JMP Clinical 7.1.1 Validation Package

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JMP Clinical Version: 7.1.1

Adding the Nicardipine Study

JMP Clinical ships with the data from a Nicardipine study. The data files are located in the Sample Data in your Installation directory (typically C:\Program Files\SASHome\JMPClinical\14\LifeSciences\Sample Data\Nicardipine).

- Click  to open the Add Study dialog.
- Specify the name of the study. For the validation add-in to work, this name must be Nicardipine.
- Click the Clinical radio button to specify the type of study.
- Specify the file paths to the SDTM and ADaM folders either by typing the path directly or clicking the Browse… button.
- Click the Run button to add the study.

When the study has been successfully added, the Results: Add Study window opens. Close this window before installing the JMP Clinical Validation Add-in.

Installing the JMP Clinical Validation Add-in

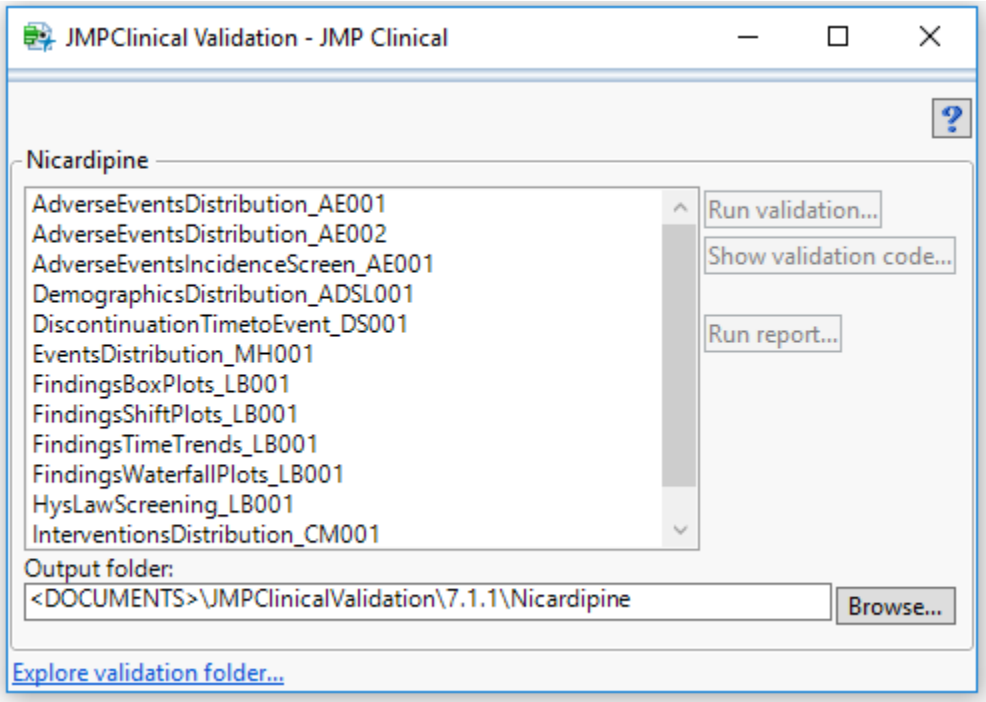
To install the JMP Clinical Validation Add-in, drag JMPClinicalValidationRunner.jmpaddin from <SASHome>/JMPClinical/14/Clinical/Add-in/ into any open JMP window. Click Install when asked Install JMP Add-In "JMP Clinical Validation" (com.jmp.clinicalvalidation)?

Once the add-in is installed, it can be accessed from the Add-Ins menu at the top of the JMP window. This menu can be accessed either by opening the JMP home window or by hovering over the blue bar at the top of the review builder.

Using the JMP Clinical Validation Add-in

To use the JMP Clinical Validation add-in, first open JMP Clinical and set the current study to Nicardipine. If the current study does not have any validation programs, a window will pop up stating "There are no validation programs for the study" when the add-in is launched.

When the add-in is launched, a new window will appear with the list of available validation programs for the selected study.



Reports can be chosen from this list to run validation, show validation code, or run report.

- Run Validation: Runs each validation program to produce the log and output. The output folder will open when the programs are finished running. The output folder location can be changed using the browse button next to the Output folder text box.
- Show Validation code: Opens the SAS code for each validation program.
- Run Report: Opens and runs each JMP Clinical Report template associated with the validation program.

To view the validation package shipped with JMP Clinical, click on the Explore validation folder… link. This will open a folder containing the validation output, programs, README document, review templates, and variable requirements usage.

- Output: Contains a folder for each validation report with the log and output to use for validation.
- Programs: The SAS code for each validation report.
- README: Documentation on how to install and use the add-in as well as how to validate each report using the provided output and templates. The help button in the top right corner of the add-in will link to the PDF version of the documentation kept in this folder.

