Getting Started: SAS® Visual Data Mining and Machine Learning

Overview

SAS® Visual Data Mining and Machine Learning combines data wrangling, exploration, feature engineering, and modern statistical, data mining and machine learning techniques in a single, scalable in memory processing environment.

As part of the *Project Data Sphere* Platform, authorized users can use SAS Visual Data Mining and Machine Learning to:

- **ACCESS** downloadable cancer clinical trial data that has been provided to the *Project Data Sphere* Platform
- **EXPLORE** data using SAS Studio and SAS Data Studio to learn more about the various datasets contributed with a study
- **VISUALIZE** data using SAS Visual Analytics to better share findings with individuals of all backgrounds
- **HARMONIZE** data using SAS Data Studio to compare or combine data from various studies to drive further research
- **DESIGN MODELS** using SAS Model Studio to discover new insights

Legal Disclaimer

Any sample code are provided as-is and SAS has no obligation to provide continued support for their use. Use of any part or all of this code is not guaranteed to fulfill any legal or other requirements of any specific data governance standard or law governing de-identification of data. Users assume all responsibility for ensuring that the final publication of any de-identified data meets all legal requirements for release of such data. Users assume all legal and ethical responsibility for determining the appropriateness of releasing data analyzed and/or modified using this code.

How to Access

Becoming an Authorized User of *Project Data Sphere*

To use SAS Visual Data Mining and Machine Learning or other SAS analytical tools, the user must first be an Authorized User of the *Project Data Sphere* website.

a. For additional information on becoming an Authorized User, see the separate "How To Guide: Becoming an Authorized User" document located in the Resources section of the *Project Data Sphere* website.
b. After receiving Authorized User login credentials, the user can click on the "Sign in" link in the upper right-hand corner of the *Project Data Sphere* website to access the SAS analytical tools.

Accessing SAS Visual Data Mining and Machine Learning

1. In the navigation bar, click Access Data.

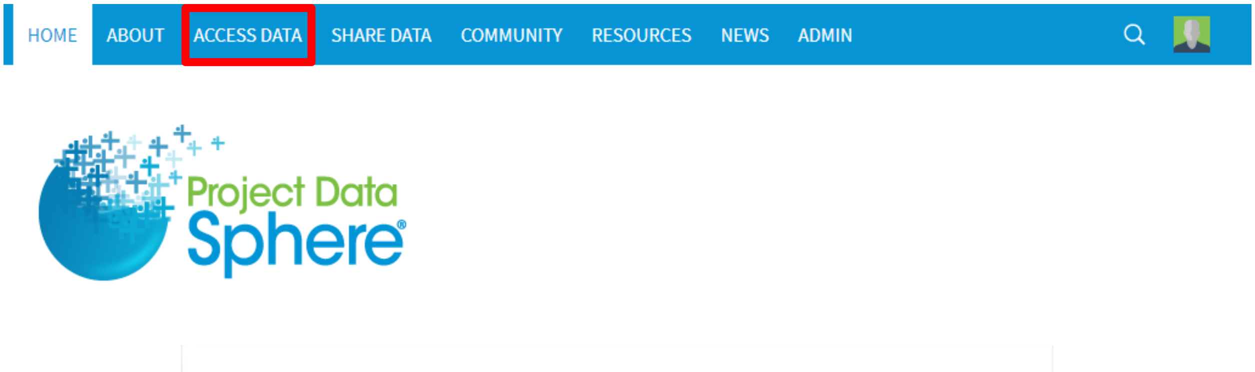


Figure 1: Navigating to the Access Data page

2. Click the SAS Visual Data Mining and Machine Learning button (pictured below) either on the Access Data page or within the detailed information page of any contribution.

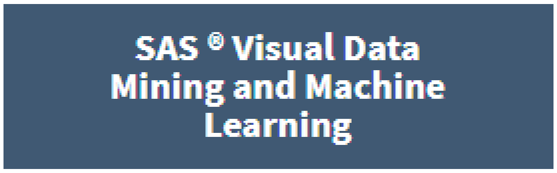
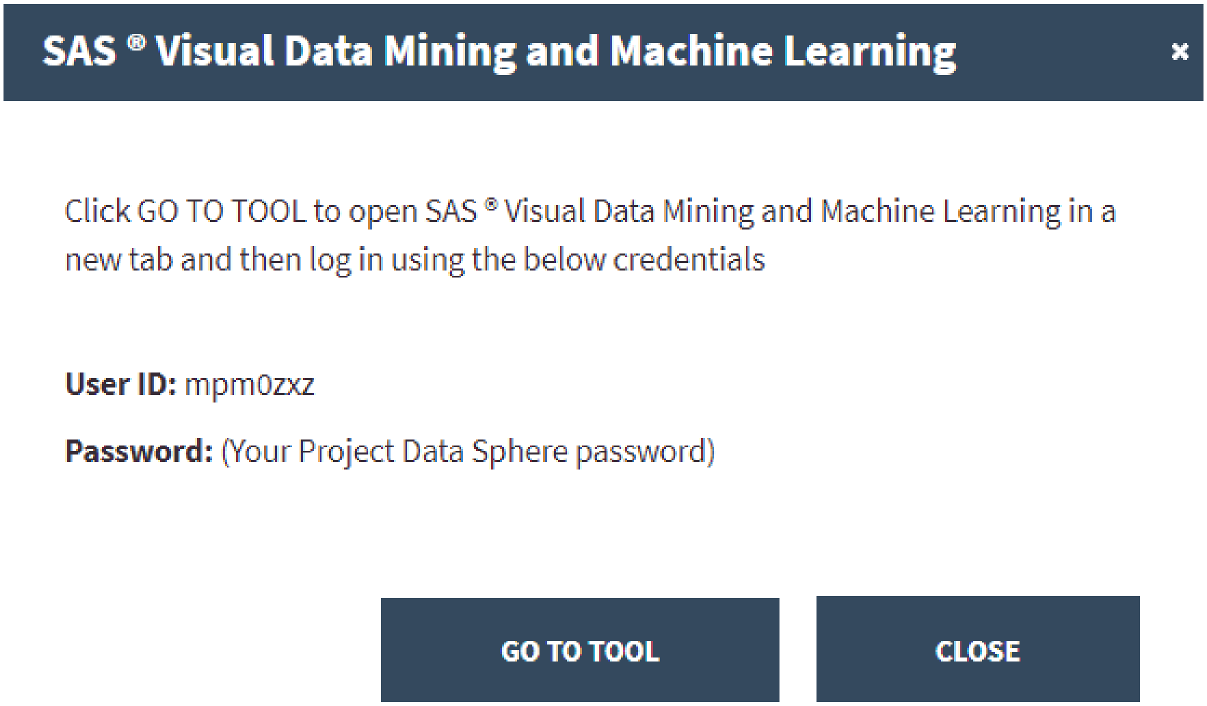


Figure 2: Access SAS Visual Data Mining and Machine Learning from the Access Data page

3. A dialog will be displayed with instructions on accessing the tool. After reading the instructions, click 'GO TO TOOL' and a new tab will be opened.
    a. Note: You must use your own user ID, not the one picture in the figure below.



SAS ® Visual Data Mining and Machine Learning

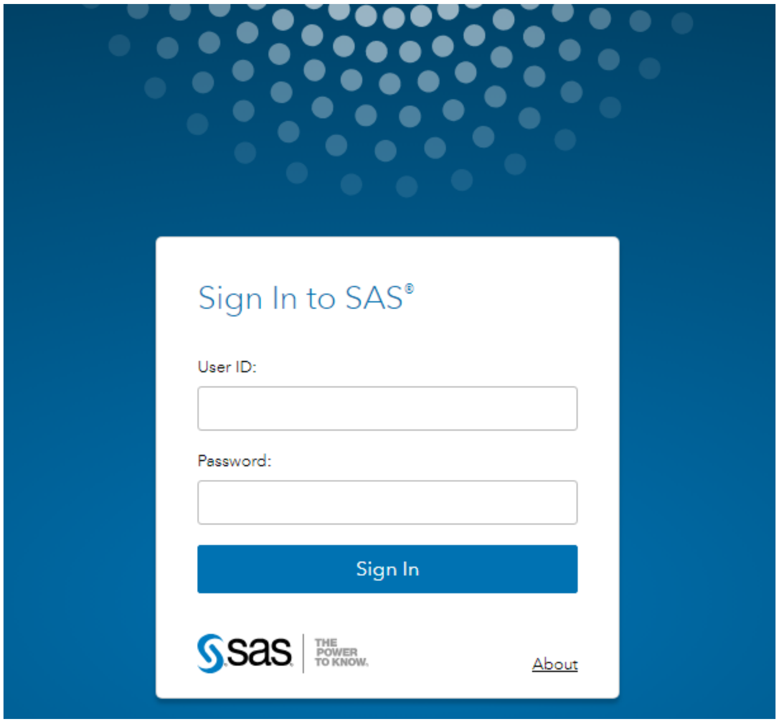
Click GO TO TOOL to open SAS ® Visual Data Mining and Machine Learning in a new tab and then log in using the below credentials

User ID: mpm0zxz

Password: (Your Project Data Sphere password)

Figure 3: Instructions for logging into SAS Visual Data Mining and Machine Learning

4. Following the instructions from the dialog, log into SAS Visual Data Mining and Machine Learning using the specified username and password.



Sign In to SAS®

User ID:

Password:

Figure 4: SAS Logon screen

5. After logging in for the first time, you may be prompted to select a profile picture and a theme, but you can skip this setup if desired.

Quick Start

After logging in, the user will be directed to the SAS Drive. SAS Drive is the hub for the SAS Viya applications that enables you to easily view, organize, and share your content from one place. The availability of the features in SAS Drive depends on the applications that have been installed, and the features and permissions that have been specified by your administrator.

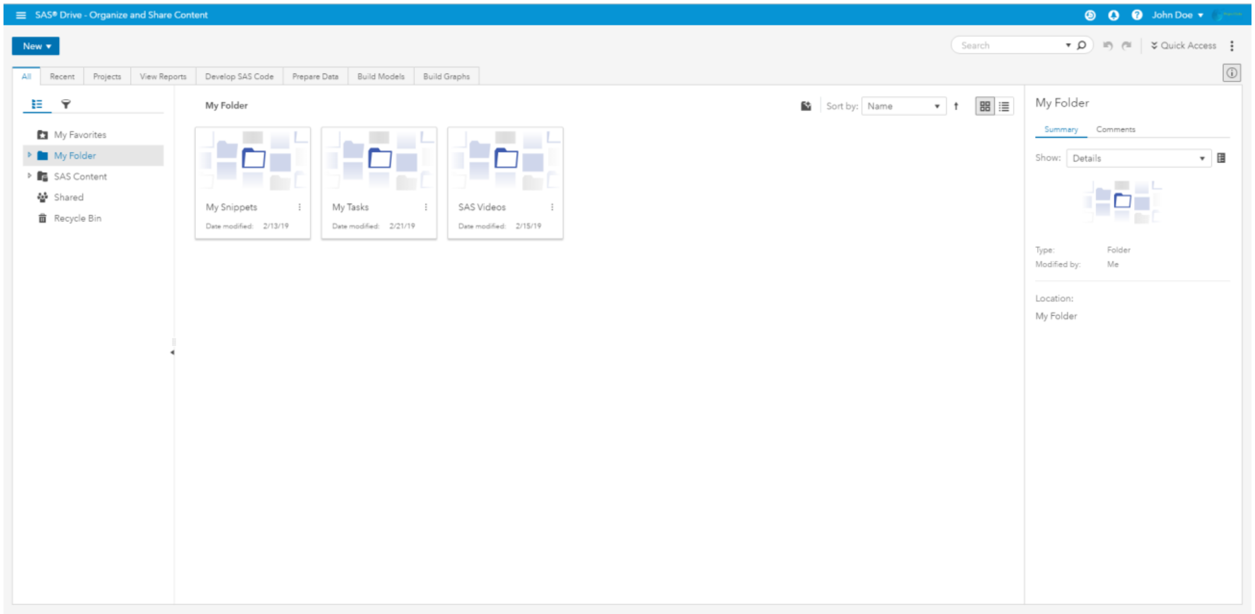


Figure 5: SAS Drive

The application switcher is in the top left and can be used to access the different applications available.

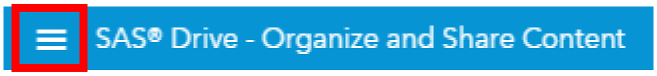


Figure 6: SAS Application Switcher Icon

These actions can be used to access the following tools:

- View Reports: SAS Report Viewer
- Develop SAS Code: SAS Studio
- Prepare Data: Data Studio
- Explore and Visualize Data: SAS Visual Analytics
- Build Models: Model Studio
- Explore Lineage: SAS Lineage Viewer
- Build Graphs: SAS Graph Builder

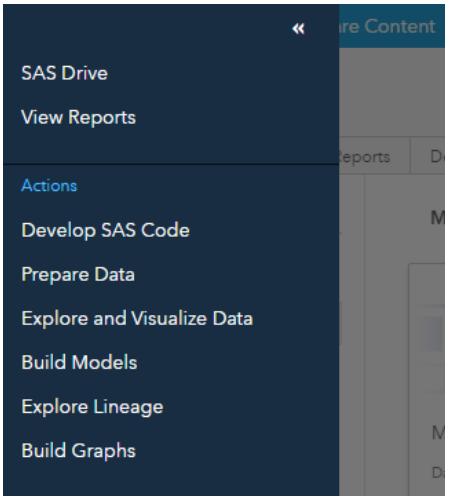


Figure 7: Application Switcher

In addition, while not featured in our Getting Started guides, users also have access to SAS Report Viewer, SAS Lineage Viewer, and SAS Graph Builder which allow users to view reports, understand the relationships between objects in your SAS Viya applications, and to create custom graph objects respectively.

What's Next?

To learn more about the different applications available with SAS Visual Data Mining and Machine Learning, check out the Quick Start guides created by the *Project Data Sphere* team.

The guides can be worked through independently, but all are related to a single example of the analytics lifecycle using *Project Data Sphere*'s DREAM Challenge data sets. In each guide, a user will navigate through a different application to prepare, explore, visualize, or model data.

- Getting Started: Locating a contribution in the SAS Visual Data Mining and Machine Learning environment – Learn how the *Project Data Sphere* contributions are organized in the SAS analytic tools.
- Getting Started: SAS® Studio – Learn how to load *Project Data Sphere* contributions into SAS Studio to start exploring and writing SAS programs.
- Getting Started: SAS® Data Studio – Learn how to transform data using Data Studio to prepare it for later analytics.
- Getting Started: SAS® Visual Analytics – Learn how to quickly create reports to visualize and explore data.
- Getting Started: SAS® Model Studio – Learn how to create analytic pipelines in Model Studio to perform machine learning.
- Getting Started: API Access to SAS® Visual Data Mining and Machine Learning using Python – Learn how to use SAS analytics through a Python environment.
- Getting Started: API Access to SAS® Visual Data Mining and Machine Learning using R – Learn how to use SAS analytics through an R environment.

Additional Videos

SAS® Viya™: The Big Picture

Getting Started with SAS Visual Data Mining and Machine Learning 8.1 on SAS Viya

SAS Visual Data Mining and Machine Learning on SAS Viya: Overview

Need Help?

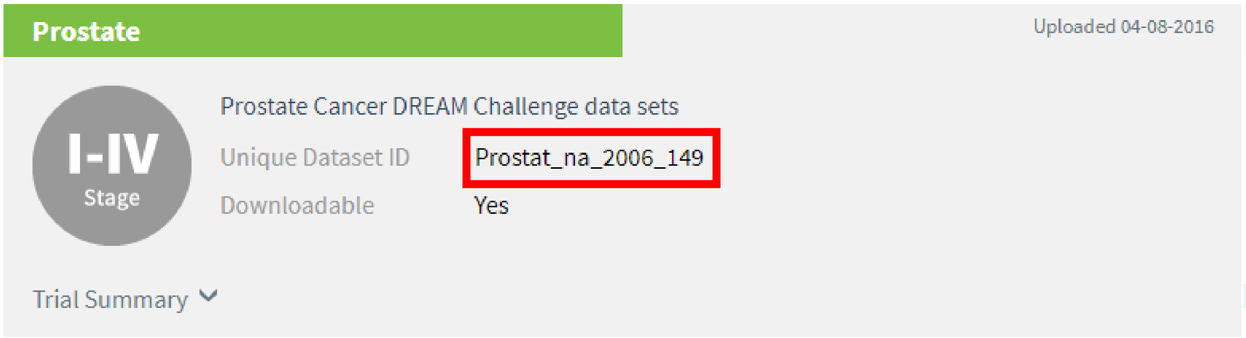
Are you still not sure how to get started or need help? Get in touch with the *Project Data Sphere* team using the Contact Us feature.

You can also check the SAS Support Communities where you can ask questions and get help for a community of SAS experts!

Getting Started: Locating a contribution in the SAS Visual Data Mining and Machine Learning environment

The Unique Dataset ID

All downloadable contributions are automatically available to the SAS analytic tools on the *Project Data Sphere* platform. Contributions are organized into directories identified by their Unique Dataset ID. The Unique Dataset ID can be identified by finding a contribution on the Access Data page or a specific contribution details page.



Prostate

Uploaded 04-08-2016

I-IV Stage

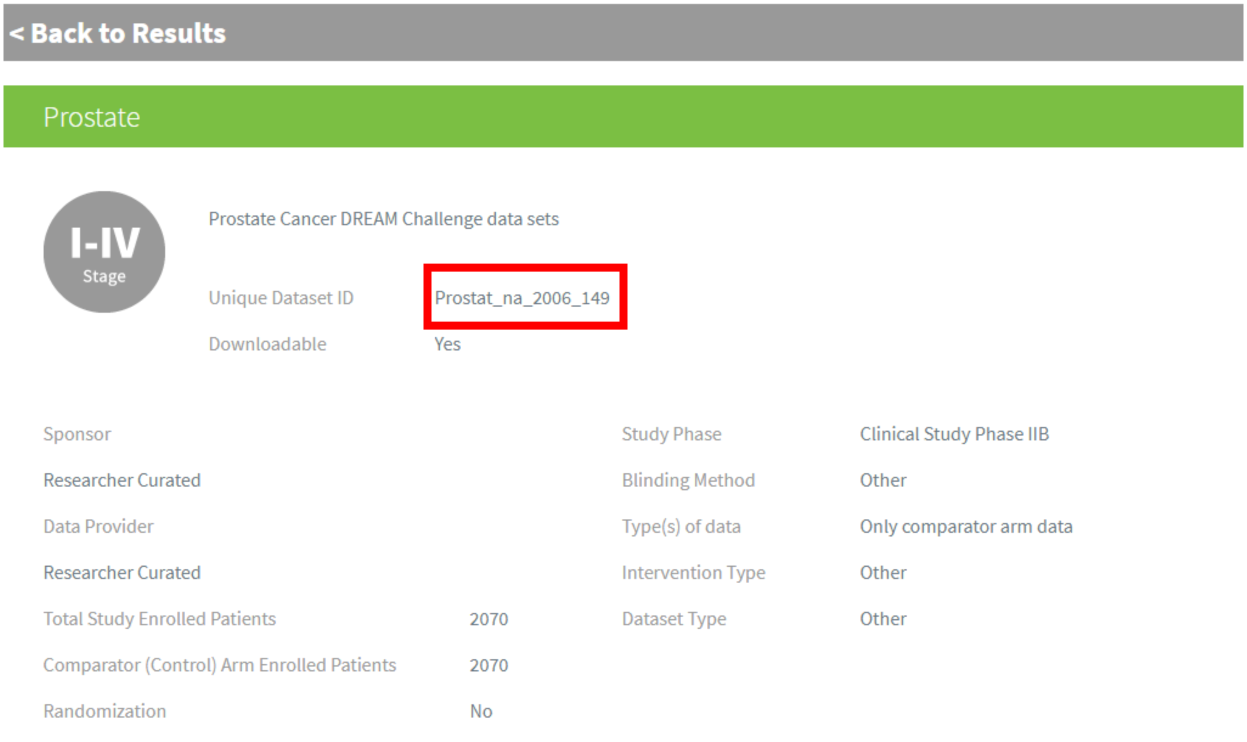
Prostate Cancer DREAM Challenge data sets

Unique Dataset ID Prostat_na_2006_149

Downloadable Yes

Trial Summary

Figure 8: Identifying a Unique Dataset ID on the Access Data Page



< Back to Results

Prostate

I-IV Stage

Prostate Cancer DREAM Challenge data sets

Unique Dataset ID Prostat_na_2006_149

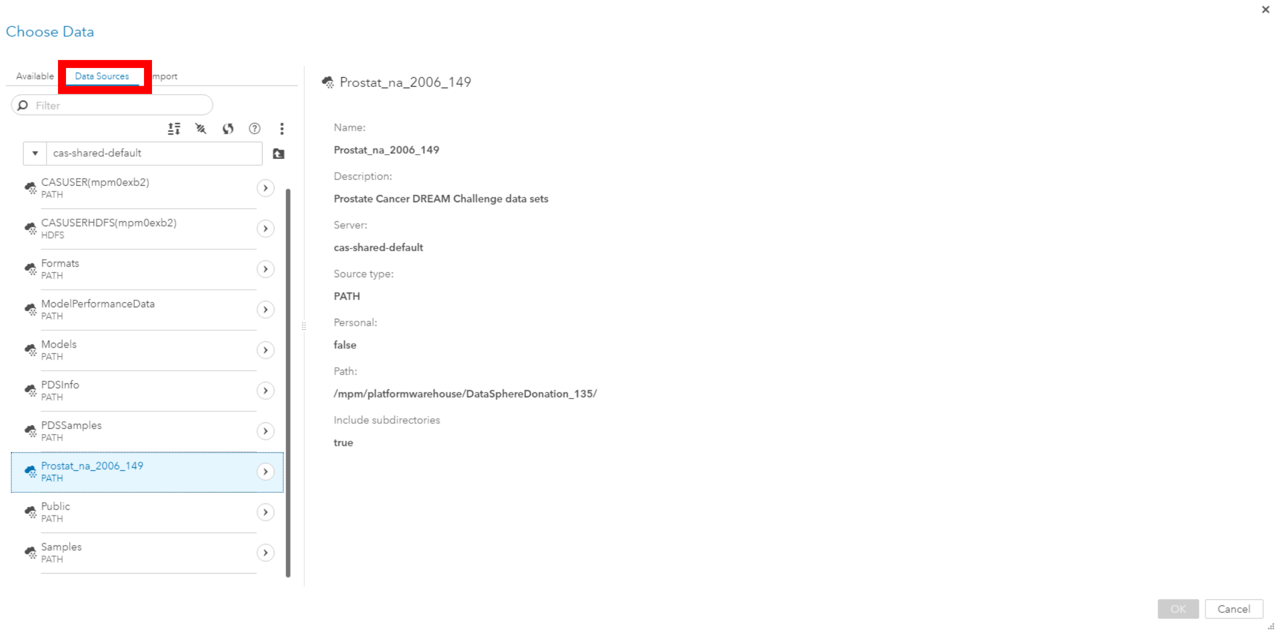
Downloadable Yes

Sponsor		Study Phase	Clinical Study Phase IIB
Researcher Curated		Blinding Method	Other
Data Provider		Type(s) of data	Only comparator arm data
Researcher Curated		Intervention Type	Other
Total Study Enrolled Patients	2070	Dataset Type	Other
Comparator (Control) Arm Enrolled Patients	2070		
Randomization	No		

Figure 9: Identifying the Unique Dataset ID on a Contribution Contents page

Finding the CASLib

In SAS Visual Data Mining and Machine Learning, you can find a contribution either using SAS Studio or the Data Explorer dialog available in most applications (Please see the Getting Started guides for more details). In the Data Explorer dialog, click the Data Sources tab and then click cas-shared-default. You should then be able to find the contribution by its Unique Dataset ID.



