

SAS Institute Japan Ltd. Toru Tsunoda (Toru.Tsunoda@sas.com)



Data Mapping

Problem Definition



- Source Data mapped to Destination Data based on Standards
 - Time-consuming process
- Standards and Implementation Guides leave room for individual interpretation
 - Inconsistent Mappings Not what a "Standard" should be
- Mapping is generally done in individual SAS programs
 - Lacks collection of central metadata/mappings
 - Only way to re-use previous mappings is copying programs



History of Clinical Data Mapping tools

Various SAS tools

CDR(Clinical Data Repository) plus MDR(Meta Data Repository)

Clinical Data Integration

Analytics Pro

(PC-SAS)



Programing tool using GUI

Life Science Analytics Framework

(ex SAS Drug Development)



Data Mapper

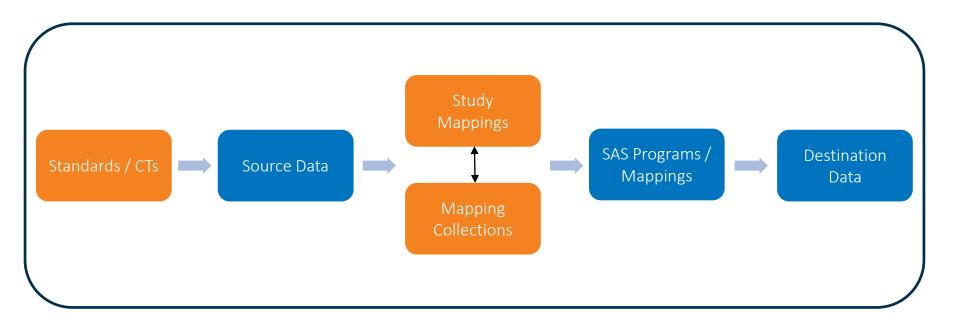
Programing tool (ex LSAF Extension)

using Machine Learning





Data Mapping using "Data Mapper" Solution

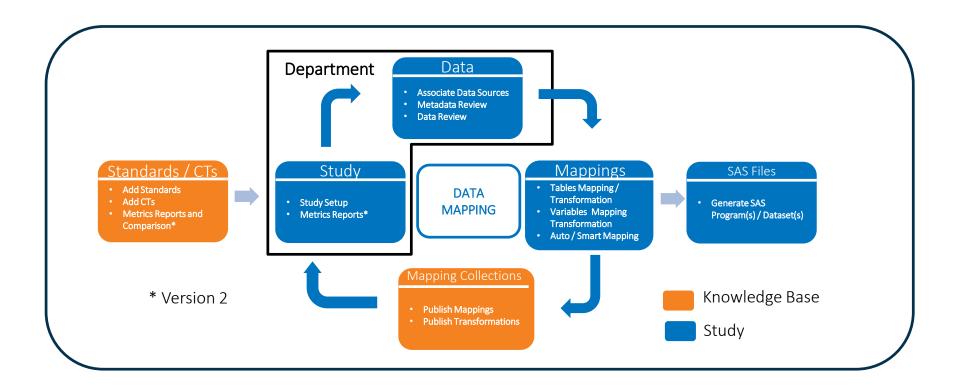




Solution

- User interface to mapping process
- Libraries Collection of mapping rules in central database
- Collect data and standards, and allow user to define rules for mapping
- Ability to re-use mapping rules in future studies
- Auto Mapping One-to-One mapping Rule between Source Data and its variable, to Destination Data and its variable
 - e.g. adverse.patid → AE.USUBJID
 - Next study, adverse.patid is automatically mapped
- Smart Mapping Similar Variables mapped in past provide guidelines to map new variables
 - e.g. adverse.ptid → AE.USUBJID
 - Suggested mapping based on previous mapping, adverse.Patid → AE.USUBJID
- Generate the SAS programs based on defined mapping

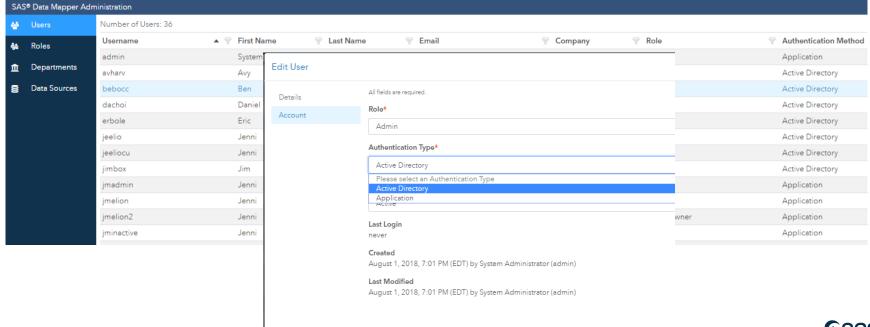






Administration - Users

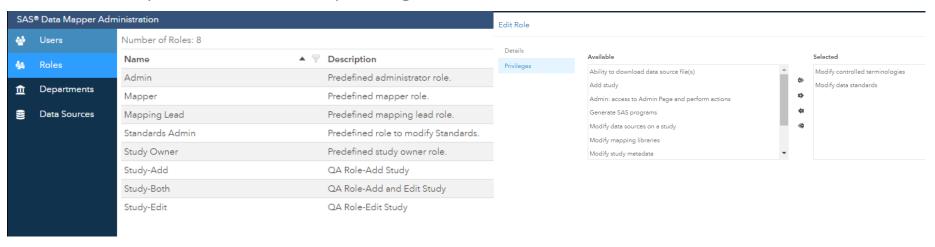
- Users Ability to register user in system
- Authentication Type: Application / Active Directory