- ReviewTemplates: A JMP Clinical review template with the options used for each report.
- VariableRequirementsUsage: PDF files of the variable requirements and usage saved from each JMP Clinical review template.

After the SAS validation programs and the JMP Clinical review templates are run, the output in the output folder can be used to compare against the JMP Clinical report to confirm the results. Instructions on how to do this for each report are provided in the list of reports below.

Table of Reports

Demographics Distribution

Review Template	DemographicsDistribution_ADSL001.jmpcrt
Program	DemographicsDistribution_ADSL001.sas
Log	DemographicsDistribution_ADSL001.log
Output	DemographicsDistribution_ADSL001.lst DemographicsDistribution.pdf
Variable Requirements Usage	DemographicsDistribution_ADSL001.pdf
Notes	- Subset on safety population and excluded screen failures - Only Planned treatment variables exist in the dataset, so Planned treatment was used even though the default setting is Actual treatment - Using AGE, created age category variable in the table - PROC FREQ or PROC MEANS were used to replicate the numbers in the distributions and tables - PROC ANOVA and PROC TTEST were used to check the Oneway ANOVA section for Age when the checkbox for "Perform treatment comparison analysis for demographic variables" is checked - PROC FREQ was used to replicate the contingency analysis and tests done for Sex and Race when the checkbox for "Perform treatment comparison analysis for demographic variables" is checked - Create Summary of Demographics with PROC TABULATE - Demographic Tables in the Demographics distribution report can be compared against the table in DemographicsDistribution.pdf from the output folder

Interventions Distribution

Review Template	InterventionsDistribution_CM001.jmpcrt
Program	InterventionsDistribution_CM001.sas
Log	InterventionsDistribution_CM001.log
Output	InterventionsDistribution_CM001.lst SummaryOfConcomitantMedication.pdf
Variable Requirements Usage	InterventionsDistribution_CM001.pdf
Notes	- Subset on safety population and excluded screen failures - Only Planned treatment variables exist in the dataset, so Planned treatment was used even though the default setting is Actual treatment - Merged ADSL and CM by USUBJID - Counts were generated by Dictionary-Derived Term - PROC REPORT was used to write the concomitant medications table to file. - Counts Table in the Concomitant Medication distribution report can be compared against the table in InterventionsDistribution_CM001.pdf from the output folder

Adverse Events Distribution

Review Template	AdverseEventsDistribution_AE001.jmpcrt
Program	AdverseEventsDistribution_AE001.sas
Log	AdverseEventsDistribution_AE001.log
Output	AdverseEventsDistribution_AE001.lst AdverseEventsDistribution_AE001.sas7bdat AdverseEventsDistribution_AE001.pdf
Variable Requirements Usage	AdverseEventsDistribution_AE001.pdf
Assumptions	AdverseEventsDistribution_AE001.sas7bdat is created by sorting the AE data by TRT01P, USUBJID, AEBODSYS, AEDECOD, descending AESER, descending AESEV, and AESTDY and then taking the first record per AEDECOD.
Notes	Counts graph in the report can be recreated from the dataset AdverseEventsDistribution_AE001.sas7bdat using Graph Builder. Counts table in the distribution report can be compared against the table in AdverseEventsDistribution_AE001.pdf from the output folder. The Distributions section of the report can be recreated from the dataset AdverseEventsDistribution_AE001.sas7bdat using the Distributions platform in JMP.

Review Template	AdverseEventsDistribution_AE002.jmpcrt
Program	AdverseEventsDistribution_AE002.sas
Log	AdverseEventsDistribution_AE002.log
Output	AdverseEventsDistribution_AE002.lst AdverseEventsDistribution_AE002.sas7bdat AdverseEventsDistribution_AE002.pdf
Variable Requirements Usage	AdverseEventsDistribution_AE002.pdf
Assumptions	Incidence rates are calculated using the date and time from AESTDTC.
Notes	Counts graph in the report can be recreated from the dataset AdverseEventsDistribution_AE002.sas7bdat using Graph Builder. Counts table in the distribution report can be compared against the table in AdverseEventsDistribution_AE002.pdf from the output folder. The Distributions section of the report can be recreated from the dataset AdverseEventsDistribution_AE002.sas7bdat using the Distributions platform in JMP.