Name:
Prostat_na_2006_149

Description:
Prostate Cancer DREAM Challenge data sets

Server:
cas-shared-default

Source type:
PATH

Personal:
false

Path:
/mpm/platformwarehouse/DataSphereDonation_135/

Include subdirectories
true

Figure 10: Data Explorer Dialog

Note: If a contribution contains sub directories then you must use SAS Studio to access them. See Getting Started: SAS® Studio for more information.

Getting Started: SAS® Studio

Overview

SAS Studio provides a web browser-based programming environment which lets you access your files and do all your SAS coding from anywhere. The environment will be familiar to SAS programmers who just want to write code, but SAS Studio also includes visual point-and-click tasks that generate code – so you don't have to. In addition, users will have the ability to create and use existing code snippet libraries of often repeated tasks. Lastly, SQL queries can easily be generated allowing users to select, sort, filter, and join on tables to begin their data exploration.

https://support.sas.com/en/software/studio.html

Quick Start

In this Quick Start, we will learn how to access a *Project Data Sphere* contribution using SAS Studio.

1. Log into SAS Visual Data Mining and Machine Learning.
2. In the application switcher click on Develop SAS Code to navigate to SAS Studio.

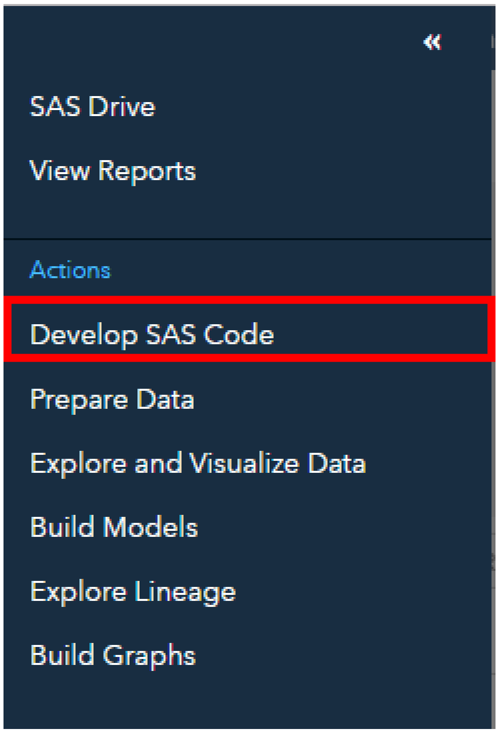


Figure 11: Navigate to SAS Studio by clicking Develop SAS Code in the App Switcher

3. Once in SAS Studio, we're going to add a custom task created by the *Project Data Sphere* team to help with loading contributions. First, click the Explorer icon in the navigate pane and then navigate to SAS Content -> PDS -> Samples. Next, right click 'Create Libref for PDS Contribution.ctm' and select 'Add to My Tasks'. In the dialog that is displayed, click OK.

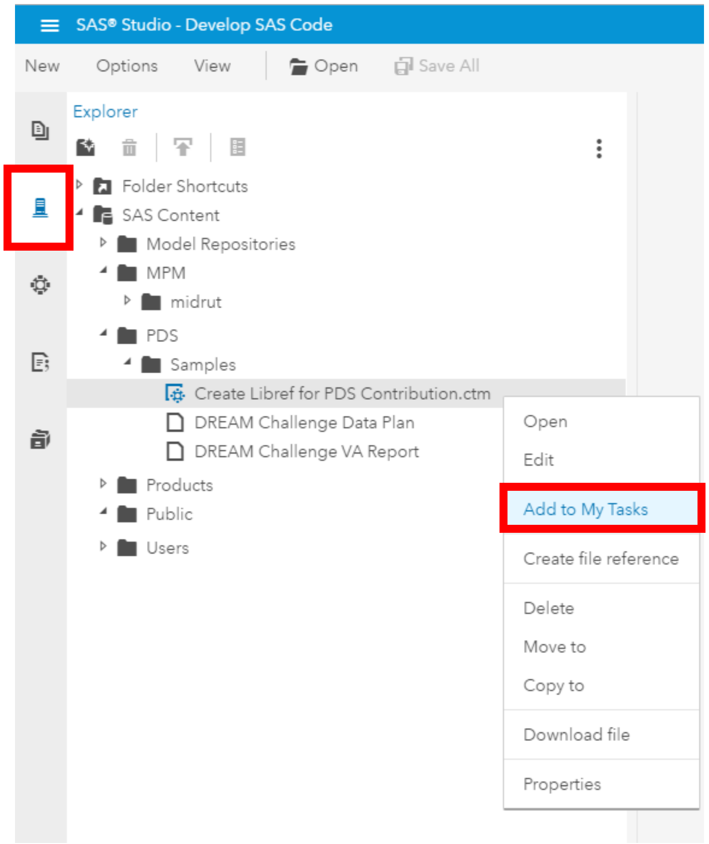


Figure 12: Adding custom task to My Tasks

4. To open the custom task, click the Tasks icon in the navigation pane and then double click the task displayed under 'My Tasks'.

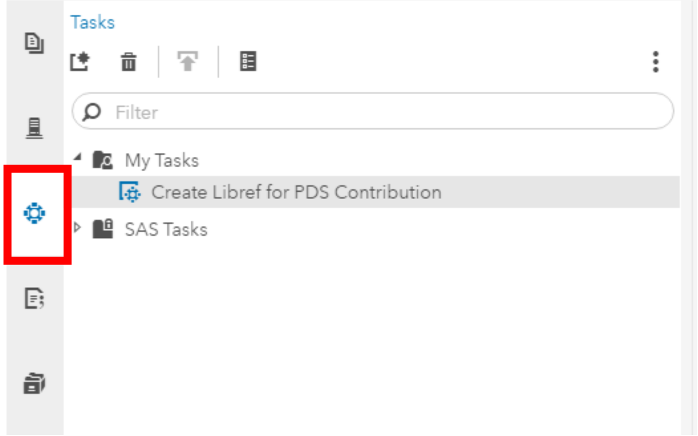
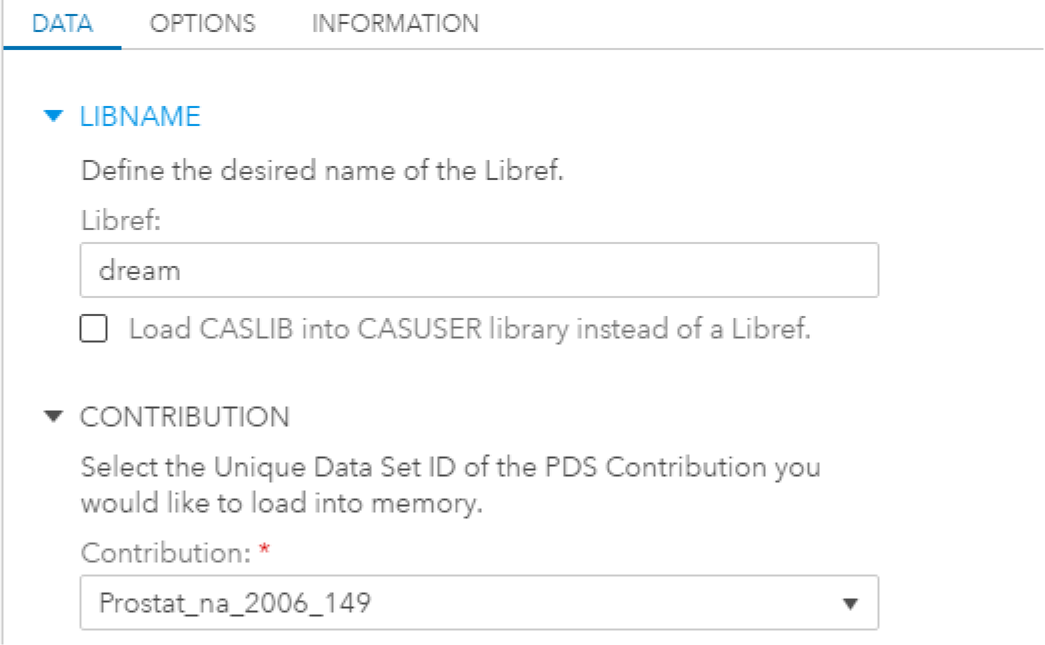


Figure 13: Opening a SAS Studio Task

5. After the task has been opened in a new tab, the user can enter the desired name of their libname and select a contribution (Caslib) for which to load into memory. Remember, the name of the Caslib corresponds to the Unique Dataset ID.
    a. For this example, 'dream' was chosen for the libname because the datasets are from the DREAM challenge and the CASLib 'Prostat_na_2006_149' was selected.

b. In addition, if you would like to load and save the data from a contribution into your CASUSER library you can check the checkbox. For this example, we will leave the checkbox unchecked.



DATA OPTIONS INFORMATION

LIBNAME

Define the desired name of the Libref.

Libref:

dream

□ Load CASLIB into CASUSER library instead of a Libref.

CONTRIBUTION

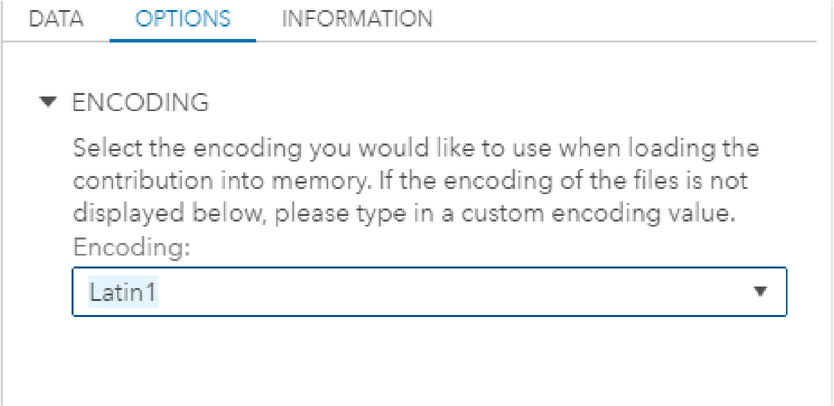
Select the Unique Data Set ID of the PDS Contribution you would like to load into memory.

Contribution: *

Prostat_na_2006_149

Figure 14: Task Data tab

6. In most cases this should be all you have to do, but the DREAM challenge data does not match the default configuration expected by SAS Viya (the default is UTF-8). Click the OPTIONS tab and change the selected encoding to Latin1.



DATA OPTIONS INFORMATION

ENCODING

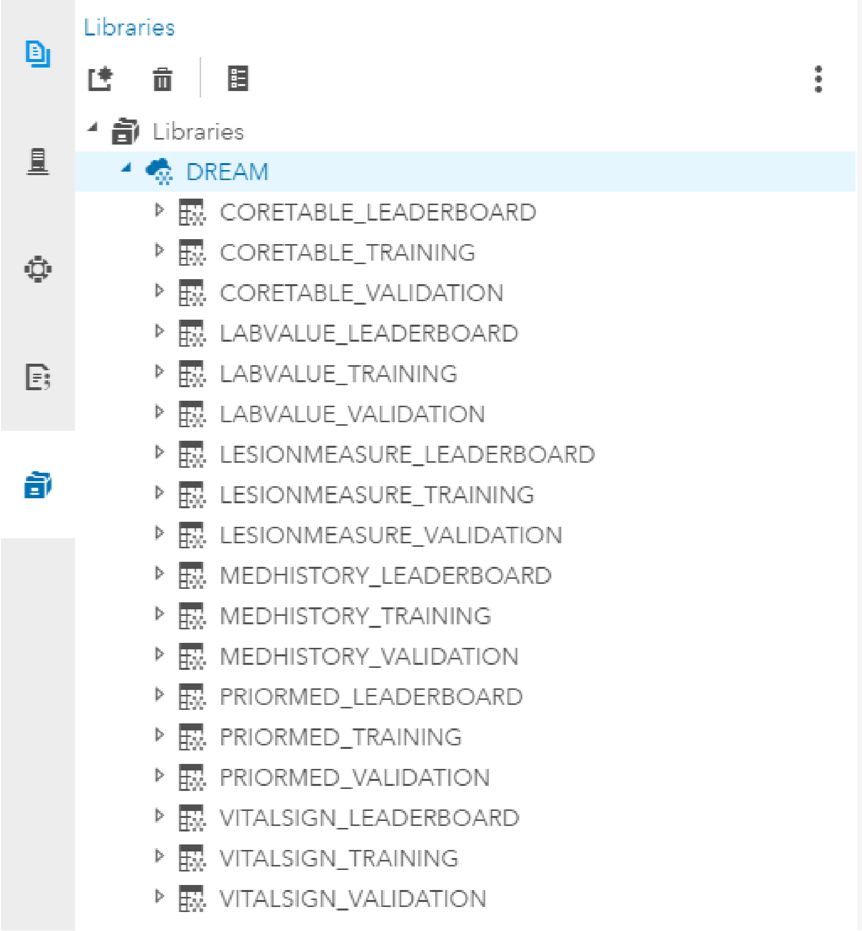
Select the encoding you would like to use when loading the contribution into memory. If the encoding of the files is not displayed below, please type in a custom encoding value.

Encoding:

Latin1

Figure 15: Task Option tab

7. Click the Submit button!
8. Lastly, navigate to the Libraries section of the navigation pane by clicking the Libraries icon. You will find all the data files in the DREAM challenge contribution have been loaded into the specified library.



- Libraries
  - DREAM
    - CORETABLE_LEADERBOARD
    - CORETABLE_TRAINING
    - CORETABLE_VALIDATION
    - LABVALUE_LEADERBOARD
    - LABVALUE_TRAINING
    - LABVALUE_VALIDATION
    - LESIONMEASURE_LEADERBOARD
    - LESIONMEASURE_TRAINING
    - LESIONMEASURE_VALIDATION
    - MEDHISTORY_LEADERBOARD
    - MEDHISTORY_TRAINING
    - MEDHISTORY_VALIDATION
    - PRIORMED_LEADERBOARD
    - PRIORMED_TRAINING
    - PRIORMED_VALIDATION
    - VITALSIGN_LEADERBOARD
    - VITALSIGN_TRAINING
    - VITALSIGN_VALIDATION

Figure 16: Data files loaded into Library

You're all done! Now you can begin exploring the individual data files and start programming with them in SAS Studio.

Documentation

https://www.sas.com/en_us/software/studio.html

Additional Videos

SAS® Viya™ CAS Libraries (Caslibs) Simplified

Understanding Caslibs and Loading Data in SAS® Viya™

Using the DATA Step in SAS® Viya™

Accessing SAS® Viya® Tasks in SAS® Studio or SAS® Enterprise Guide®

SAS® Viya™ Programming for SAS® 9 Programmers: Overview

Getting Started: Data Studio

Overview

SAS Data Studio provides an easy way to prepare data for analysis. With Data Studio users can create plans containing a variety of data transformations such as joining tables, appending data to tables, transposing columns, and creating calculated columns. Users can also view profiles of tables to view metrics such as pattern and frequency distributions. Data Studio is a self-service application, which users without data management programming skills can use to transform data to solve their analytic problems.

Quick Start

In this Quick Start, we will prepare data for visualization and model building. To do this, we will learn how to use Data Studio to transform a table from the DREAM challenge contribution into an analytics-ready state.

1. Log into SAS Visual Data Mining and Machine Learning.
2. First, we must load data from the PDSSamples CASLib into our CASUSER CASLib.
    a. Note: If you have completed this step in another Getting Started guide, then you can proceed to step 3. The PDSSamples CASLib contains sample files for the Getting Started guides and is different from the files used in Getting Started: SAS® Studio.
    b. In the application switcher, click on Develop SAS Code to navigate to SAS Studio.

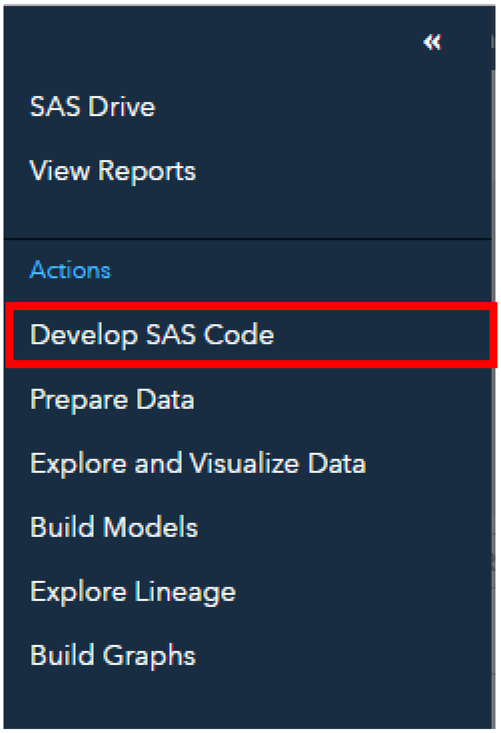
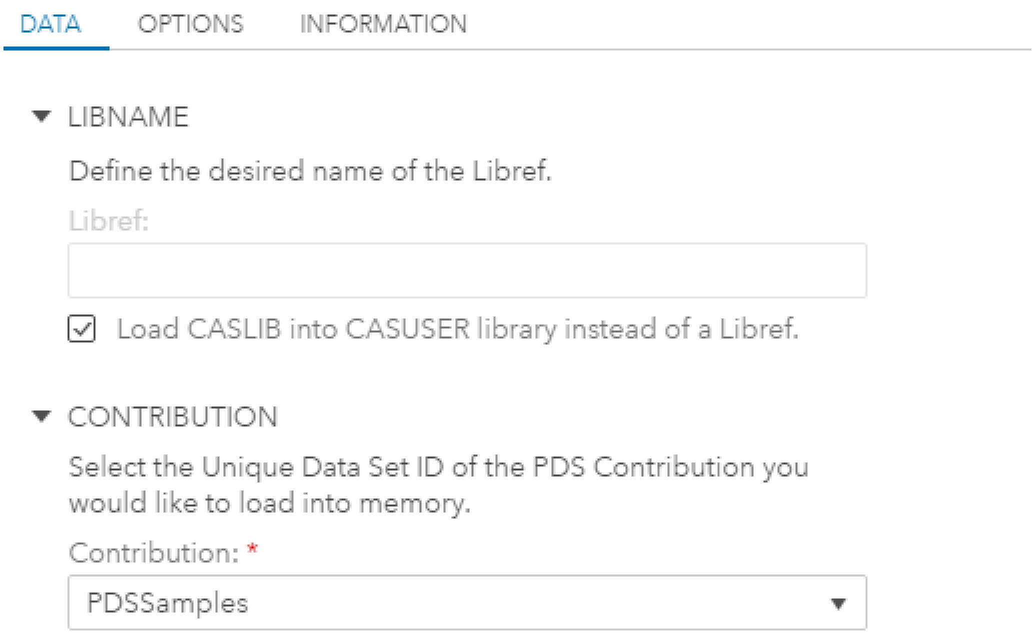


Figure 17: Navigate to SAS Studio by clicking Develop SAS Code in the App Switcher

    c. Using the ‘Create Libref for PDS Contribution’ task under My Tasks load the data from the PDSSamples into your CASUSER library.



LIBNAME

Define the desired name of the Libref.

Libref:

☑ Load CASLIB into CASUSER library instead of a Libref.

CONTRIBUTION

Select the Unique Data Set ID of the PDS Contribution you would like to load into memory.

