire	APPROVED