Adverse Events Incidence Screen

Review Template	AdverseEventsIncidenceScreen_AE001.jmpcrt
Program	AdverseEventsIncidenceScreen_AE001.sas
Log	AdverseEventsIncidenceScreen_AE001.log
Output	AdverseEventsIncidenceScreen_AE001.pdf aeincidencescreen_ae001.sas7bdat
Variable Requirements Usage	AdverseEventsIncidenceScreen_AE001.pdf
Assumptions	- Subset on safety population and excluded screen failures - Only Planned treatment variables exist in the dataset, so Planned treatment was used even though the default setting is Actual treatment - Merged ADSL and AE by USUBJID - Macro was created to subset AE data by each AEDECOD - all 2X2 tables constructed from AE incidence and treatment arm
Notes	- PROC FREQ was used to generate all statistics - P values from Cochran-Mantel-Haenszel test - Risk Difference (NIC .15 – Placebo), Relative Risk (NIC .15 vs Placebo), Odds Ratio (NIC.15 vs Placebo) were generated from PROC FREQ - PROC SGPLOT to generate Bubble Plot of -log10(Raw P-value) by Risk Difference (NIC .15 -Placebo), Sized by Counts of AE - Bubble Plot in the AE Incidence Screen report can be compared against the graph in AdverseEventsIncidenceScreen_AE001.pdf from the output folder

Events Distribution

Review Template	EventsDistribution_MH001.jmpcrt
Program	EventsDistribution_MH001.sas
Log	EventsDistribution_MH001.log
Output	MedicalHistory_001.pdf
Variable Requirements Usage	EventsDistribution_MH001.pdf
Notes	- Subset on safety population and excluded screen failures - Only Planned treatment variables exist in the dataset, so Planned treatment was used even though the default setting is Actual treatment - Merged ADSL and MH by USUBJID - Counts were generated by dictionary-derived Term - PROC REPORT was used to write the summary of Medical History table to file. - Counts table in the Medical History distribution report can be compared against the table in MedicalHistory_001.pdf from the output folder

Mortality Time to Event

Review Template	MortalityTimetoEvent_DS001.jmpcrt
Program	MortalityTimetoEvent_DS001.sas
Log	MortalityTimetoEvent_DS001.log
Output	MortalityTimetoEvent_DS001.lst MortalityTimetoEvent_DS001.pdf
Variable Requirements Usage	MortalityTimetoEvent_DS001.pdf
Notes	- Merged ADSL, DS, and DM by USUBJID, keeping all subjects found in ADSL - Created an age group variable for the default setting (0-39, 40-64, >64) - Subset on safety population and excluded screen failures - Subset DS on DSCAT='DISPOSITION EVENT' - Overall counts table of death occurrence regardless of Censor Date was created - Last Disposition Record Date defined as the censor date. o Set censor to 0 if 'DEATH' & DSSTDTC before the censor date. Calculate Survival days as DSSTDTC - RFSTDTC + 1 o Set censor to 1 if not 'DEATH' or Death Date After the censor Date. Calculate survival days as Censor Date - RFSTDTC + 1 - Used PROC LIFETEST to check survival analysis graph and numbers along with ODS output CensoredSummary, HomTests, Means, Quartiles, and ProductLimitEstimates. - Used PROC FREQ to recreate mosaic plot - Used PROC PHREG to check hazard ratios along with ODS output HazardRatios - Overall Survival analysis and Hazard Ratio Estimates for Subgroup of Demographics from Overall Survival Report.rtf in the report can be compared against the table in MortalityTimetoEvent_DS001.pdf from the output folder

Discontinuation Time to Event

Review Template	DiscontinuationTimetoEvent_DS001.jmpcrt
Program	DiscontinuationTimetoEvent_DS001.sas
Log	DiscontinuationTimetoEvent_DS001.log
Output	DiscontinuationTimetoEvent_DS001.lst MosaicPlot.png SurvivalPlot.png
Variable Requirements Usage	DiscontinuationTimetoEvent_DS001.pdf
Notes	- Merged ADSL, DS, and DM by USUBJID, keeping all subjects found in ADSL - Subset on safety population and excluded screen failures - Subset DS on DSCAT='DISPOSITION EVENT' - Define Events as Discontinuations due to Adverse events or deaths - Last Disposition Record Date defined as the censor date. o Set censor to 0 if DEDECOD='DEATH' or "ADVERSE EVENT" Calculate Time to event as DSSTDTC – RFSTDTC +1 o Set censor to 1 if not "DEATH" nor "ADVERSE EVENT" o Set censor to 1 if not in DS, use RFENDTC as censor cutoff date, Calculate Time to event as Censor Date -RFSTDTC+1 - Used PROC LIFETEST to check survival analysis graph and numbers along with ODS output CensoredSummary, HomTests, Means, Quartiles, and ProductLimitEstimates. - Used PROC FREQ to recreate mosaic plot - Used PROC PHREG to check hazard ratios along with ODS output HazardRatios - Survival Plot and Mosaic Plot in the Discontinuation Time to Event report can be compared against the SurvivalPlot.png and Mosaic Plot from the output folder