Contribution: * PDSSamples

Figure 18 SAS Studio task to load data from PDSSamples to CASUSER library

3. Next, in the application switcher, click on Prepare Data to navigate to SAS Data Studio.

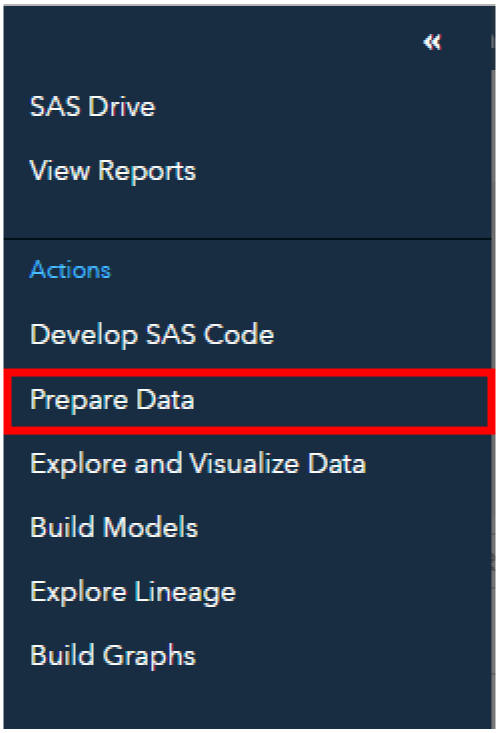


Figure 19: Navigate to SAS Data Studio by clicking Prepare Data in the App Switcher

4. Once in Data Studio, click 'New Plan'.

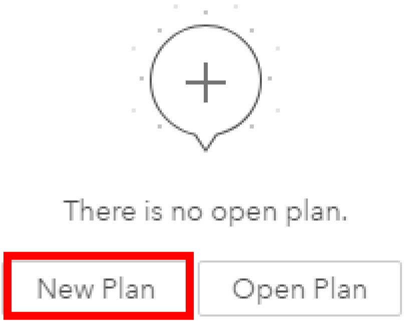
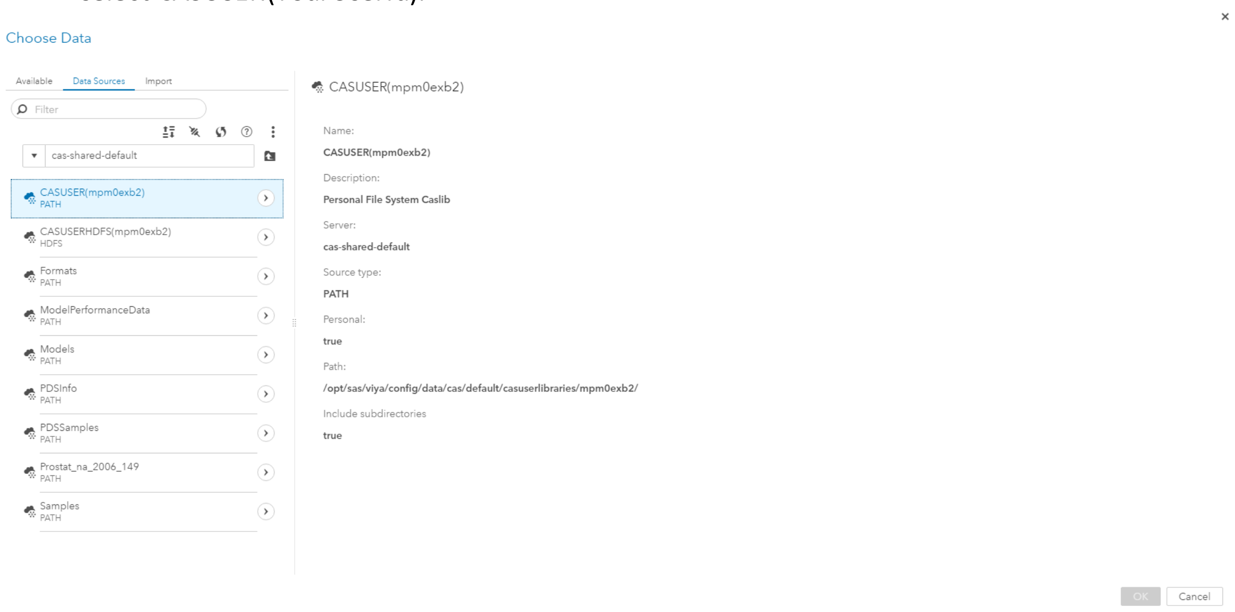


Figure 20: Click 'New Plan' to start a new Plan

5. Next, we must select the table we're going to transform. In the Choose Data dialog that opens, select Data Sources from the top three tabs and then select cas-shared-default, and then finally select CASUSER(YourUserId).



CASUSER(mpm0exb2)

Name:
CASUSER(mpm0exb2)

Description:
Personal File System Caslib

Server:
cas-shared-default

Source type:
PATH

Personal:
true

Path:
/opt/sas/viya/config/data/cas/default/casuserlibraries/mpm0exb2/

Include subdirectories
true

Figure 21: Choosing table to use in Data Studio

6. Next, double click on CASUSER.
7. To prepare data in Data Studio, the table we want to transform must first be loaded into memory. We want to work on the DC_CORE_TABLE.sashdat, but it may already be loaded into memory for us. The table is already loaded into memory if there is a row titled DC_CORE_TABLE and it has a lightning bolt icon to its left.

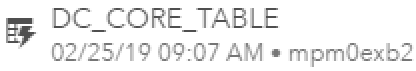
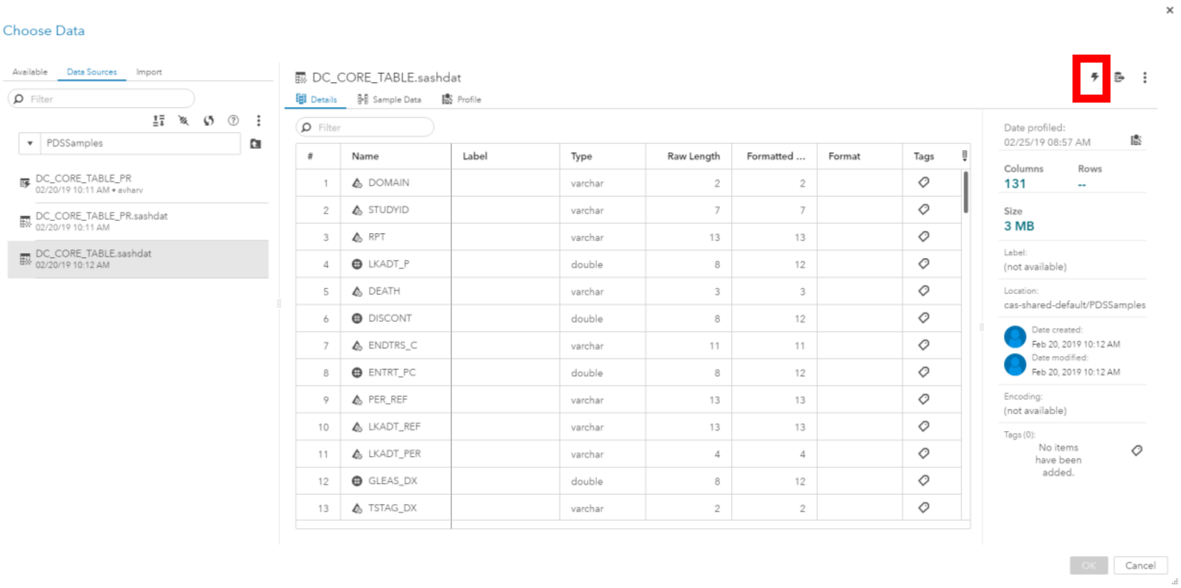


Figure 22: The DC_CORE_TABLE loaded into memory

8. If you do not see the in memory table, then select DC_CORE_TABLE.sashdat and then click the lightning bolt icon in the top right. Otherwise, just proceed to the next step.

a. From this view you can view details about the columns in the table, view a sample of the first 100 rows, and even profile the table to find more insights.



#	Name	Label	Type	Raw Length	Formatted ...	Format	Tags
1	DOMAIN		varchar	2	2		
2	STUDYID		varchar	7	7		
3	RPT		varchar	13	13		
4	LKADT_P		double	8	12		
5	DEATH		varchar	3	3		
6	DISCONT		double	8	12		
7	ENDTRS_C		varchar	11	11		
8	ENTRT_PC		double	8	12		
9	PER_REF		varchar	13	13		
10	LKADT_REF		varchar	13	13		
11	LKADT_PER		varchar	4	4		
12	GLEAS_DX		double	8	12		
13	TSTAG_DX		varchar	2	2		

Date profiled:
02/25/19 08:57 AM

Columns 131

Rows --

Size 3 MB

Label:
(not available)

Location:
cas-shared-default/PDSSamples

Date created:
Feb 20, 2019 10:12 AM

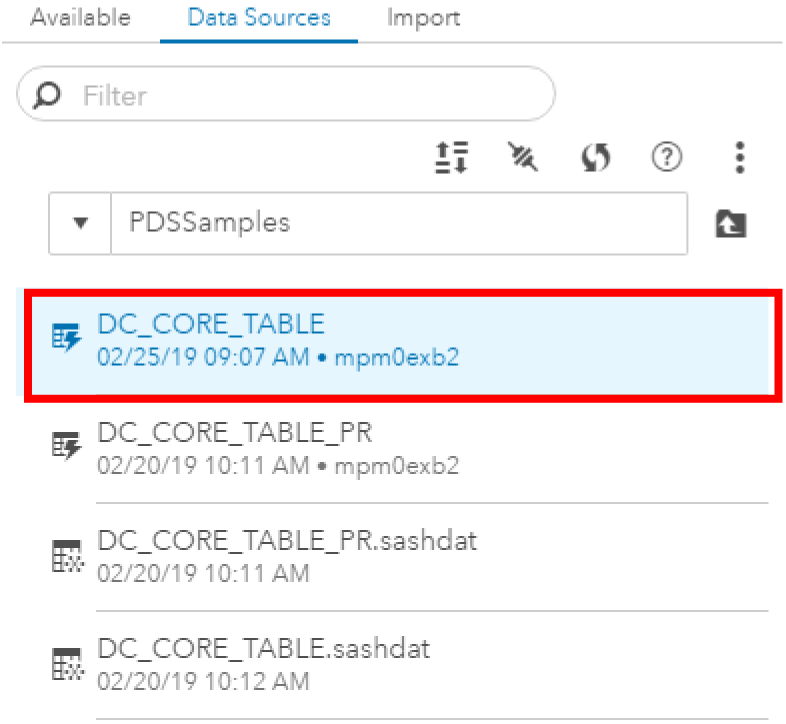
Date modified:
Feb 20, 2019 10:12 AM

Encoding:
(not available)

Tags (0):
No items have been added.

Figure 23: View information about a selected table

9. Select the in-memory table DC_CORE_TABLE (not DC_CORE_TABLE.sashdat) and then click OK.



DC_CORE_TABLE
02/25/19 09:07 AM • mpm0exb2

DC_CORE_TABLE_PR
02/20/19 10:11 AM • mpm0exb2

DC_CORE_TABLE_PR.sashdat
02/20/19 10:11 AM

DC_CORE_TABLE.sashdat
02/20/19 10:12 AM

Figure 24: DC_CORE_TABLE loaded into memory

10. Now that we have selected a table we can begin to transform it for our analytic goals. The first step we are going to take is to add a Custom Code transform to add labels to the columns in the table and transform the various flag columns in the table to store ‘Y’ and ‘N’. To do this, click the Code item in the left pane and then click ‘Add Transform’.

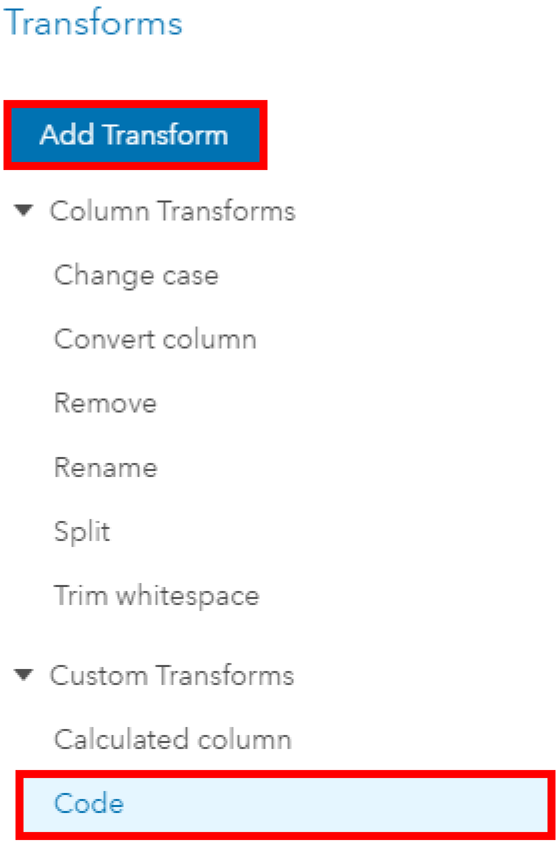


Figure 25: Adding Custom Code Transform

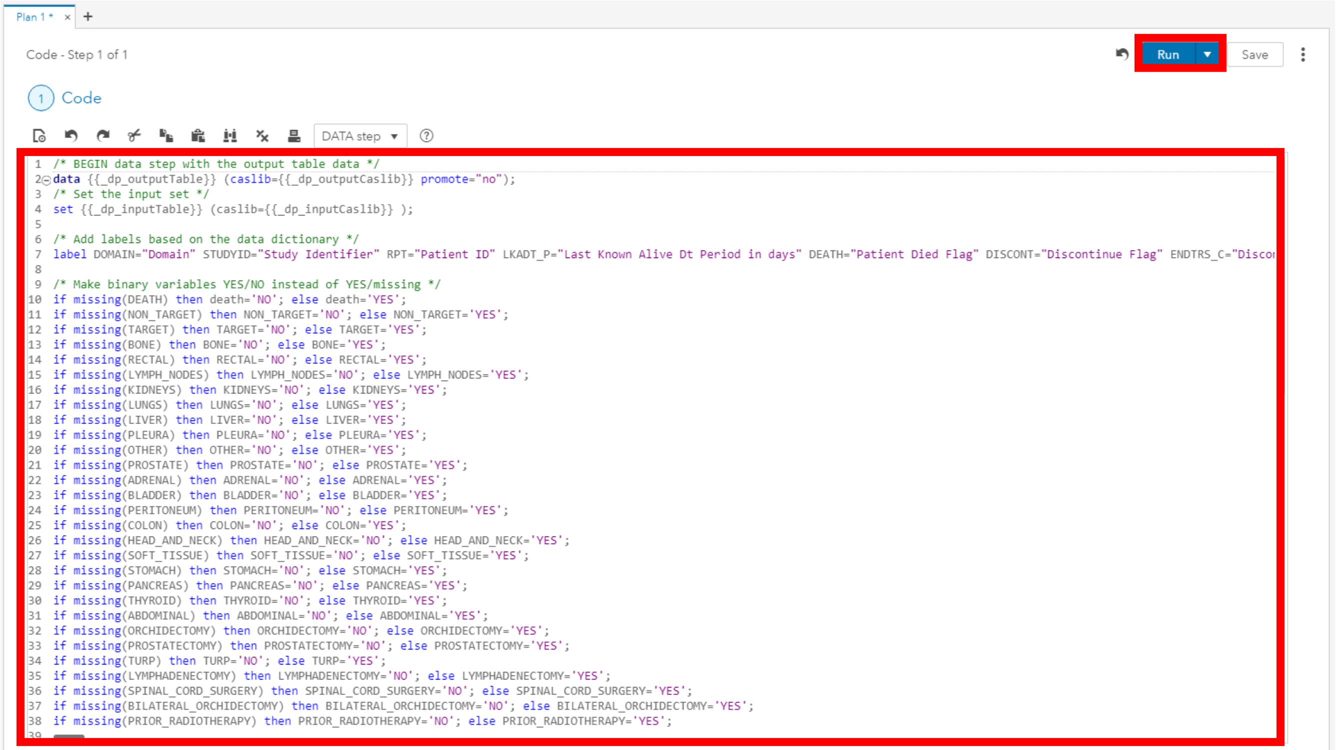
11. In the Code transform step that is created, copy the following code snippet and in the program editor paste it below line 5:

```
/* Add labels based on the data dictionary */
label DOMAIN="Domain" STUDYID="Study Identifier" RPT="Patient ID" LKADT_P="Last Known
Alive Dt Period in days" DEATH="Patient Died Flag" DISCONT="Discontinue Flag"
ENDTRS_C="Discontinue Trt Reason (category)" ENTRT_PC="Discontinue Trt Date Period in
days" PER_REF="Reference Day used for ENTRT_PC" LKADT_REF="Reference Day used for
LKADT_P" LKADT_PER="Period unit for period values, LKADT_P" GLEAS_DX="Gleason Score at
Initial diagnosis" TSTAG_DX="Primary Tumor-stage Score at Initial diagnosis" AGEGRP="Age
Group" AGEGRP2="Age Group (3 category)" RACE_C="Race" BMI="Baseline Body Mass Index
(kg/m2)" HEIGHTBL="Baseline Height in cm" HGTBLCAT="Baseline Height in cm category"
WEIGHTBL="Baseline Weight in kg" WGTBLCAT="Baseline Weight in kg category"
REGION_C="Region of the World" SMOKE="Ever Smoked" SMOKFREQ="Smoking Frequency"
SMOKSTAT="Current Smoking Status" ECOG_C="Baseline Patient Performance Status"
TRT1_ID="Treatment 1 product " TRT2_ID="Treatment 2 product (docetaxel)"
```

TRT3_ID="Treatment 3 product (prednisone except AZ)" ALP="BASELINE LAB VALUE: ALKALINE PHOSPHATASE U/L" ALT="BASELINE LAB VALUE: ALANINE TRANSAMINASE U/L" AST="BASELINE LAB VALUE: ASPARTATE AMINOTRANSFERASE U/L" CA="BASELINE LAB VALUE: CALCIUM MMOL/L" CREAT="BASELINE LAB VALUE: CREATININE UMOL/L" HB="BASELINE LAB VALUE: HEMOGLOBIN G/DL" LDH="BASELINE LAB VALUE: LACTATE DEHYDROGENASE U/L" NEU="BASELINE LAB VALUE: NEUTROPHILS 10^9/L" PLT="BASELINE LAB VALUE: PLATELET COUNT 10^9/L" PSA="BASELINE LAB VALUE: PROSTATE SPECIFIC ANTIGEN NG/ML" TBILI="BASELINE LAB VALUE: TOTAL BILIRUBIN UMOL/L" TESTO="BASELINE LAB VALUE: TESTOSTERONE NMOL/L" WBC="BASELINE LAB VALUE: WHITE BLOOD CELLS 10^9/L" CREACL="BASELINE LAB VALUE: CREATININE CLEARANCE ML/MIN" NA="BASELINE LAB VALUE: SODIUM MMOL/L" MG="BASELINE LAB VALUE: MAGNESIUM MMOL/L" PHOS="BASELINE LAB VALUE: PHOSPHORUS MMOL/L" ALB="BASELINE LAB VALUE: ALBUMIN G/L" TPRO="BASELINE LAB VALUE: TOTAL PROTEIN G/L" RBC="BASELINE LAB VALUE: RED BLOOD CELLS 10^12/L" LYM="BASELINE LAB VALUE: LYMPHOCYTES 10^9/L" BUN="BASELINE LAB VALUE: BLOOD UREA NITROGEN MMOL/L" CCRC="BASELINE LAB VALUE: CALCULATED CREATININE CLEARANCE ML/MIN" GLU="BASELINE LAB VALUE: GLUCOSE MMOL/L" CREACLCA="BASELINE LAB VALUE: CREATININE CLEARANCE CALCUL. (COCKCROFT AND GAULT) ML/MIN" NON_TARGET="Baseline Non-Target Lesion(s)" TARGET="Baseline Target Lesion(s)" BONE="Baseline Bone Lesion(s)" RECTAL="Baseline Rectal Lesion(s)" LYMPH_NODES="Baseline Lymph Node Lesion(s)" KIDNEYS="Baseline Kidney Lesion(s)" LUNGS="Baseline Lung Lesion(s)" LIVER="Baseline Liver Lesion(s)" PLEURA="Baseline Pleura Lesion(s)" OTHER="Baseline Other Lesion(s)" PROSTATE="Baseline Prostate Lesion(s)" ADRENAL="Baseline Adrenal Lesion(s)" BLADDER="Baseline Bladder Lesion(s)" PERITONEUM="Baseline Peritoneum Lesion(s)" COLON="Baseline Colon Lesion(s)" HEAD_AND_NECK="Baseline Head and Neck Lesion(s)" SOFT_TISSUE="Baseline Soft Tissue Lesion(s)" STOMACH="Baseline Stomach Lesion(s)" PANCREAS="Baseline Pancreas Lesion(s)" THYROID="Baseline Thyroid Lesion(s)" ABDOMINAL="Baseline Abdominal Lesion(s)" ORCHIDECTOMY="Prior Orchidectomy(includes bilateral)" PROSTATECTOMY="Prior Prostatectomy" TURP="Prior Turp" LYMPHADENECTOMY="Prior Bilateral Lymphadenectomy" SPINAL_CORD_SURGERY="Prior Spinal Cord Surgery" BILATERAL_ORCHIDECTOMY="Prior Bilateral Orchidectomy" PRIOR_RADIOTHERAPY="Prior Radiotherapy" ANALGESICS="Prior analgesics" ANTI_ANDROGENS="Prior Anti-Androgens" GLUCOCORTICOID="Prior Glucocorticoids" GONADOTROPIN="Prior Gomadotropin" BISPHOSPHONATE="Prior Bisphosponate" CORTICOSTEROID="Prior Corticosteroid" IMIDAZOLE="Prior Imidazole" ACE_INHIBITORS="Prior ACE Inhibitors" BETA_BLOCKING="Prior Beta Blocking Agents" HMG_COA_REDUCT="Prior HMG COA Reductase Inhibitors" ESTROGENS="Prior Estrogens" ANTI_ESTROGENS="Prior Anti-Estrogens" ARTTHROM="MEDICAL HISTORY: ARTERIAL THROMBOSIS" CEREBACC="MEDICAL HISTORY: CEREBROVASCULAR ACCIDENT (HEMORRHAGIC AND/OR ISCHEMIC)" CHF="MEDICAL HISTORY: CONGESTIVE HEART FAILURE" DVT="MEDICAL HISTORY: DEEP VENOUS THROMBOSIS (DVT)" DIAB="MEDICAL HISTORY: DIABETES" GASTREFL="MEDICAL HISTORY: GASTROESOPHAGEAL REFLUX DISEASE (GERD)" GIBLEED="MEDICAL HISTORY: GASTROINTESTINAL (GI) BLEED" MI="MEDICAL HISTORY: MYOCARDIAL INFARCTION (MI)" PUD="MEDICAL HISTORY: PEPTIC ULCER DISEASE (PUD)" PULMEMB="MEDICAL HISTORY: PULMONARY EMBOLISM (PE)" PATHFRAC="MEDICAL HISTORY: PATHOLOGICAL BONE

```
FRACTURES" SPINCOMP="MEDICAL HISTORY: SPINAL CORD COMPRESSION" COPD="MEDICAL
HISTORY: CHRONIC OBSTRUCTIVE PULMONARY DISEASE" MHBLOOD="MEDICAL HISTORY (Body
system): BLOOD & LYMPHATIC SYSTEM" MHCARD="MEDICAL HISTORY (Body system): CARDIAC
DISORDERS" MHCONGEN="MEDICAL HISTORY (Body system): CONGENITAL, FAMILIAL &
GENETIC" MHEAR="MEDICAL HISTORY (Body system): EAR & LABYRINTH" MHENDO="MEDICAL
HISTORY (Body system): ENDOCRINE DISORDERS" MHEYE="MEDICAL HISTORY (Body system):
EYE DISORDERS" MHGASTRO="MEDICAL HISTORY (Body system): GASTROINTESTINAL
DISORDERS" MHGEN="MEDICAL HISTORY (Body system): GEN DISORD & ADMIN SITE"
MHHEPATO="MEDICAL HISTORY (Body system): HEPATOBILIARY DISORDERS"
MHIMMUNE="MEDICAL HISTORY (Body system): IMMUNE SYSTEM DISORDERS"
MHINFECT="MEDICAL HISTORY (Body system): INFECTIONS & INFESTATIONS"
MHINJURY="MEDICAL HISTORY (Body system): INJURY, POISON & PROCEDURAL"
MHINVEST="MEDICAL HISTORY (Body system): INVESTIGATIONS" MHMETAB="MEDICAL
HISTORY (Body system): METABOLISM & NUTRITION" MHMUSCLE="MEDICAL HISTORY (Body
system): MUSC/SKELETAL & CONNECT TISSUE" MHNEOPLA="MEDICAL HISTORY (Body system):
NEOPLASMS BENIGN, MALIG & UNSPEC" MHNERV="MEDICAL HISTORY (Body system):
NERVOUS SYSTEM DISORDERS" MHPSYCH="MEDICAL HISTORY (Body system): PSYCHIATRIC
DISORDERS" MHRENAL="MEDICAL HISTORY (Body system): RENAL & URINARY DISORDERS"
MHRESP="MEDICAL HISTORY (Body system): RESP, THORACIC & MEDIASTINAL"
MHSKIN="MEDICAL HISTORY (Body system): SKIN & SUBCUTANEOUS TISSUE"
MHSOCIAL="MEDICAL HISTORY (Body system): SOCIAL CIRCUMSTANCES" MHSURG="MEDICAL
HISTORY (Body system): SURGICAL & MEDICAL PROCEDURES" MHVASC="MEDICAL HISTORY
(Body system): VASCULAR DISORDERS";

/* Make binary variables YES/NO instead of YES/missing */
if missing(DEATH) then death='NO'; else death='YES';
if missing(NON_TARGET) then NON_TARGET='NO'; else NON_TARGET='YES';
if missing(TARGET) then TARGET='NO'; else TARGET='YES';
if missing(BONE) then BONE='NO'; else BONE='YES';
if missing(RECTAL) then RECTAL='NO'; else RECTAL='YES';
if missing(LYMPH_NODES) then LYMPH_NODES='NO'; else LYMPH_NODES='YES';
if missing(KIDNEYS) then KIDNEYS='NO'; else KIDNEYS='YES';
if missing(LUNGS) then LUNGS='NO'; else LUNGS='YES';
if missing(LIVER) then LIVER='NO'; else LIVER='YES';
if missing(PLEURA) then PLEURA='NO'; else PLEURA='YES';
if missing(OTHER) then OTHER='NO'; else OTHER='YES';
if missing(PROSTATE) then PROSTATE='NO'; else PROSTATE='YES';
if missing(ADRENAL) then ADRENAL='NO'; else ADRENAL='YES';
if missing(BLADDER) then BLADDER='NO'; else BLADDER='YES';
if missing(PERITONEUM) then PERITONEUM='NO'; else PERITONEUM='YES';
if missing(COLON) then COLON='NO'; else COLON='YES';
if missing(HEAD_AND_NECK) then HEAD_AND_NECK='NO'; else HEAD_AND_NECK='YES';
if missing(SOFT_TISSUE) then SOFT_TISSUE='NO'; else SOFT_TISSUE='YES';
if missing(STOMACH) then STOMACH='NO'; else STOMACH='YES';
if missing(PANCREAS) then PANCREAS='NO'; else PANCREAS='YES';
if missing(THYROID) then THYROID='NO'; else THYROID='YES';
if missing(ABDOMINAL) then ABDOMINAL='NO'; else ABDOMINAL='YES';
if missing(ORCHIDECTOMY) then ORCHIDECTOMY='NO'; else ORCHIDECTOMY='YES';
if missing(PROSTATECTOMY) then PROSTATECTOMY='NO'; else PROSTATECTOMY='YES';
if missing(TURP) then TURP='NO'; else TURP='YES';
if missing(LYMPHADENECTOMY) then LYMPHADENECTOMY='NO'; else
LYMPHADENECTOMY='YES';
if missing(SPINAL_CORD_SURGERY) then SPINAL_CORD_SURGERY='NO'; else
SPINAL_CORD_SURGERY='YES';
if missing(BILATERAL_ORCHIDECTOMY) then BILATERAL_ORCHIDECTOMY='NO'; else
BILATERAL_ORCHIDECTOMY='YES';
if missing(PRIOR_RADIOTHERAPY) then PRIOR_RADIOTHERAPY='NO'; else
PRIOR_RADIOTHERAPY='YES';
if missing(ANALGESICS) then ANALGESICS='NO'; else ANALGESICS='YES';
if missing(ANTI_ANDROGENS) then ANTI_ANDROGENS='NO'; else ANTI_ANDROGENS='YES';
if missing(GLUCOCORTICOID) then GLUCOCORTICOID='NO'; else GLUCOCORTICOID='YES';
if missing(GONADOTROPIN) then GONADOTROPIN='NO'; else GONADOTROPIN='YES';
if missing(BISPHOSPHONATE) then BISPHOSPHONATE='NO'; else BISPHOSPHONATE='YES';
if missing(CORTICOSTEROID) then CORTICOSTEROID='NO'; else CORTICOSTEROID='YES';
if missing(IMIDAZOLE) then IMIDAZOLE='NO'; else IMIDAZOLE='YES';
if missing(ACE_INHIBITORS) then ACE_INHIBITORS='NO'; else ACE_INHIBITORS='YES';
if missing(BETA_BLOCKING) then BETA_BLOCKING='NO'; else BETA_BLOCKING='YES';
if missing(HMG_COA_REDUCT) then HMG_COA_REDUCT='NO'; else HMG_COA_REDUCT='YES';
if missing(ESTROGENS) then ESTROGENS='NO'; else ESTROGENS='YES';
if missing(ANTI_ESTROGENS) then ANTI_ESTROGENS='NO'; else ANTI_ESTROGENS='YES';
if missing(ARTTHROM) then ARTTHROM='NO'; else ARTTHROM='YES';
if missing(CEREBACC) then CEREBACC='NO'; else CEREBACC='YES';
if missing(CHF) then CHF='NO'; else CHF='YES';
if missing(DVT) then DVT='NO'; else DVT='YES';
if missing(DIAB) then DIAB='NO'; else DIAB='YES';
if missing(GASTREFL) then GASTREFL='NO'; else GASTREFL='YES';
if missing(GIBLEED) then GIBLEED='NO'; else GIBLEED='YES';
if missing(MI) then MI='NO'; else MI='YES';
if missing(PUD) then PUD='NO'; else PUD='YES';
if missing(PULMEMB) then PULMEMB='NO'; else PULMEMB='YES';
if missing(PATHFRAC) then PATHFRAC='NO'; else PATHFRAC='YES';
if missing(SPINCOMP) then SPINCOMP='NO'; else SPINCOMP='YES';
if missing(COPD) then COPD='NO'; else COPD='YES';
if missing(MHBLOOD) then MHBLOOD='NO'; else MHBLOOD='YES';
if missing(MHCARD) then MHCARD='NO'; else MHCARD='YES';
if missing(MHCONGEN) then MHCONGEN='NO'; else MHCONGEN='YES';
if missing(MHEAR) then MHEAR='NO'; else MHEAR='YES';
if missing(MHENDO) then MHENDO='NO'; else MHENDO='YES';
if missing(MHEYE) then MHEYE='NO'; else MHEYE='YES';
if missing(MHGASTRO) then MHGASTRO='NO'; else MHGASTRO='YES';
if missing(MHGEN) then MHGEN='NO'; else MHGEN='YES';
if missing(MHHEPATO) then MHHEPATO='NO'; else MHHEPATO='YES';
if missing(MHIMMUNE) then MHIMMUNE='NO'; else MHIMMUNE='YES';
if missing(MHINFECT) then MHINFECT='NO'; else MHINFECT='YES';
if missing(MHINJURY) then MHINJURY='NO'; else MHINJURY='YES';
if missing(MHINVEST) then MHINVEST='NO'; else MHINVEST='YES';
if missing(MHMETAB) then MHMETAB='NO'; else MHMETAB='YES';
if missing(MHMUSCLE) then MHMUSCLE='NO'; else MHMUSCLE='YES';
if missing(MHNEOPLA) then MHNEOPLA='NO'; else MHNEOPLA='YES';
if missing(MHNERV) then MHNERV='NO'; else MHNERV='YES';
if missing(MHPSYCH) then MHPSYCH='NO'; else MHPSYCH='YES';
if missing(MHRENAL) then MHRENAL='NO'; else MHRENAL='YES';
if missing(MHRESP) then MHRESP='NO'; else MHRESP='YES';
if missing(MHSKIN) then MHSKIN='NO'; else MHSKIN='YES';
if missing(MHSOCIAL) then MHSOCIAL='NO'; else MHSOCIAL='YES';
if missing(MHSURG) then MHSURG='NO'; else MHSURG='YES';
if missing(MHVASC) then MHVASC='NO'; else MHVASC='YES';
```



```
/* BEGIN data step with the output table data */
data {{_dp_outputTable}} (caslib={{_dp_outputCaslib}} promote="no");
/* Set the input set */
set {{_dp_inputTable}} (caslib={{_dp_inputCaslib}} );

/* Add labels based on the data dictionary */
label DOMAIN="Domain" STUDYID="Study Identifier" RPT="Patient ID" LKADT_P="Last Known Alive Dt Period in days" DEATH="Patient Died Flag" DISCONT="Discontinue Flag" ENDTRS_C="Discor

/* Make binary variables YES/NO instead of YES/missing */
if missing(DEATH) then death='NO'; else death='YES';
if missing(NON_TARGET) then NON_TARGET='NO'; else NON_TARGET='YES';
if missing(TARGET) then TARGET='NO'; else TARGET='YES';
if missing(BONE) then BONE='NO'; else BONE='YES';
if missing(RECTAL) then RECTAL='NO'; else RECTAL='YES';
if missing(LYMPH_NODES) then LYMPH_NODES='NO'; else LYMPH_NODES='YES';
if missing(KIDNEYS) then KIDNEYS='NO'; else KIDNEYS='YES';
if missing(LUNGS) then LUNGS='NO'; else LUNGS='YES';
if missing(LIVER) then LIVER='NO'; else LIVER='YES';
if missing(PLEURA) then PLEURA='NO'; else PLEURA='YES';
if missing(OTHER) then OTHER='NO'; else OTHER='YES';
if missing(PROSTATE) then PROSTATE='NO'; else PROSTATE='YES';
if missing(ADRENAL) then ADRENAL='NO'; else ADRENAL='YES';
if missing(BLADDER) then BLADDER='NO'; else BLADDER='YES';
if missing(PERITONEUM) then PERITONEUM='NO'; else PERITONEUM='YES';
if missing(COLON) then COLON='NO'; else COLON='YES';
if missing(HEAD_AND_NECK) then HEAD_AND_NECK='NO'; else HEAD_AND_NECK='YES';
if missing(SOFT_TISSUE) then SOFT_TISSUE='NO'; else SOFT_TISSUE='YES';
if missing(STOMACH) then STOMACH='NO'; else STOMACH='YES';
if missing(PANCREAS) then PANCREAS='NO'; else PANCREAS='YES';
if missing(THYROID) then THYROID='NO'; else THYROID='YES';
if missing(ABDOMINAL) then ABDOMINAL='NO'; else ABDOMINAL='YES';
if missing(ORCHIDECTOMY) then ORCHIDECTOMY='NO'; else ORCHIDECTOMY='YES';
if missing(PROSTATECTOMY) then PROSTATECTOMY='NO'; else PROSTATECTOMY='YES';
if missing(TURP) then TURP='NO'; else TURP='YES';
if missing(LYMPHADENECTOMY) then LYMPHADENECTOMY='NO'; else LYMPHADENECTOMY='YES';
if missing(SPINAL_CORD_SURGERY) then SPINAL_CORD_SURGERY='NO'; else SPINAL_CORD_SURGERY='YES';
if missing(BILATERAL_ORCHIDECTOMY) then BILATERAL_ORCHIDECTOMY='NO'; else BILATERAL_ORCHIDECTOMY='YES';
if missing(PRIOR_RADIOTHERAPY) then PRIOR_RADIOTHERAPY='NO'; else PRIOR_RADIOTHERAPY='YES';
```

Figure 26: Custom Code Transform in Data Studio

12. After updating the custom code transform, click Run. You should see the updates made to the table by the custom code in the table below.

13. Next, we'll add a Remove transform to drop some columns from the source table that are not needed. In the transform pane, select the Remove item and then click Add Transform.

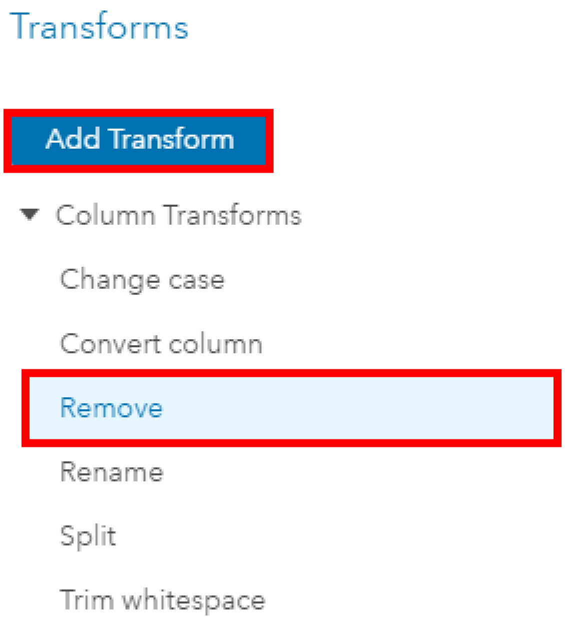
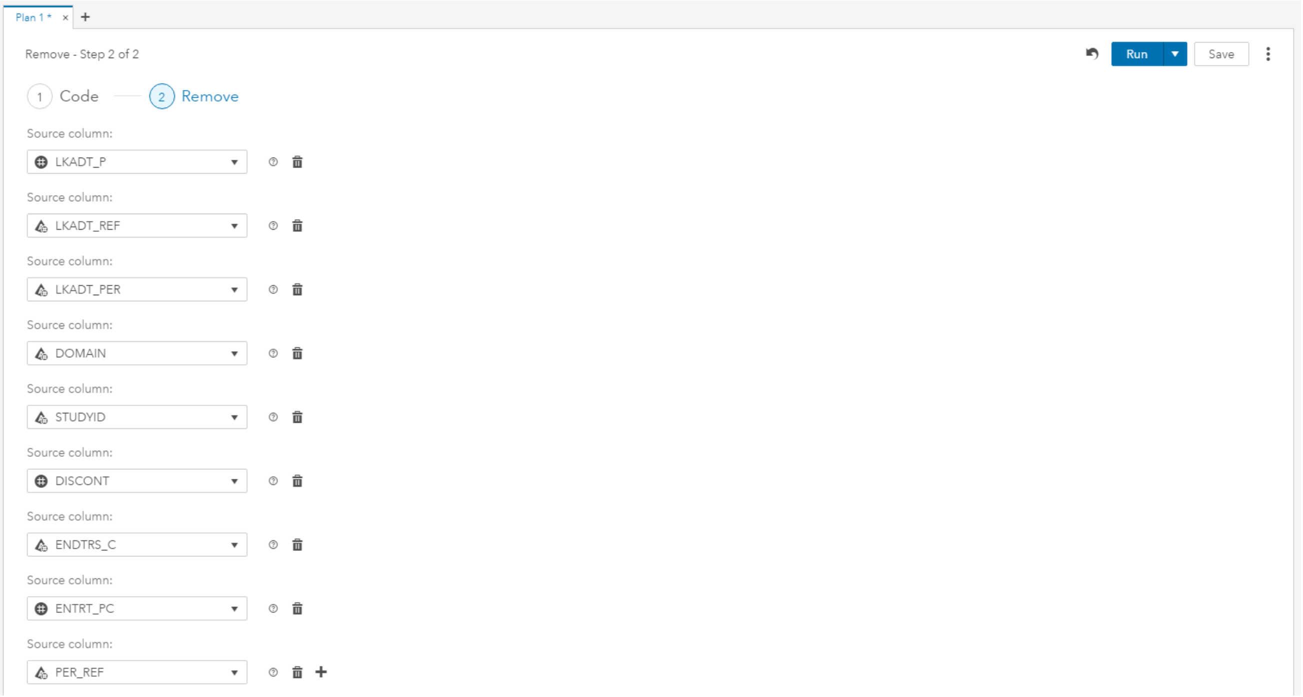


Figure 27: Adding Remove Transform

14. In the Remove transform step, drop the following columns: LKADT_P, LKADT_REF, LKADT_PER, DOMAIN, STUDYID, DISCONT, ENDTRS_C, ENTRT_PC, and PER_REF.



Remove - Step 2 of 2

Source column: LKADT_P

Source column: LKADT_REF

Source column: LKADT_PER

Source column: DOMAIN

Source column: STUDYID

Source column: DISCONT

Source column: ENDTRS_C

Source column: ENTRT_PC

Source column: PER_REF

Figure 28: The Remove Transform with columns selected for removal

15. Click Run.

16. In our last step, we're going to rename some columns using the Rename transform. In the transform pane, select the Rename item and then click Add Transform.

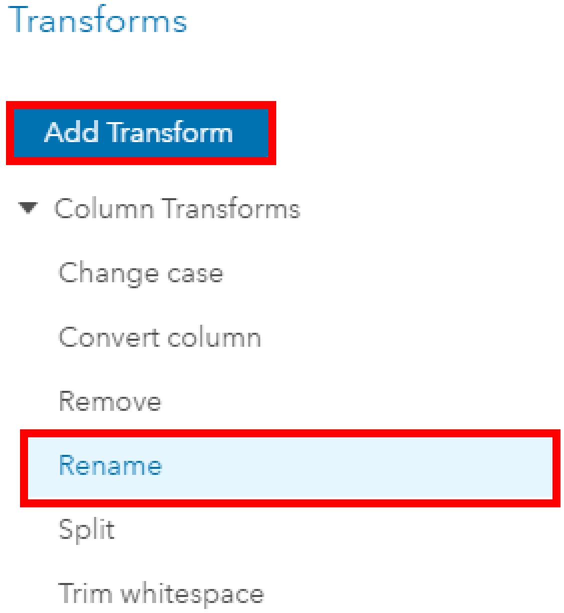
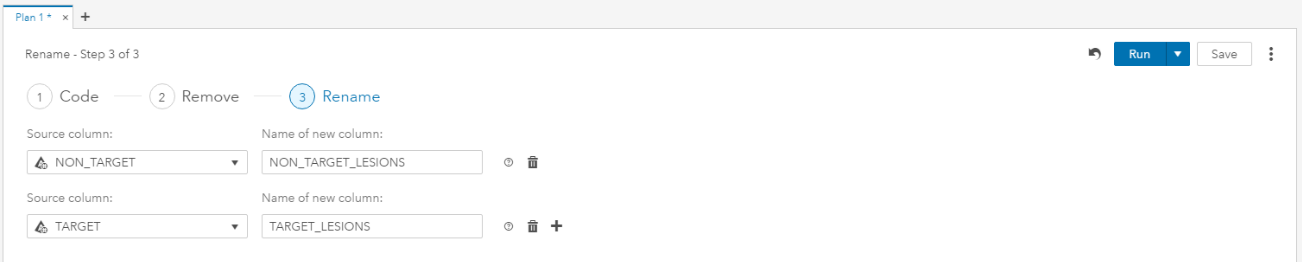


Figure 29: Adding a 'Rename' transform to the data plan

17. In the rename transform step, rename the NON_TARGET column to NON_TARGET_LESIONS and the TARGET column to TARGET_LESIONS. This rename will make it more easily known what information those columns store.
    a. Note, you may have to click 'View all columns' at the bottom of the source column dropdown to find the NON_TARGET and TARGET columns.