Findings Time Trends

Review Template	FindingsTimeTrends_LB001.jmpcrt
Program	FindingsTimeTrends_LB001.sas
Log	FindingsTimeTrends_LB001.log
Output	FindingsTimeTrends_LB001.sas7bdat FindingsTimeTrends_LB001.pdf
Variable Requirements Usage	FindingsTimeTrends_LB001.pdf
Assumptions	- Observed Laboratory Test Results with no normalization were used. - Use mean for multiple measurements on the same VISITNUM - Compute averages for each Visit number over the whole dataset
Notes	- Laboratory Test Results Time Trend Plots were created using PROC SGPLOT - Plots of Laboratory Test Results Treatment Time Trends and counts vs Visit Number distribution in the Findings Time Trends report can be compared against the plots in FindingsTimeTrends_LB001.pdf from the output folder

Findings Box Plots

Review Template	FindingsBoxPlots_LB001.jmpcrt
Program	FindingsBoxPlots_LB001.sas
Log	FindingsBoxPlots_LB001.log
Output	FindingsBoxPlots_LB001.lst FindingsBoxPlots_LB001.sas7bdat FindingsBoxPlots_LB001.pdf
Variable Requirements Usage	FindingsBoxPlots_LB001.pdf
Assumptions	To derive the baseline value, keep only records where LBBLFL='Y'. If multiple records exist on the same day, then take the mean per day. If multiple baseline records exist after taking the mean per day, take the last record per subject per lab test. If multiple post-baseline records exist, then take the mean per lab test per visit number.
Notes	Change from Baseline Box Plots in the report can be recreated from the dataset FindingsBoxPlots_LB001.sas7bdat using Graph Builder. Change from Baseline Summary Statistic Tables can be compared against the table in FindingsBoxPlots_LB001.pdf from the output folder.

Findings Waterfall Plots

Review Template	FindingsWaterfallPlots_LB001.jmpcrt
Program	FindingsWaterfallPlots_LB001.sas
Log	FindingsWaterfallPlots_LB001.log
Output	FindingsWaterfallPlots_LB001.lst FindingsWaterfallPlots_LB001.sas7bdat
Variable Requirements Usage	FindingsWaterfallPlots_LB001.pdf
Assumptions	To derive the baseline value, keep only records where LBBLFL='Y'. If multiple baseline records exist, take the last record per subject per lab test. For post-baseline records if multiple records exist, then take the mean per lab test per visit number.
Notes	Laboratory Test Results Waterfall Plots in the report can be recreated from the dataset FindingsWaterfallPlots_LB001.sas7bdat using Graph Builder.

Hy's Law Screening

Review Template	HysLawScreening_LB001.jmpcrt
Program	HysLawScreening_LB001.sas
Log	HysLawScreening_LB001.log
Output	HysLawScreening_LB001.lst HysLawScreening_LB001.sas7bdat HysLawScreening_LB001_by_day.sas7bdat HysLawScreening_LB001.pdf
Variable Requirements Usage	HysLawScreening_LB001.pdf
Notes	The Liver Test Elevations Plot and Scatterplot Matrix can be recreated from the dataset HysLawScreening_LB001.sas7bdat using Graph Builder. Peak Liver Lab Tests per Subject by Study Day can be recreated from the dataset HysLawScreening_LB001_by_day.sas7bdat using Graph Builder. Contingency Analysis of Elevated AT Tests By Planned Treatment for Period 01 can be recreated from the dataset HysLawScreening_LB001.sas7bdat using Fit Y by X. Distributions can be recreated from the dataset HysLawScreening_LB001.sas7bdat using the Distributions platform in JMP. Tables in the report for AT Test Elevation and Possible Hy's Law Cases, ALT Counts and Percents, AST Counts and Percents, AST Counts and Percents, BILI Counts and Percents, ALP Counts and Percents, Counts of Missing Liver Lab Records, and Counts of Subjects Missing All Tests can be compared against the table in HysLawScreening_LB001.pdf from the output folder.

Findings Shift Plots

Review Template	FindingsShiftPlots_LB001.jmpcrt
Program	FindingsShiftPlots_LB001.sas
Log	FindingsShiftPlots_LB001.log
Output	FindingsShiftPlots_LB001.sas7bdat FindingsShiftPlots_LB001.pdf
Variable Requirements Usage	FindingsShiftPlots_LB001.pdf
Assumptions	To derive the baseline value, keep only records where LBBLFL='Y'. If multiple baseline records exist, take the last record per subject per lab test. For post-baseline records if multiple records exist, then take the mean per lab test per visit number. "ULN" Normalization of Lab Measurements was used: to divide the measured lab values by the value considered to be the upper limit of the normal range (ULN) of values. Log2 transformation of normalized Lab measurements were calculated.
Notes	- Laboratory Test Results Shift Plots Trial Mean vs Baseline were created using PROC SGPLOT - Test Results Shift Tables were created using PROC FREQ - Laboratory Test Results Shift Plots in the report can be compared against the plots in FindingsShiftPlots_LB001.pdf from the output folder