Rename - Step 3 of 3

Source column: NON_TARGET
Name of new column: NON_TARGET_LESIONS

Source column: TARGET
Name of new column: TARGET_LESIONS

Figure 30: The Rename transform with columns selected to rename

18. Click Run.

If you would like to save your plan and transform table. Following the below steps:

19. Click the SAVE button.

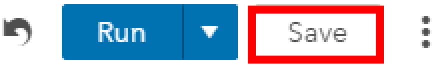
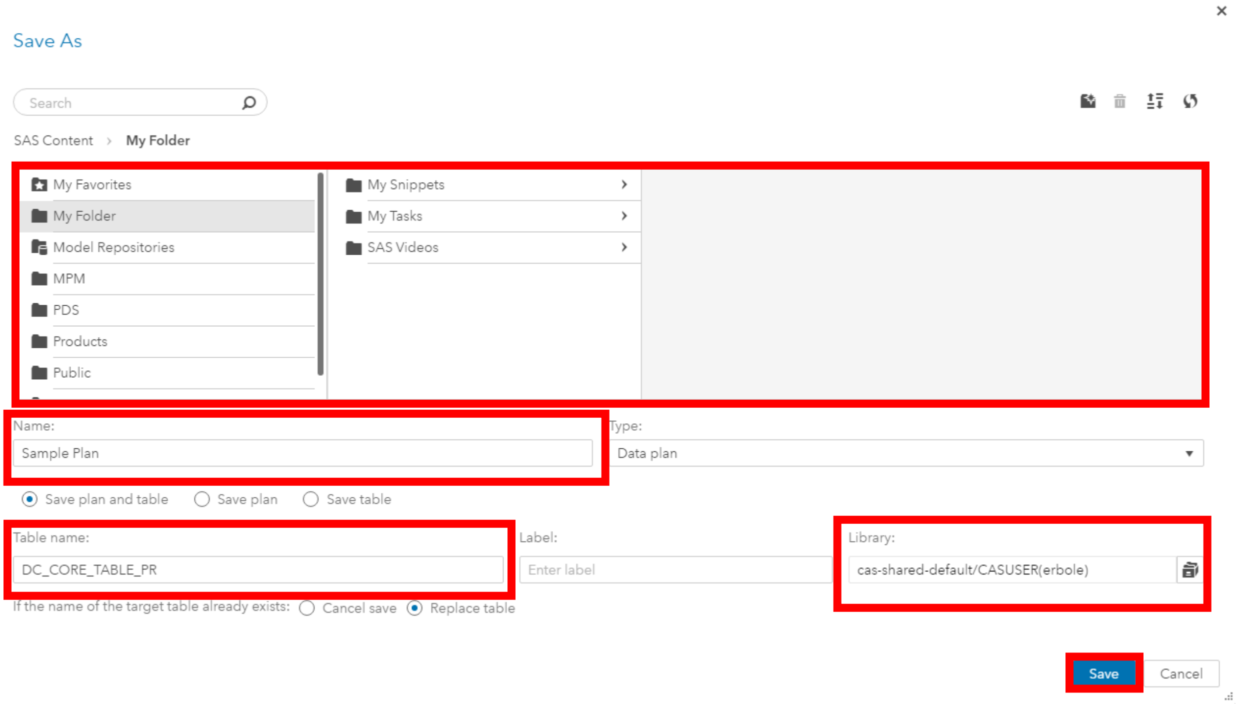


Figure 31: Saving a Data Plan in Data Studio

20. In the Save As dialog, you can save the data plan is your My Folder and the table in your CASUSER library.
    a. In the tree view, you may select the directory in which you save your data plan. We suggest saving it under My Folder, which should be selected by default
    b. Under name, you may name the data plan anything you desire
    c. Under table name, you may name the transformed DC_CORE_TABLE. We suggest naming it DC_CORE_TABLE_PR
    d. Under library, you may select the CasLib to store the transformed table in. You must select you CASUSER library.
21. Lastly, slick the Save button.



Name: Sample Plan

Type: Data plan

● Save plan and table ○ Save plan ○ Save table

Table name: DC_CORE_TABLE_PR

Label: Enter label

Library: cas-shared-default/CASUSER(erbole)

If the name of the target table already exists: ○ Cancel save ● Replace table

Figure 32: Data Studio Save As Dialog

You're all done! This Quick Start should have shown you the power available with Data Studio to quickly transform data to fit your research and analytic goals.

Documentation

[SAS® Data Studio 2.2: User's Guide]

Additional Videos

Using SAS® Data Explorer to Load SAS® Data Sets

Using SAS® Data Explorer to Profile Data for Better Understanding

Using SAS® Data Studio to Prepare and Transform Data into the Desired Format

Getting Started: Model Studio

Overview

SAS Model Studio is an integrated visual environment that provides a suite of analytic data mining tools to facilitate end-to-end data mining analysis. In Model Studio, users can leverage the visual web interface to assemble, configure, build, and compare data mining models and pipelines for a wide range of analytic data mining tasks. Data miners of all levels can use Model Studio and most tasks can be used by individuals who have minimal SAS programming experience.

Quick Start

In this Quick Start, we will learn how to use Model Studio to create various machine learning models and pipelines with the goal of finding the pipeline that best classifies the data.

We will be using the DC_CORE_TABLE_PR table that we created in the Getting Started: Data Studio guide. If you have not completed that Getting Started guide or want to skip it, you can use the sample table located in the PDSSamples CASLib.

1. Log into SAS Visual Data Mining and Machine Learning.
2. First, we must load data from the PDSSamples CASLib into our CASUSER CASLib.
    a. Note: If you have completed this step in another Getting Started guide, then you can proceed to step 3. The PDSSamples CASLib contains sample files for the Getting Started guides and is different from the files used in Getting Started: SAS® Studio.
    b. In the application switcher, click on Develop SAS Code to navigate to SAS Studio.

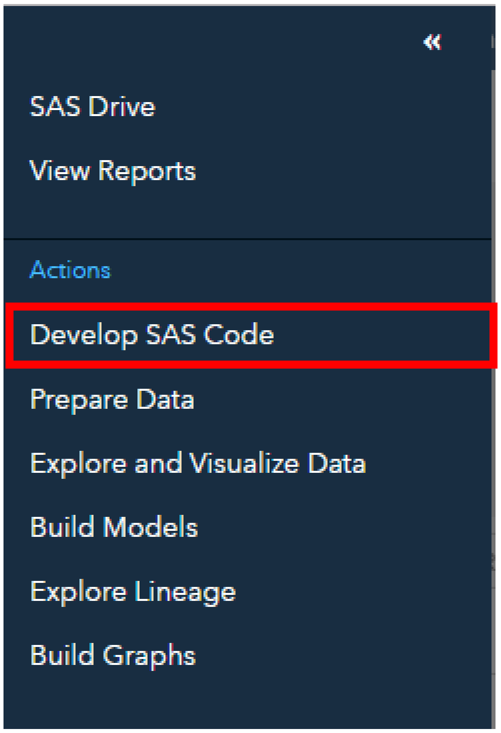
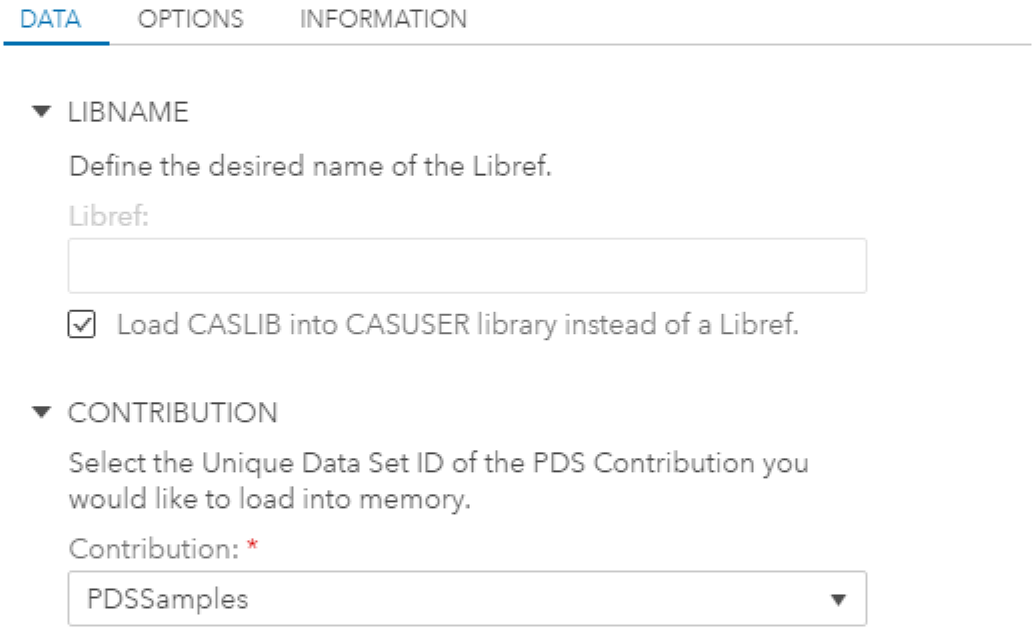


Figure 33: Navigate to SAS Studio by clicking Develop SAS Code in the App Switcher

c. Using the 'Create Libref for PDS Contribution' task under My Tasks load the data from the PDSSamples into your CASUSER library.



DATA OPTIONS INFORMATION

▼ LIBNAME

Define the desired name of the Libref.

Libref:

☑ Load CASLIB into CASUSER library instead of a Libref.

▼ CONTRIBUTION

Select the Unique Data Set ID of the PDS Contribution you would like to load into memory.

Contribution: *

PDSSamples ▼

Figure 34 SAS Studio task to load data from PDSSamples to CASUSER library

3. Next, in the application switcher, click on Build Models to navigate to Model Studio.

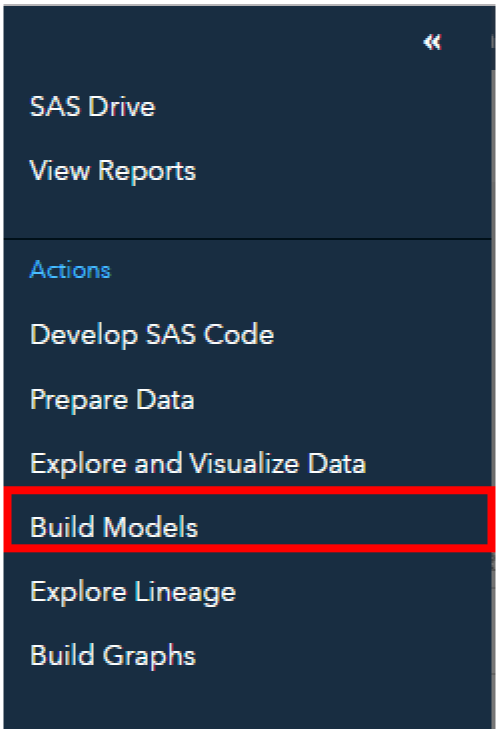


Figure 35: Navigate to SAS Model Studio by clicking Build Models in the App Switcher

4. Once in Model Studio, click the New Project button.

5. In the New Project dialog, fill out the following:
   a. Name: Any name that you desire
   b. Data Source
      i. Click Browse.
      ii. In the Browse Data dialog, select the Data Sources tab and then click cas-shared-default.

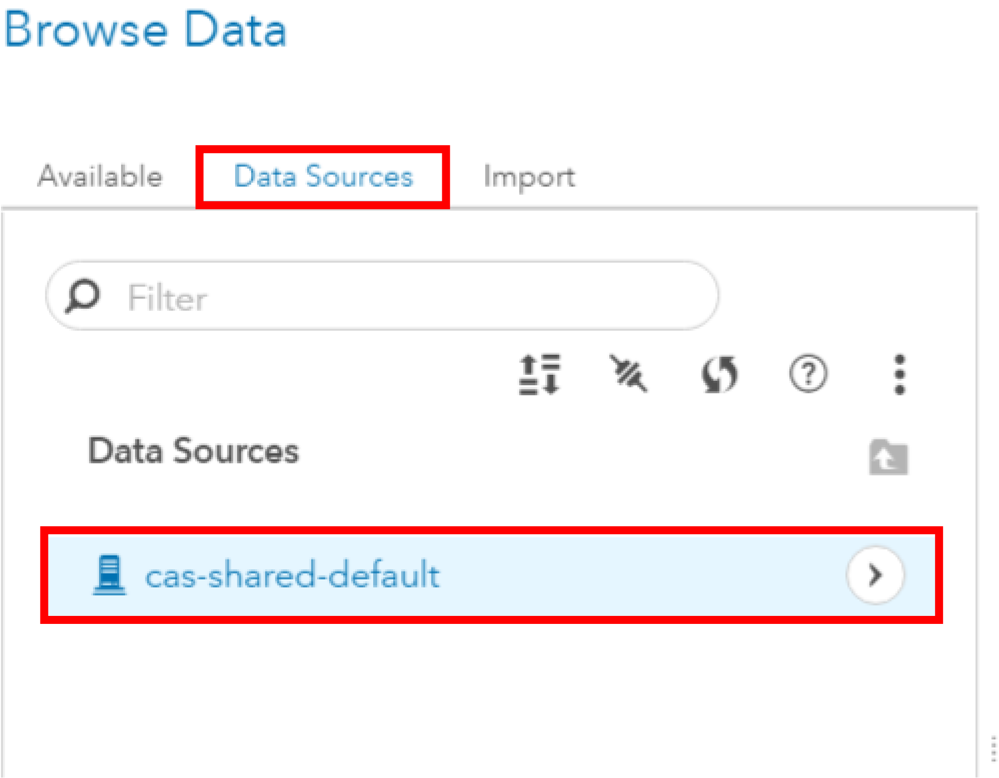
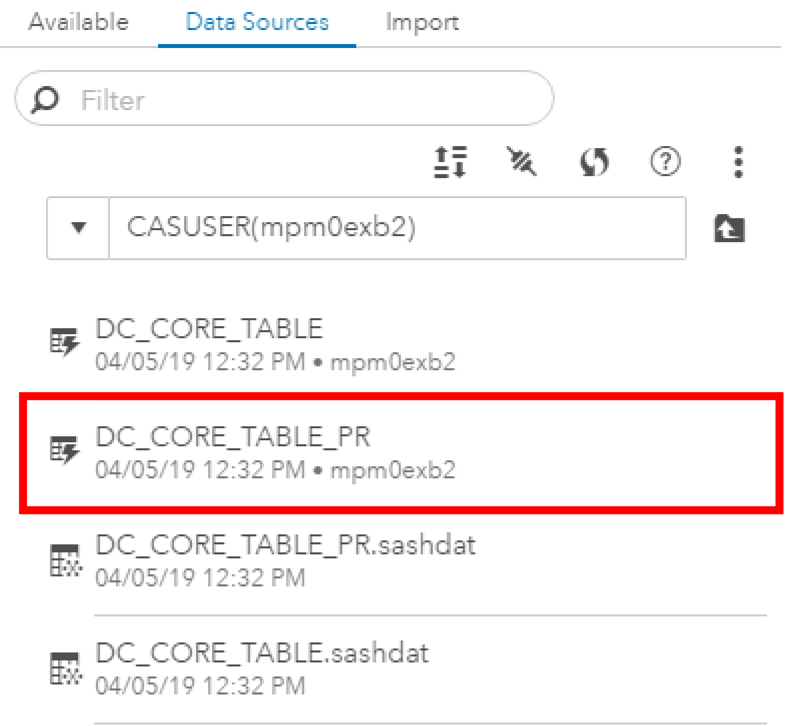


Figure 36: Browse Data Dialog

      iii. Next, go to your CASUSER library and select the ‘DC_CORE_TABLE_PR’ in-memory table you created during the Data Studio Quick Start.



CASUSER(mpm0exb2)

DC_CORE_TABLE
04/05/19 12:32 PM • mpm0exb2

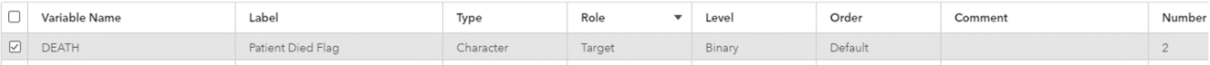
DC_CORE_TABLE_PR
04/05/19 12:32 PM • mpm0exb2

DC_CORE_TABLE_PR.sashdat
04/05/19 12:32 PM

DC_CORE_TABLE.sashdat
04/05/19 12:32 PM

Figure 37: Select table to use in Model Studio

6. Click OK and then click Save.
7. Once the project opens, we first need to make a few changes in the Data tab. We want our target variable to be the Patient Died Flag (the variable named DEATH) and Model Studio may automatically set the target variable to something else.
    a. In the table find the target variable by looking at the Role column, if it is not the DEATH variable, then click on the row and then change the Role to Input in the properties pane on the right side.
    b. Next, in the table find the DEATH variable and change its role to Target.



☐	Variable Name	Label	Type	Role	Level	Order	Comment	Number
☑	DEATH	Patient Died Flag	Character	Target	Binary	Default		2

Figure 38: Setting the target variable

8. Now we're ready to start creating analytical pipelines. Click the Pipelines tab.
9. We are going to create two new pipelines called Logistic Regression and Gradient Boosting. Double-click the default pipeline (named 'Pipeline 1') to rename it. To create the other new pipeline click the plus icon. In the New Pipeline dialog assign a name and click Save.

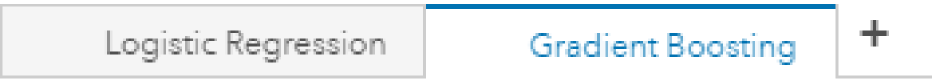


Figure 39: Newly created pipelines

10. First, let's work on the Logistic Regression pipeline. Click on the Logistic Regression tab.

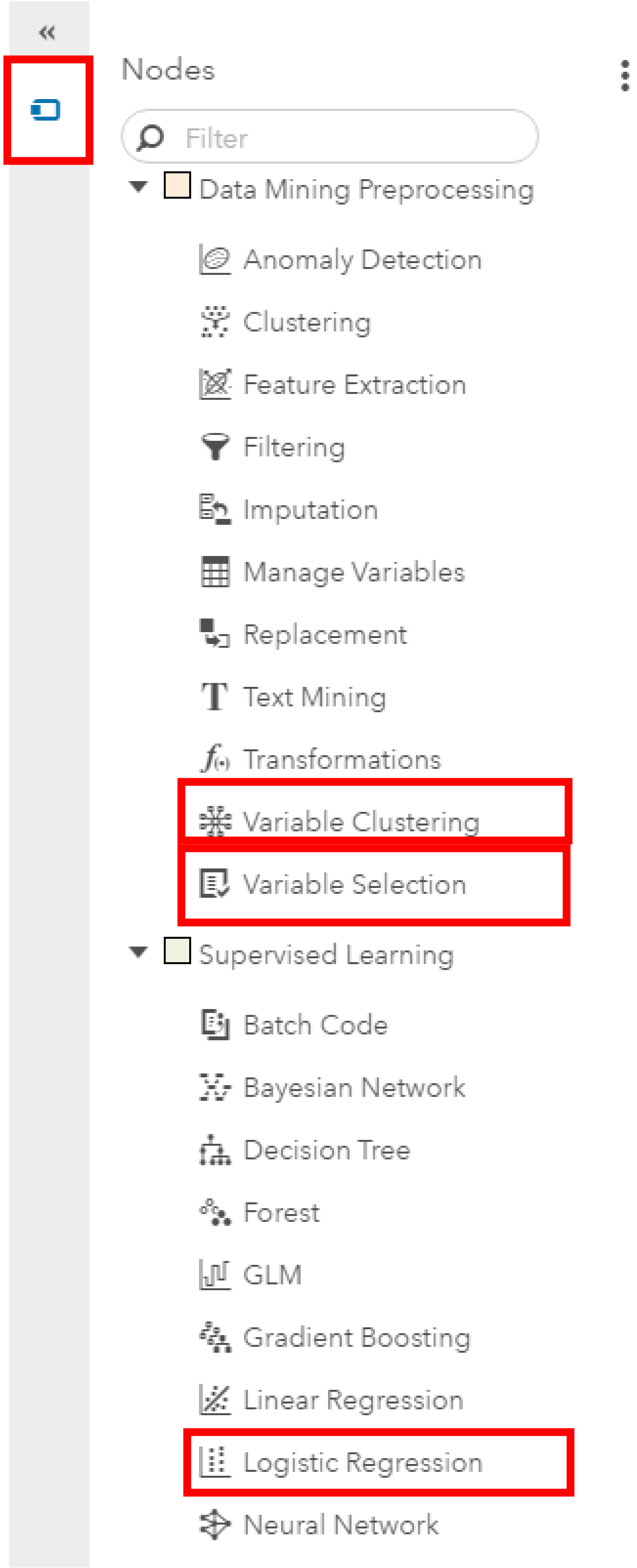


Figure 40: Select nodes from Nodes pane

a. Open the nodes pane on the left side, and then we're going to add two different data mining preprocessing nodes: Variable Selection and Variable Clustering. Drag and drop these objects onto the Data node.

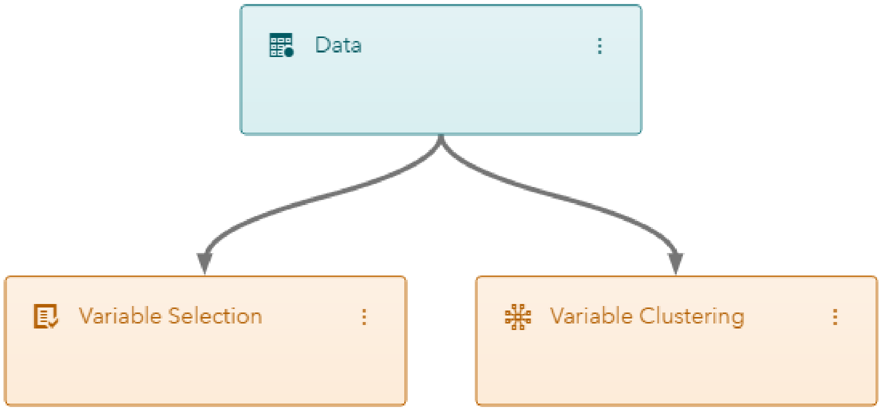


Figure 41: Added preprocessing nodes for Logistic Regression pipeline

b. After that, we're going to add three logistic regression nodes from the supervised learning section. Three should be attached to each of the preprocessing nodes and one to the data node.
    i. For each of the logistic regression nodes change the name, so it's easier to discern the different nodes and also change the configuration options for each node as noted below:
        1. Variable Selection
            a. Name: Logistic Regression (VarSel)
                i. Note: To change the name of a node, right-click the node and select rename.
            b. Options
                i. Selection Method: None
                ii. Note: To change the options, first select the options panel in the right pane.
        2. Variable Clustering
            a. Name: Logistic Regression (VarClus)
            b. Options
                i. Selection Method: None
        3. Logistic Regression
            a. Name: Logistic Regression (Backward selection)
            b. Options

i. Selection Method: Fast backward

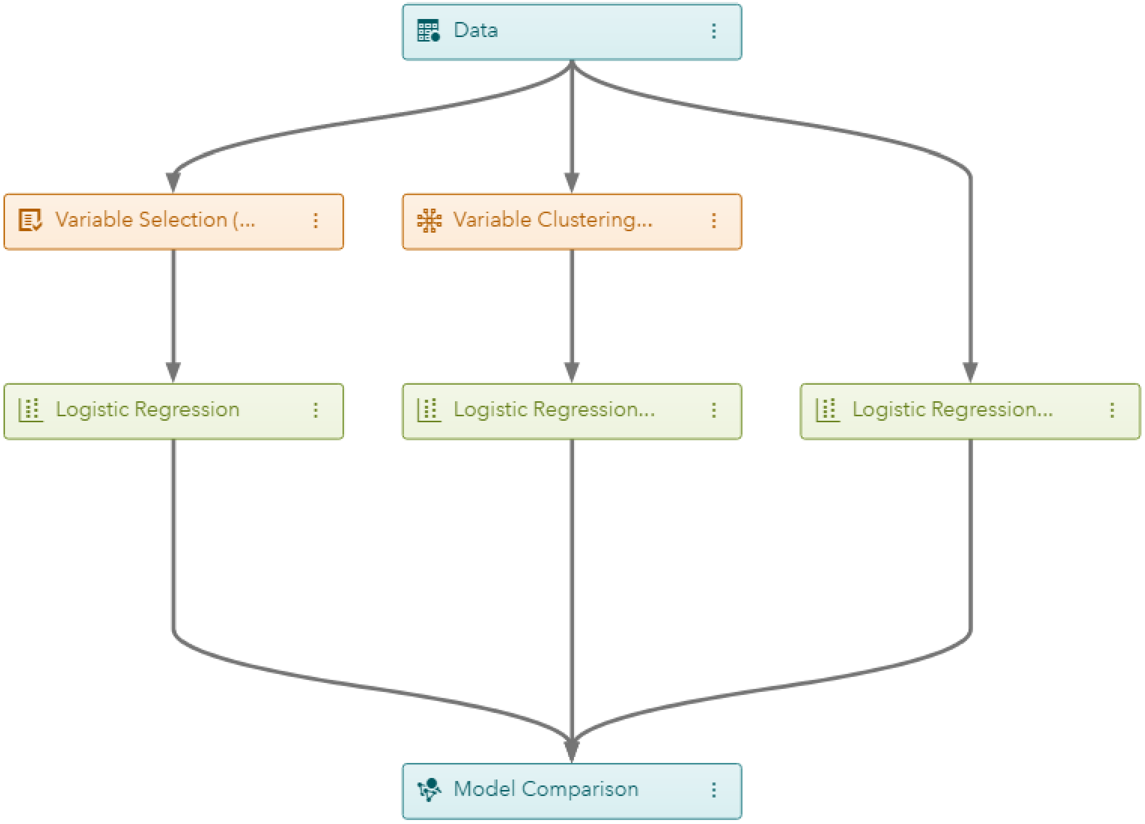


Figure 42: Completed Logistic Regression pipeline

c. Click Run to execute the pipeline.

i. Note: You can continue work while a pipeline is executing.

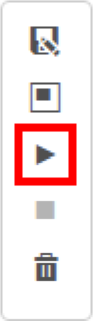


Figure 43: Executing pipeline

11. Next, let's work on the Gradient Boosting pipeline. Click on the Gradient Boosting tab.

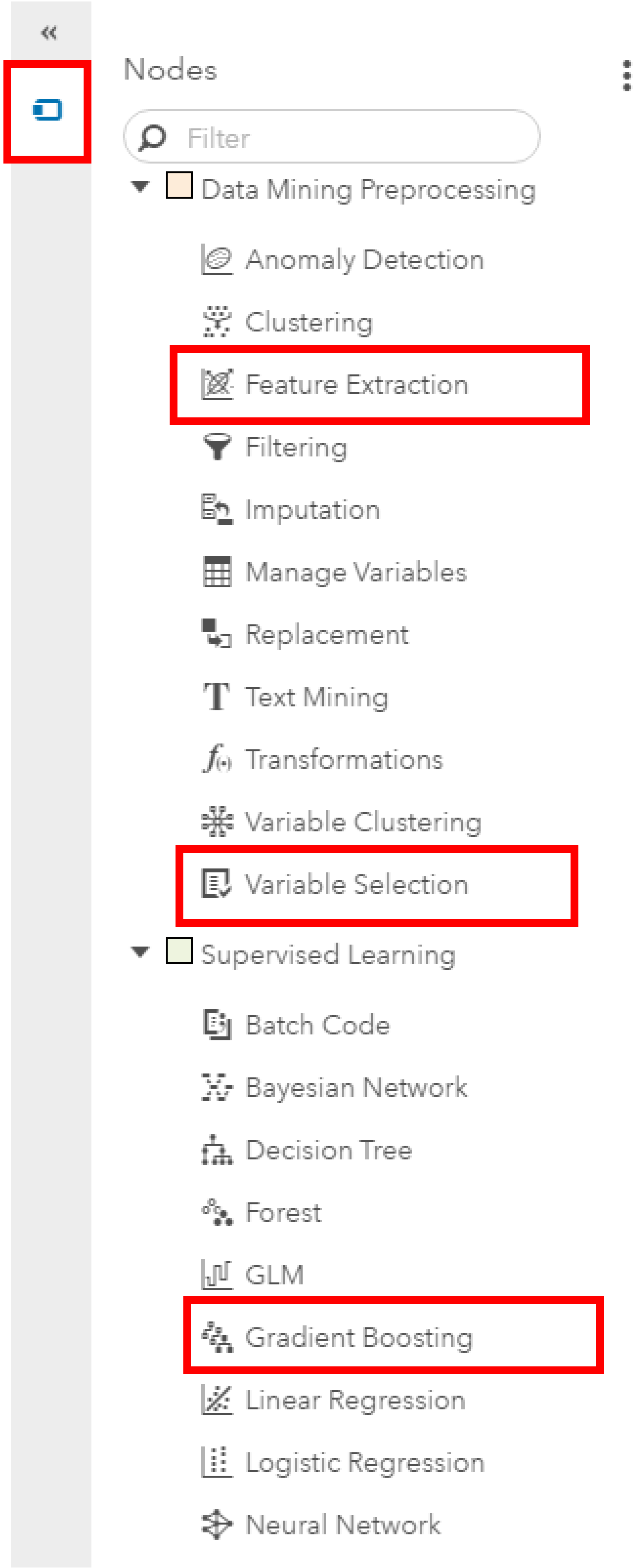


Figure 44: Selecting nodes from Nodes pane

a. Open the nodes pane on the left side, and add two different data mining preprocessing nodes: Variable Selection and Feature Extraction. Drag and drop these objects onto the Data node.

b. Next, we're going to add three Gradient Boosting nodes from the supervised learning section. Three should be attached to each of the preprocessing nodes and one to the Data node.

i. For each of the gradient boosting nodes change the name, so it's easier to discern the different nodes as noted below:

1. Variable Selection

a. Name: Gradient Boosting (VarSel)

2. Feature Extraction

a. Name: Gradient Boosting (Ext)

3. Gradient Boosting

a. Name: Gradient Boosting

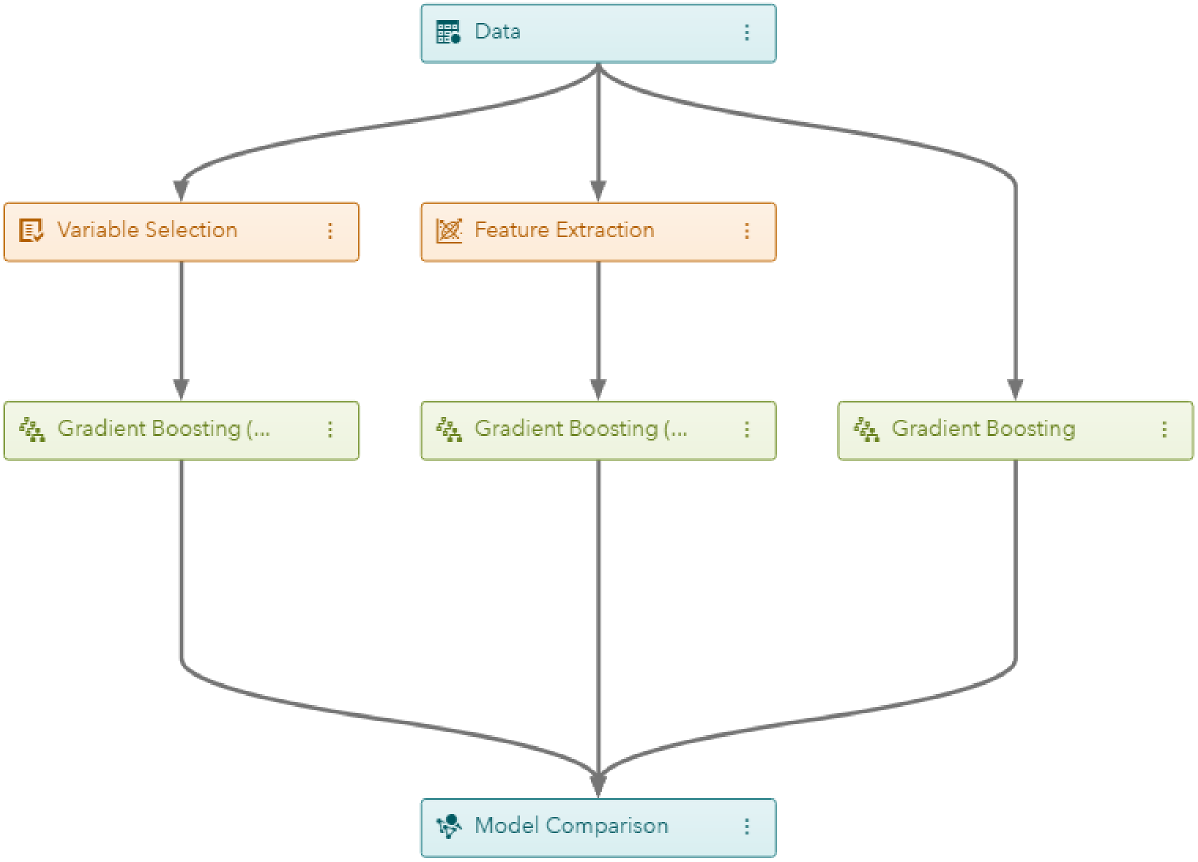
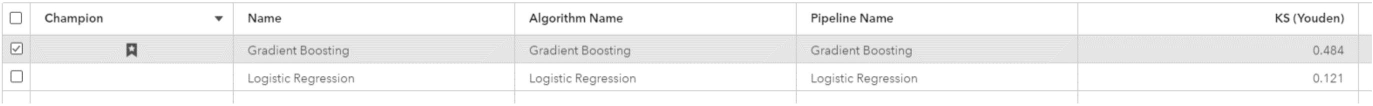


Figure 45: Completed Gradient Boosting pipeline

c. Click Run to execute the pipeline.

12. At this point, we've finished setting up all our pipelines and we can go to the Pipeline Comparison tab to see which of our pipelines performs the best. Click on the Pipeline Comparison tab.

13. In the Pipeline Comparison tab, the pipelines should be ranked by the default model performance statistic. Since this is a classification problem, the default is the KS (Youden) statistic.
    a. Note: You may receive different results from what we have received.



□	Champion ▾	Name	Algorithm Name	Pipeline Name	KS (Youden)
☑	🔖	Gradient Boosting	Gradient Boosting	Gradient Boosting	0.484
□		Logistic Regression	Logistic Regression	Logistic Regression	0.121

Figure 46: Comparing pipeline accuracy.

You're all done! With this Quick Start you've learned how to navigate Model Studio and seen how easy it is to set up analytical pipelines.

Documentation

[SAS® Visual Data Mining and Machine Learning 8.3: User's Guide]

Additional Videos

[Getting Started with Data Mining and Machine Learning Pipelines on SAS® Viya®]

[Managing Variables in Model Studio]

[The Variable Selection Node in Model Studio]

[Training Gradient Boosting Models in Model Studio]

Getting Started: SAS® Visual Analytics

Overview

SAS Visual Analytics provides a modern, integrated environment for discovery and exploration. Users, including those without advanced analytical skills, can examine and understand patterns, trends, and relationships in data. Reports and dashboards can easily be created and shared to display analyses and visualizations to help everyone get insights from data to better solve complex problems.

SAS® Visual Analytics 8.3 Video

Quick Start

In this Quick Start, we will learn how to use SAS Visual Analytics to create data visualizations in a report to present information and find new insights.

We will be using the DC_CORE_TABLE_PR table that we created in the Getting Started: Data Studio guide. If you have not completed that Getting Started guide or want to skip it, you can use the sample table located in the PDSSamples CASLib.

1. Log into SAS Visual Data Mining and Machine Learning.
2. First, we must load data from the PDSSamples CASLib into our CASUSER CASLib.
    a. Note: If you have completed this step in another Getting Started guide, then you can proceed to step 3. The PDSSamples CASLib contains sample files for the Getting Started guides and is different from the files used in Getting Started: SAS® Studio.
    b. In the application switcher, click on Develop SAS Code to navigate to SAS Studio.

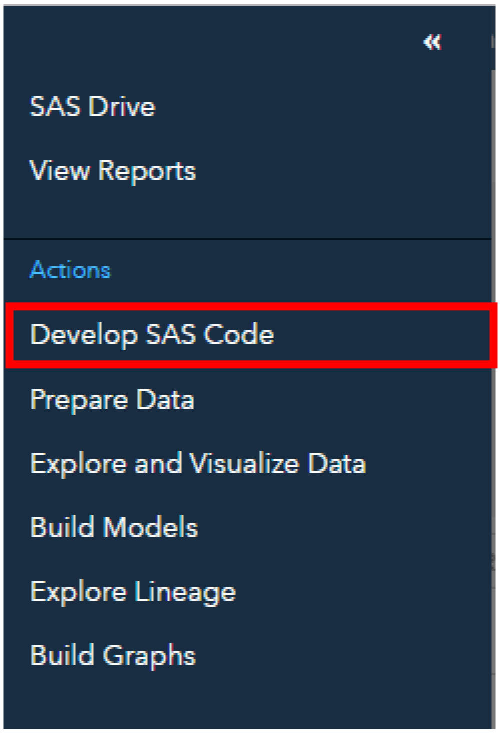
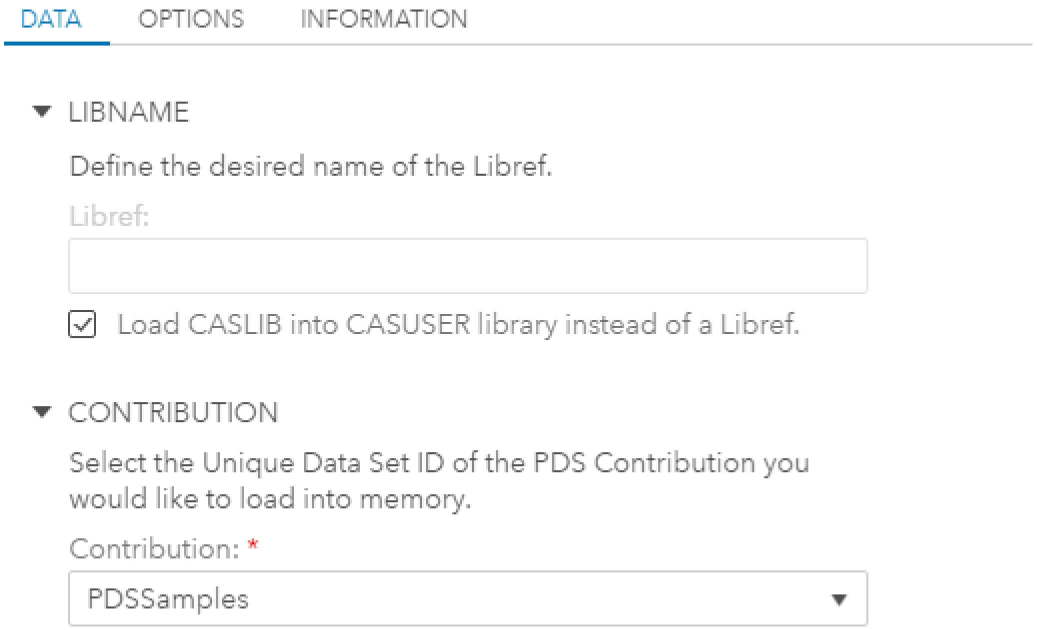


Figure 47: Navigate to SAS Studio by clicking Develop SAS Code in the App Switcher

c. Using the ‘Create Libref for PDS Contribution’ task under My Tasks load the data from the PDSSamples into your CASUSER library.



DATA OPTIONS INFORMATION

▼ LIBNAME

Define the desired name of the Libref.

Libref:

☑ Load CASLIB into CASUSER library instead of a Libref.

▼ CONTRIBUTION

Select the Unique Data Set ID of the PDS Contribution you would like to load into memory.

Contribution: *

PDSSamples ▼

Figure 48 SAS Studio task to load data from PDSSamples to CASUSER library

3. In the application switcher, click on ‘Explore and Visualize Data’ to navigate to SAS Visual Analytics.

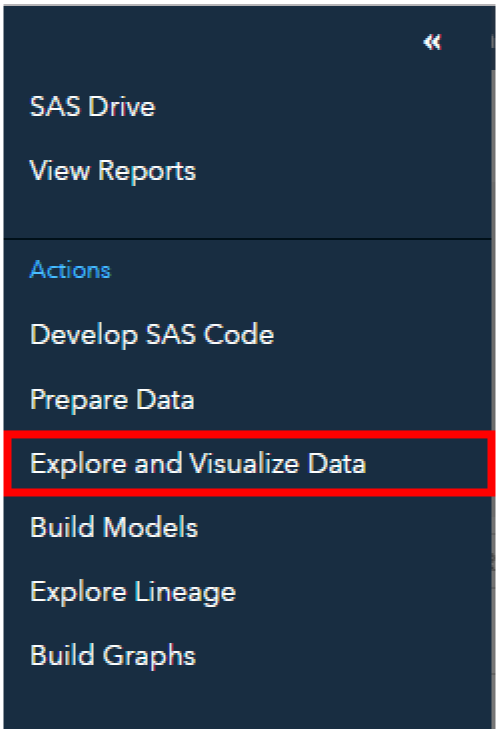
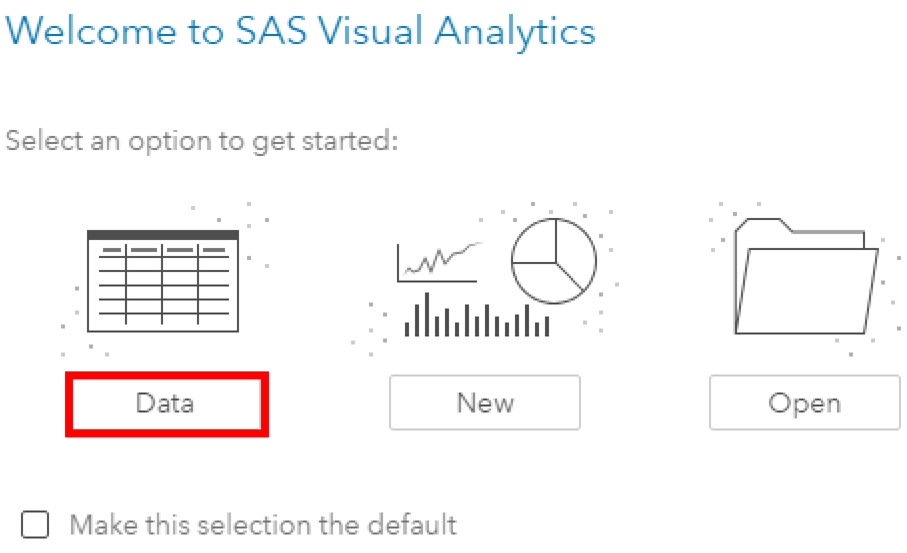


Figure 49: Navigate to SAS Visual Analytics by clicking Explore and Visualize Data in the App Switcher

4. To get started creating a SAS Visual Analytics report, we will click the ‘Data’ button.

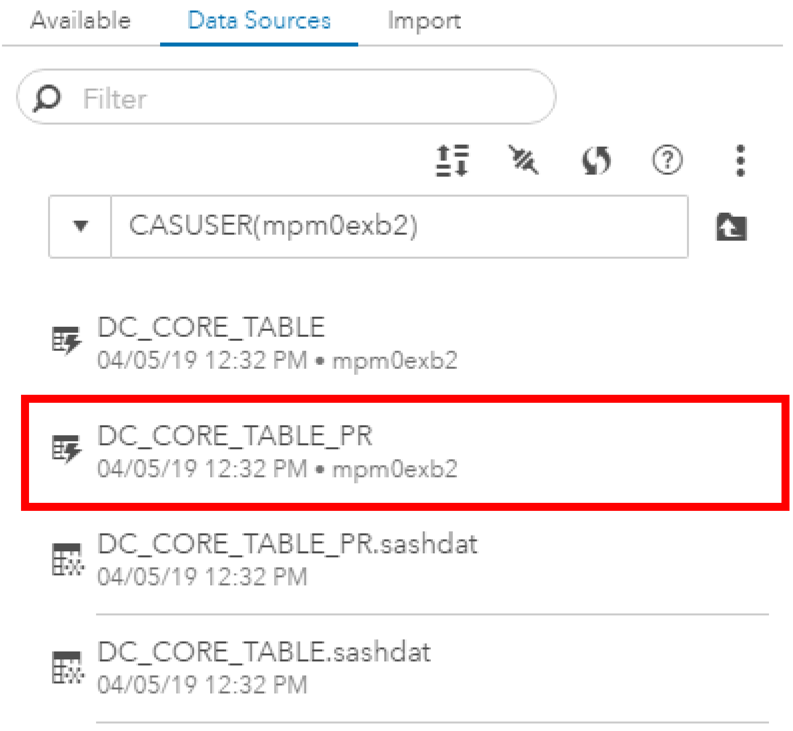

Welcome to SAS Visual Analytics

Select an option to get started:

☐ Make this selection the default

Figure 50: Creating a new SAS Visual Analytics report

5. In the Open Data Source dialog that is displayed, select the Data Sources tab and then select cas-shared-default. Next, use the ‘DC_CORE_TABLE_PR’ in-memory table stored in your CASUSER directory. After selecting the table, click OK.



CASUSER(mpm0exb2)

DC_CORE_TABLE
04/05/19 12:32 PM • mpm0exb2

DC_CORE_TABLE_PR
04/05/19 12:32 PM • mpm0exb2

DC_CORE_TABLE_PR.sashdat
04/05/19 12:32 PM

DC_CORE_TABLE.sashdat
04/05/19 12:32 PM

Figure 51: Selecting table to use for report

6. In this report, we're going to create two tabs: Variable Explanation and Demographics & Baseline Labs. Create the first tab by right-clicking 'Page 1' and renaming it to Variable Explanation. Add the other tab by clicking the plus icon and then renaming it to Demographics & Baseline Labs.
    a. Note: The left pane may be covering up the 'Page 1' tab. You can pin the left pane by clicking the push tab icon.

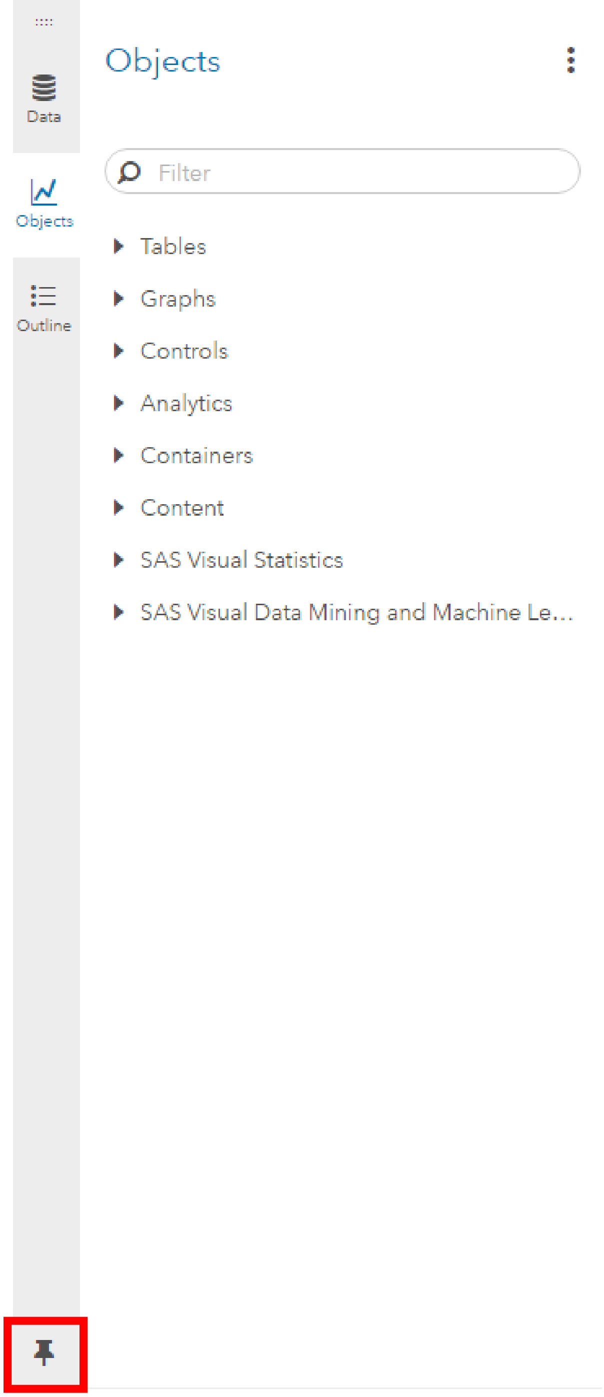


Figure 52: Pinning the left pane

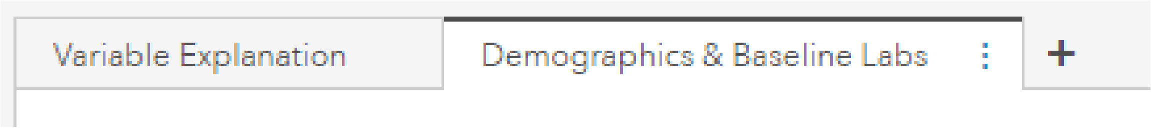


Figure 53: Creating and renaming tabs in report

7. First, we'll start with the Variable Explanation tab. Select the objects icon in the left pane and then drag and drop the 'Automated Analysis' item into the report.

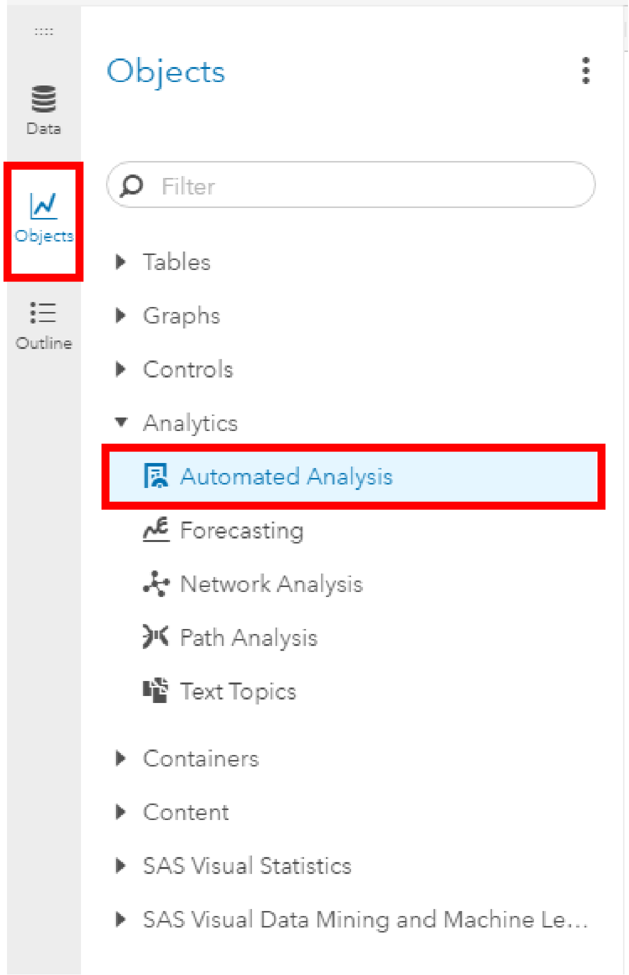
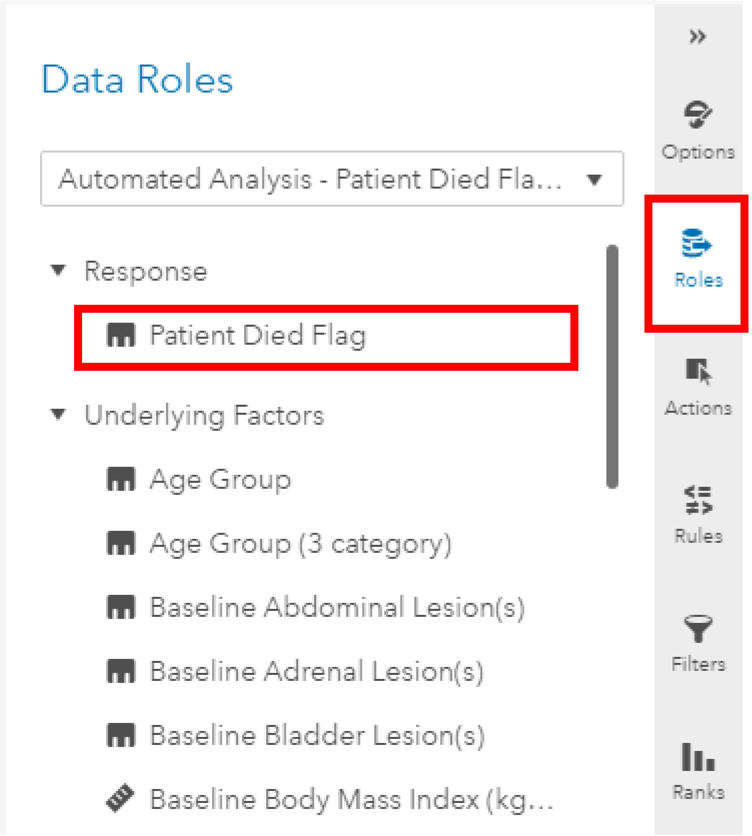


Figure 54: Adding Automated Analysis object

a. After adding the 'Automated Analysis' object to the report, you'll see a message 'The required roles have not been assigned a data item'. To define the roles for the object, click the roles icon in the right pane. Then under 'Response', select 'Patient Died Flag'.
   i. Note: The underlying factors will be automatically selected for you.



Data Roles

Automated Analysis - Patient Died Fla... ▾

▾ Response

Patient Died Flag

▾ Underlying Factors

Age Group

Age Group (3 category)

Baseline Abdominal Lesion(s)

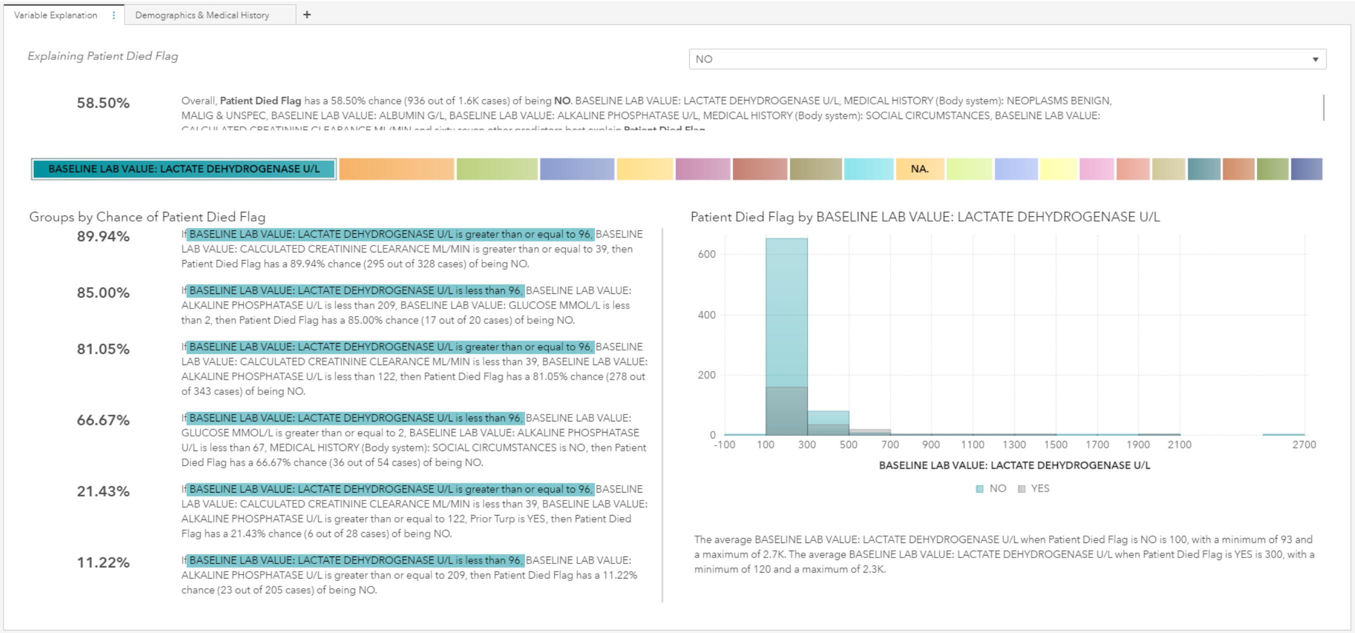
Baseline Adrenal Lesion(s)

Baseline Bladder Lesion(s)

Baseline Body Mass Index (kg...

Figure 55: Selecting role for Automated Analysis object

b. That's it! The Variable Explanation tab is now complete and you should see a report like the image below.



Explaining Patient Died Flag

NO ▾

58.50% Overall, **Patient Died Flag** has a 58.50% chance (936 out of 1.6K cases) of being **NO**. BASELINE LAB VALUE: LACTATE DEHYDROGENASE U/L, MEDICAL HISTORY (Body system): NEOPLASMS BENIGN, MALIG & UNSPEC, BASELINE LAB VALUE: ALBUMIN G/L, BASELINE LAB VALUE: ALKALINE PHOSPHATASE U/L, MEDICAL HISTORY (Body system): SOCIAL CIRCUMSTANCES, BASELINE LAB VALUE: CALCULATED CREATININE CLEARANCE ML/MIN and sixty seven other predictors best explain **Patient Died Flag**.

Groups by Chance of Patient Died Flag

89.94% If BASELINE LAB VALUE: LACTATE DEHYDROGENASE U/L is greater than or equal to 96, BASELINE LAB VALUE: CALCULATED CREATININE CLEARANCE ML/MIN is greater than or equal to 39, then Patient Died Flag has a 89.94% chance (295 out of 328 cases) of being NO.

85.00% If BASELINE LAB VALUE: LACTATE DEHYDROGENASE U/L is less than 96, BASELINE LAB VALUE: ALKALINE PHOSPHATASE U/L is less than 209, BASELINE LAB VALUE: GLUCOSE MMOL/L is less than 2, then Patient Died Flag has a 85.00% chance (17 out of 20 cases) of being NO.

81.05% If BASELINE LAB VALUE: LACTATE DEHYDROGENASE U/L is greater than or equal to 96, BASELINE LAB VALUE: CALCULATED CREATININE CLEARANCE ML/MIN is less than 39, BASELINE LAB VALUE: ALKALINE PHOSPHATASE U/L is less than 122, then Patient Died Flag has a 81.05% chance (278 out of 343 cases) of being NO.

66.67% If BASELINE LAB VALUE: LACTATE DEHYDROGENASE U/L is less than 96, BASELINE LAB VALUE: GLUCOSE MMOL/L is greater than or equal to 2, BASELINE LAB VALUE: ALKALINE PHOSPHATASE U/L is less than 67, MEDICAL HISTORY (Body system): SOCIAL CIRCUMSTANCES is NO, then Patient Died Flag has a 66.67% chance (36 out of 54 cases) of being NO.

21.43% If BASELINE LAB VALUE: LACTATE DEHYDROGENASE U/L is greater than or equal to 96, BASELINE LAB VALUE: CALCULATED CREATININE CLEARANCE ML/MIN is less than 39, BASELINE LAB VALUE: ALKALINE PHOSPHATASE U/L is greater than or equal to 122, Prior Turp is YES, then Patient Died Flag has a 21.43% chance (6 out of 28 cases) of being NO.

11.22% If BASELINE LAB VALUE: LACTATE DEHYDROGENASE U/L is less than 96, BASELINE LAB VALUE: ALKALINE PHOSPHATASE U/L is greater than or equal to 209, then Patient Died Flag has a 11.22% chance (23 out of 205 cases) of being NO.

Patient Died Flag by BASELINE LAB VALUE: LACTATE DEHYDROGENASE U/L

The average BASELINE LAB VALUE: LACTATE DEHYDROGENASE U/L when Patient Died Flag is NO is 100, with a minimum of 93 and a maximum of 2.7K. The average BASELINE LAB VALUE: LACTATE DEHYDROGENASE U/L when Patient Died Flag is YES is 300, with a minimum of 120 and a maximum of 2.3K.

Figure 56: The completed Variable Explanation report tab

8. Next, we'll work on the Demographics & Baseline Labs tab. In this tab, we're going to create some basic bar and box charts to examine the distribution of some demographics and baseline lab variables with respect to the Patient Died Flag. First, we'll add a bar chart and box chart object to the report.

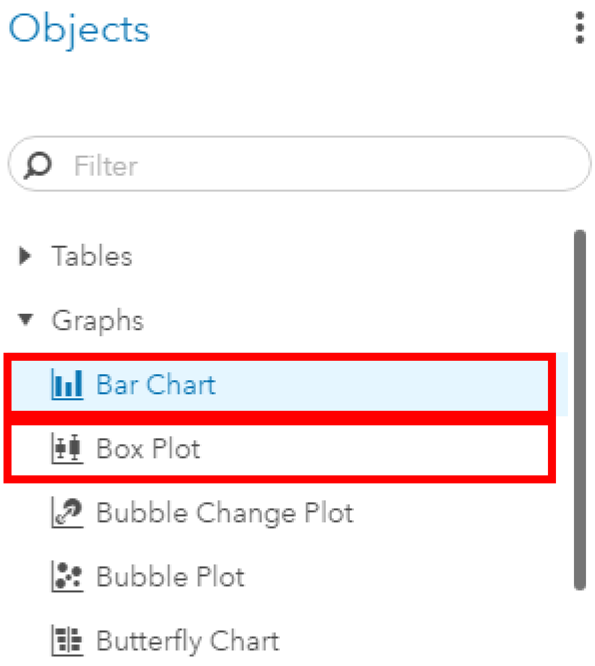
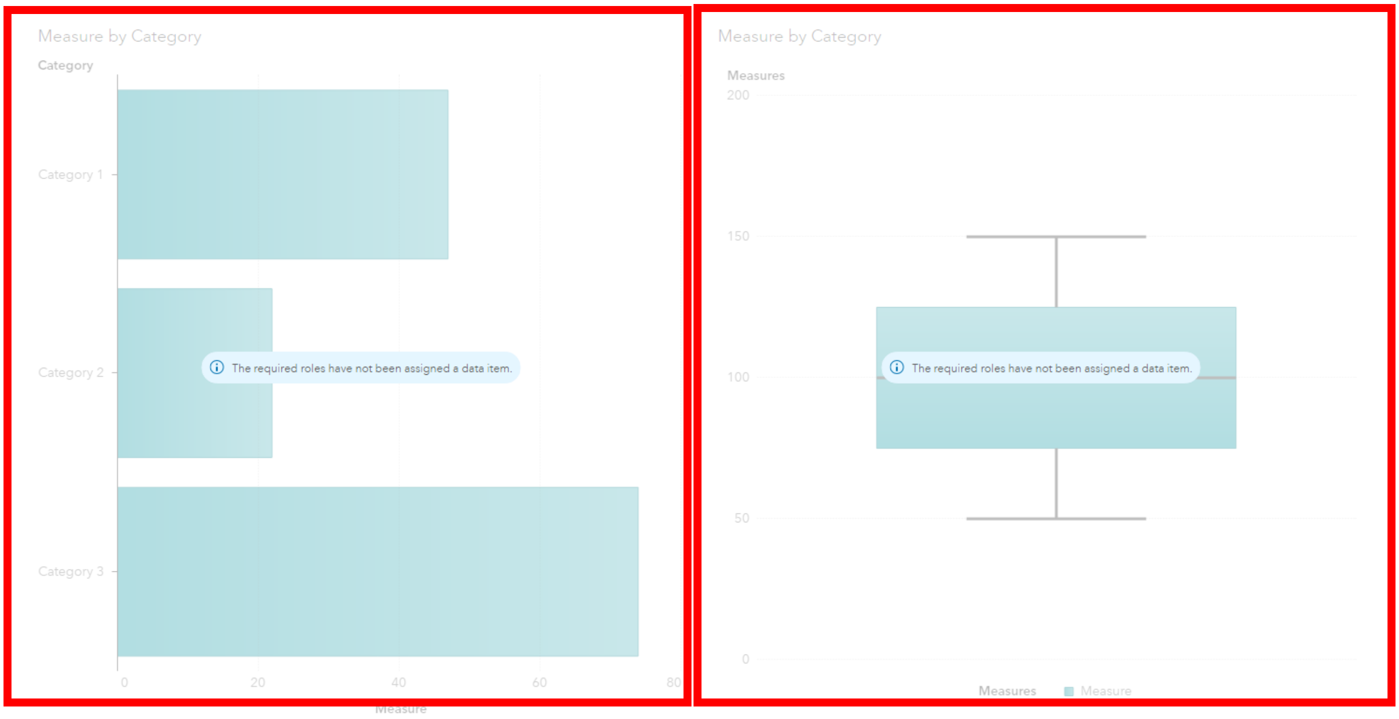


Figure 57: Adding Bar Chart objects to report



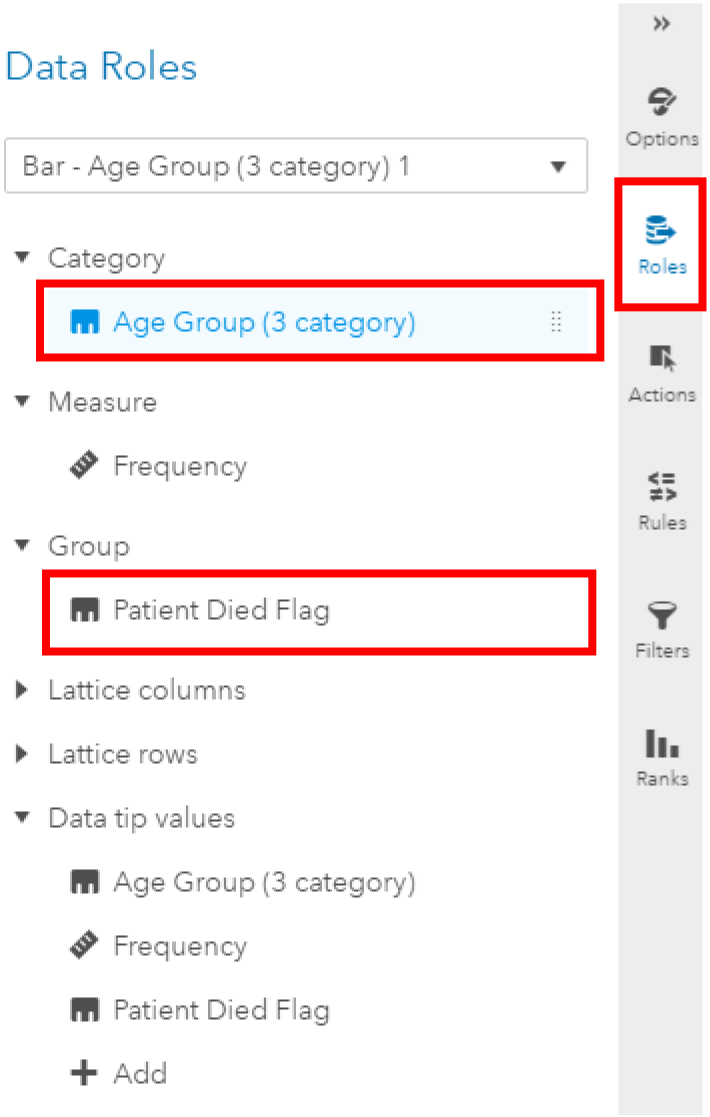
The required roles have not been assigned a data item.

The required roles have not been assigned a data item.

Figure 58: Adding a bar and box chart to report

a. The charts have been added to the tab, but now we need to set up each of them. We'll start with the left-side bar chart we want to display the frequency of the age group grouped by the patient died flag. Select the bar chart and then open the roles pane.

   i. In the roles pane, under category select 'Age Group (3 category)'. Under group, select 'Patient Died Flag'.



Data Roles

Bar - Age Group (3 category) 1

Category

- Age Group (3 category)

Measure

- Frequency

Group

- Patient Died Flag

Lattice columns

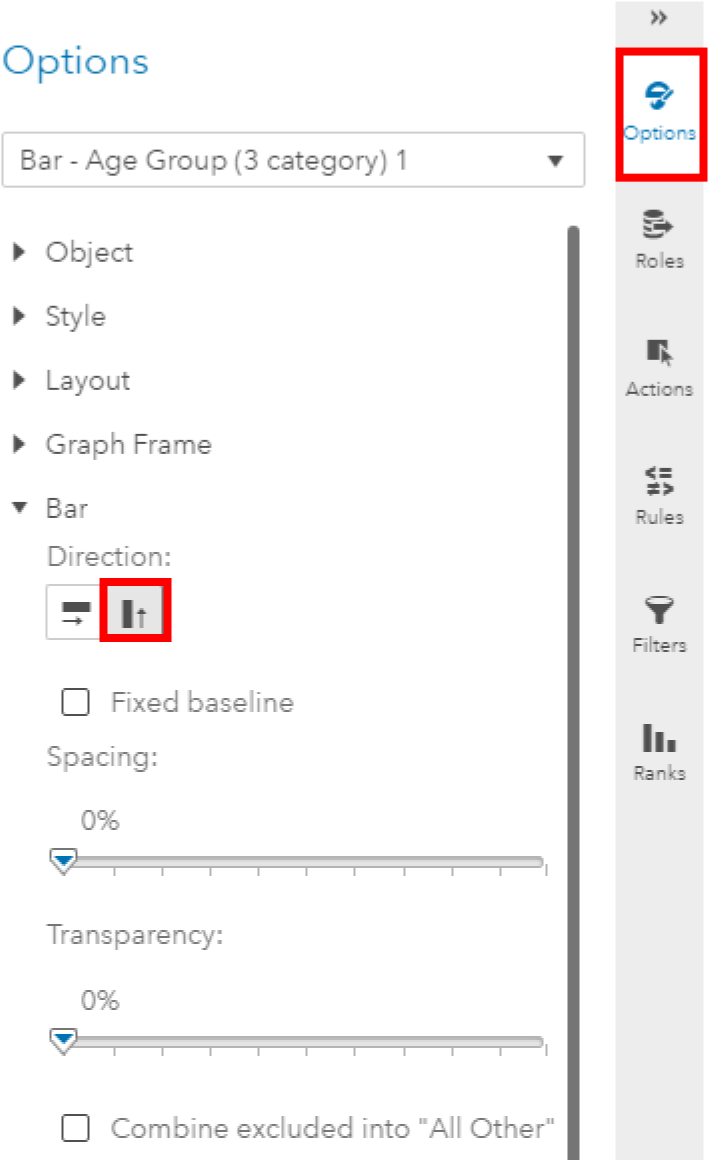
Lattice rows

Data tip values

- Age Group (3 category)
- Frequency
- Patient Died Flag
- Add

Figure 59: Define roles for bar chart

ii. Lastly, for this bar chart let's change the orientation of the bars from being horizontal to vertical. We can do that by going to the options pane and selecting the vertical icon for the direction.



Options

Bar - Age Group (3 category) 1 ▾

- ▸ Object
- ▸ Style
- ▸ Layout
- ▸ Graph Frame
- ▾ Bar

Direction:

□ Fixed baseline

Spacing:

0%

Transparency:

0%

□ Combine excluded into "All Other"

Figure 60: Settings options on the bar chart

iii. All done! The left-side bar chart is now complete.

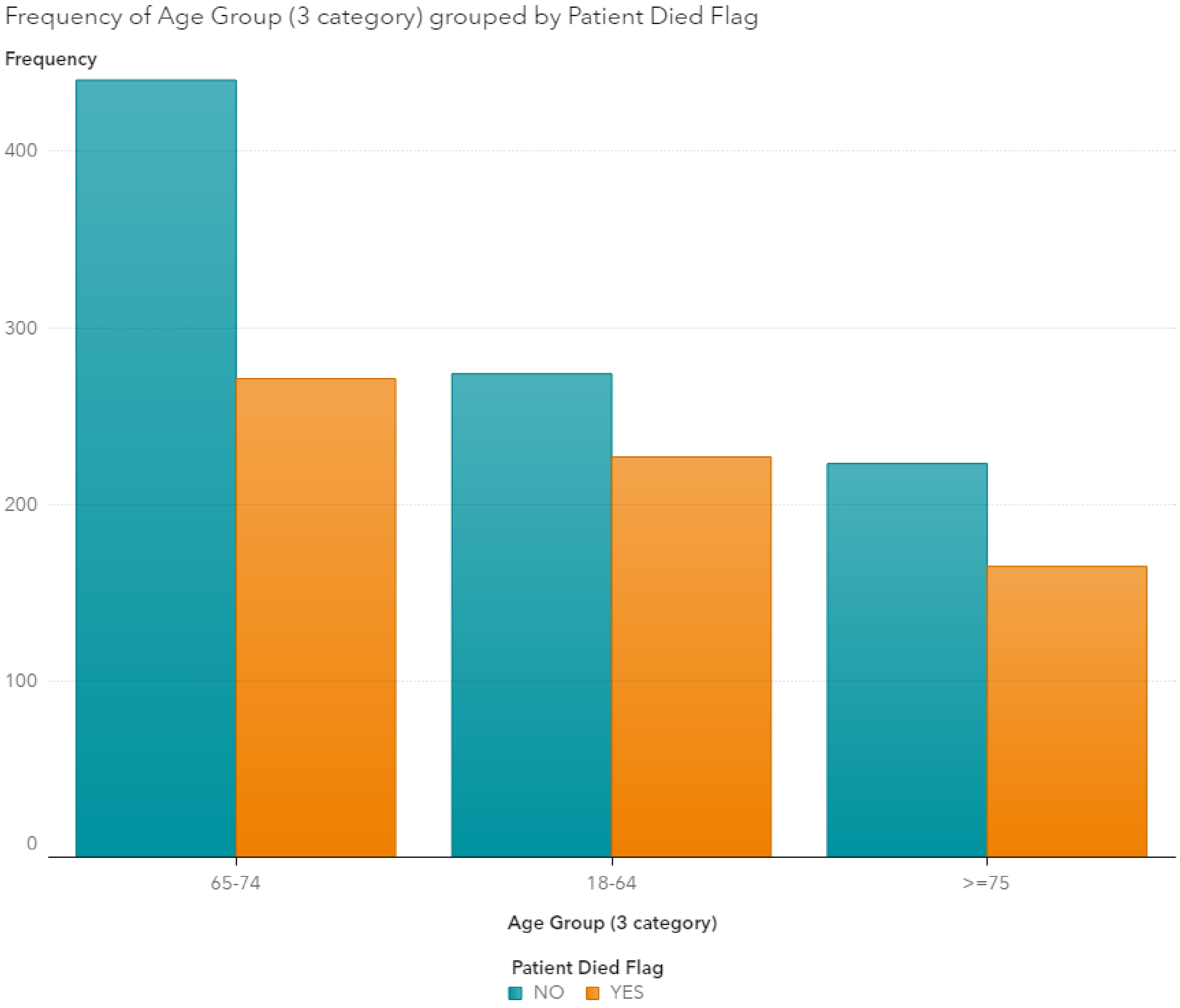
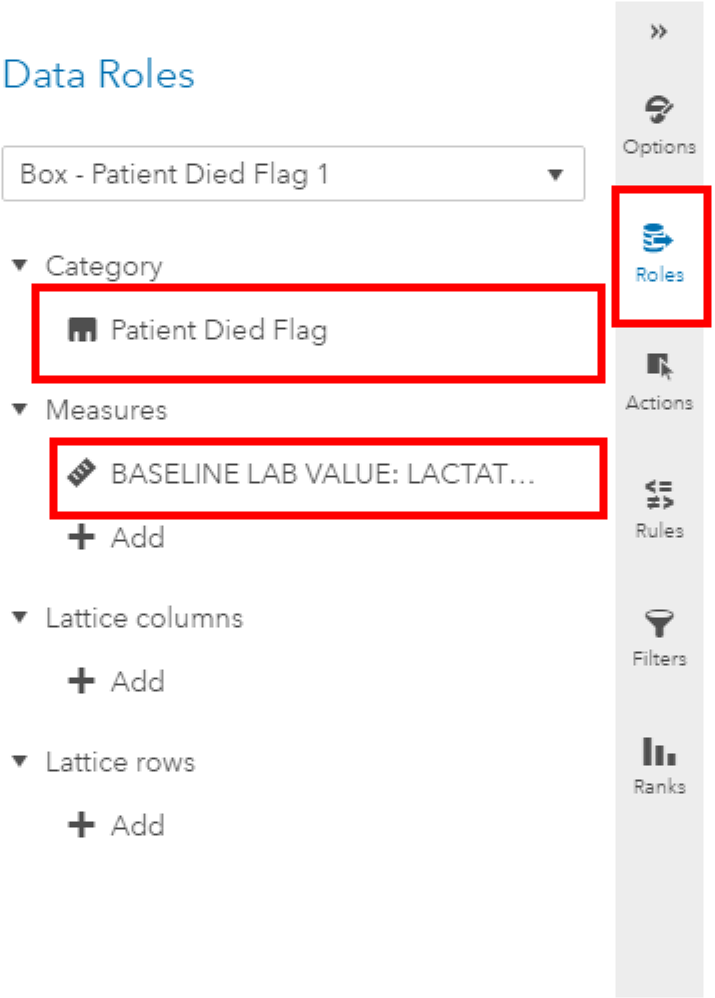


Figure 61: A bar chart displaying the age group grouped by the patient died flag

b. Next, let's work on the right-side box chart. In this box chart, we want to display BASELINE LAB VALUE: LACTATE DEHYDROGENASE U/L baseline lab grouped by the patient died flag.

  i. Select the right-side box chart and then in the roles pane, under category select the 'Patient Died Flag' column and under measure select the 'BASELINE LAB VALUE: LACTATE DEHYDROGENASE U/L' column.



Data Roles

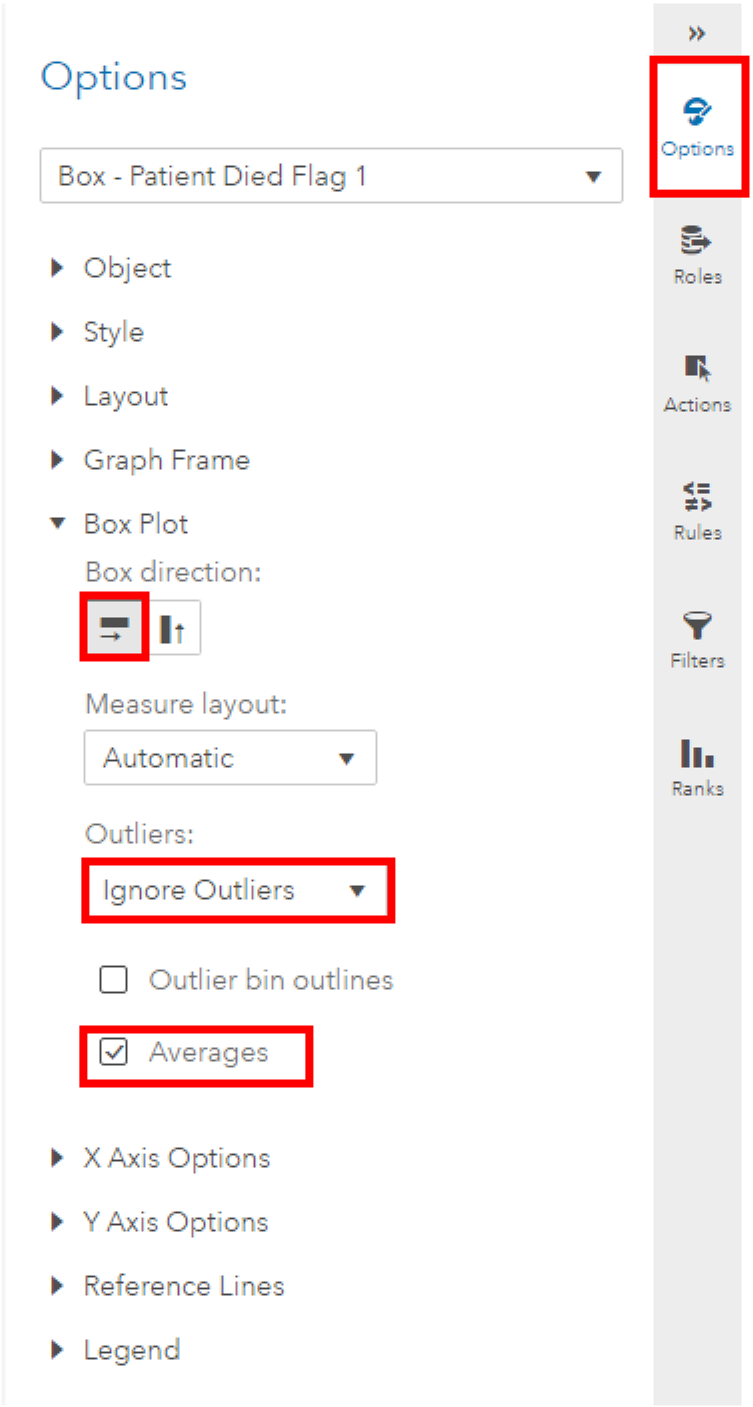
Box - Patient Died Flag 1

- Category
  - Patient Died Flag
- Measures
  - BASELINE LAB VALUE: LACTAT…
  - + Add
- Lattice columns
  - + Add
- Lattice rows
  - + Add

Figure 62: Define roles for box chart

ii. Lastly, let's change the appearance of the box chart in a few ways. Select the right Options pane and change the following:

1. Box direction: horizontal
2. Outliers: Ignore Outliers
3. Averages: True



Options

Box - Patient Died Flag 1 ▼

- Object
- Style
- Layout
- Graph Frame
- Box Plot

Box direction:

Measure layout: Automatic ▼

Outliers: Ignore Outliers ▼

☐ Outlier bin outlines

☑ Averages

- X Axis Options
- Y Axis Options
- Reference Lines
- Legend

Figure 63: Define options for box chart

9. That it's for the Demographics & Baseline Labs tab.

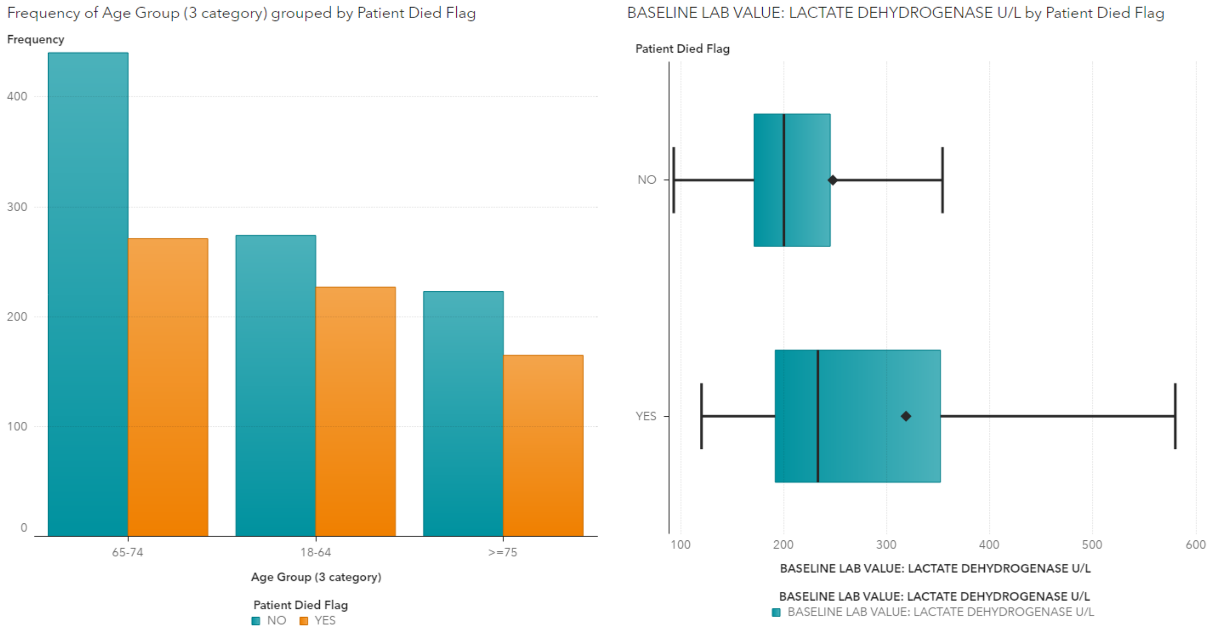


Figure 64: Completed Demographics & Baseline Labs tab

If you would like to save your report, follow the instructions below:

10. To save the report, click the save icon in the top right.

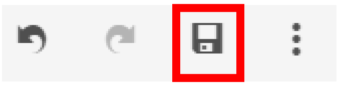
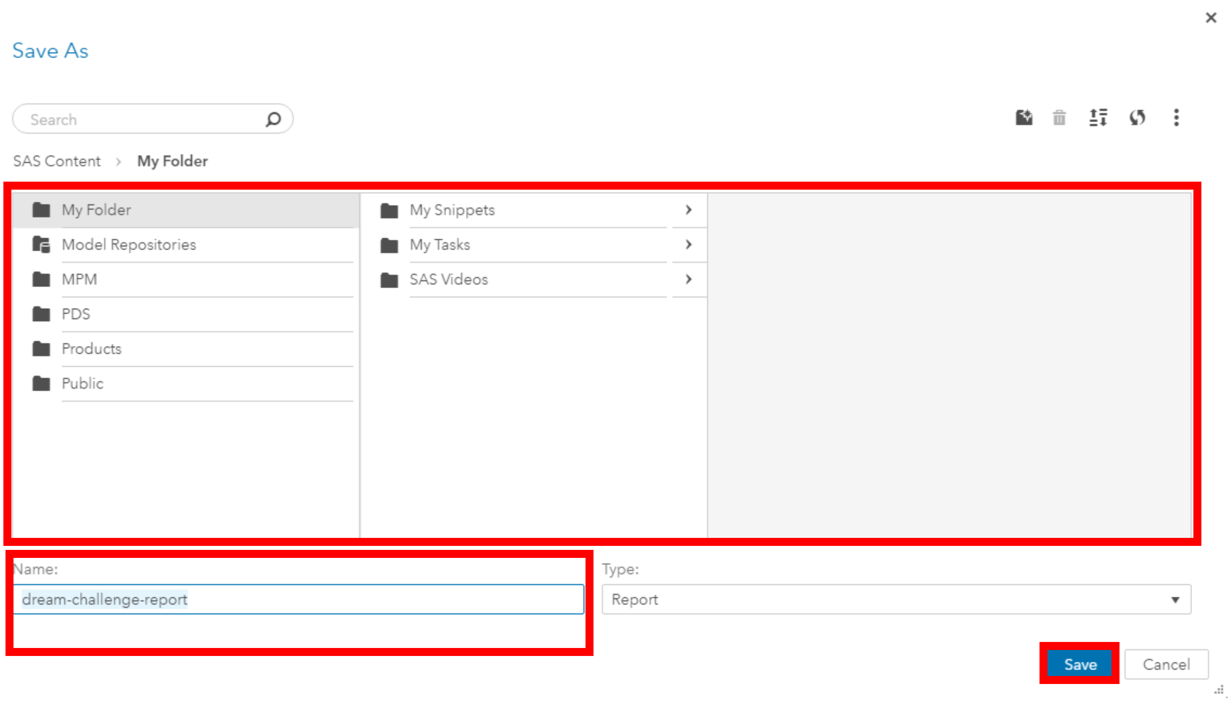


Figure 65: Save Report

11. In the Save As dialog, you must specify where you want to save the report and the name of the report. We suggest saving it in your My Folder and you can name the report whatever you desire.



Name: dream-challenge-report

Type: Report

Figure 66: Save As Dialog

12. Lastly, click the Save button.

You're all done! You should now know how to quickly create a report in SAS Visual Analytics.

Documentation

[SAS® Visual Analytics 8.3: Overview]

[SAS® Visual Analytics 8.3: Getting Started with Reports]

Additional Videos

[Creating a Basic Report in SAS® Visual Analytics on SAS® Viya®]

[Exploring Data in SAS Visual Analytics 8.1 on SAS Viya]

[Viewing a Report in SAS Visual Analytics 8.1 on SAS Viya]