Administration - Roles

- Roles Pre-defined set of Roles with different privileges
- Ability to add /remove privileges





Administration – Data Sources

• Data Sources – define data locations

SAS® Data Mapper Administration						
44	Users	Number of Data Sources: 14				
64	Roles	① Click refresh to scan for new data sources.				
m	Departments	Name	A 🗑	Path		
_		custom_formats		/tla/warehouse/oracle_content/data_sources/custom_formats		
8	Data Sources	dataSourceA		/tla/warehouse/oracle_content/data_sources/dataSourceA		
		dataSourceB		/tla/warehouse/oracle_content/data_sources/dataSourceB		
		dataSourceC		/tla/warehouse/oracle_content/data_sources/dataSourceC		
		dupe		/tla/warehouse/oracle_content/data_sources/dupe		
		empty		/tla/warehouse/oracle_content/data_sources/empty		
		FSDataSource1		/tla/warehouse/oracle_content/data_sources/FSDataSource1		
		FSDataSource2		/tla/warehouse/oracle_content/data_sources/FSDataSource2		
		NICSAH_DATA		/tla/warehouse/oracle_content/data_sources/NICSAH_DATA		



Administration - Departments

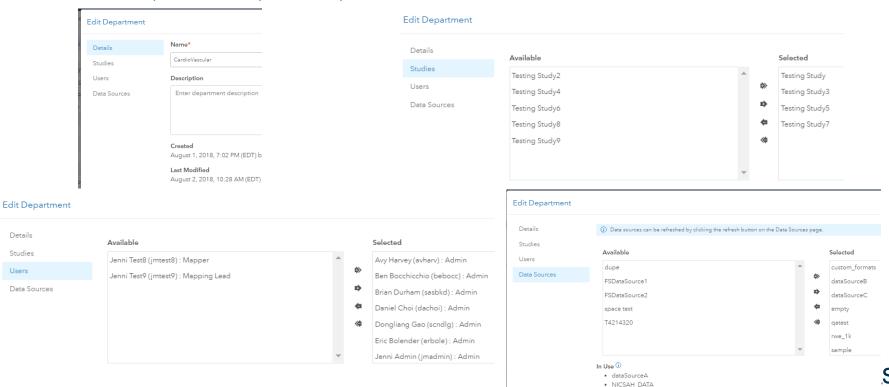
- Departments Group similar studies with associated data sources and members
- Provides better permission and data access control

SAS® Data Mapper Administration								
44	Users	Number of Departments: 13						
44	Roles	Name	▲ 🗑	Users 💡	Studies 💡	Data Sources		
		CardioVascular		34	9			
血	Departments	CNS		0	0			
2	Data Sources	Dermatology		0	0			
		Endocrinology		0	0			
		Gastroenterology		0	0			



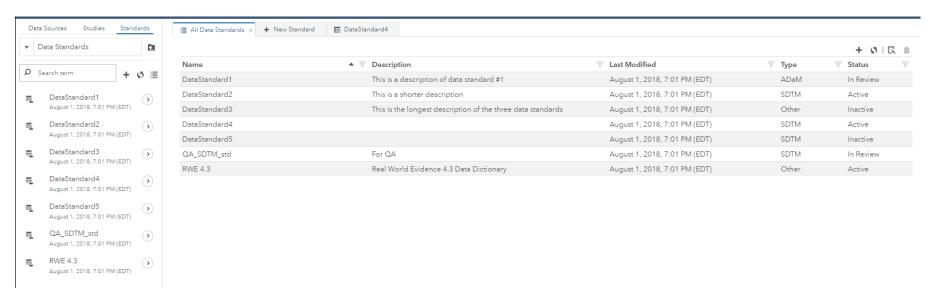
Administration - Departments

Details / Studies / Users / Data Sources



Knowledge Base - Standards

- Register Standard by Importing
- View list of Registered Standards





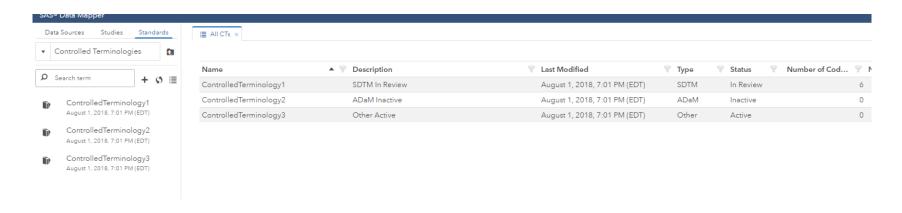
Knowledge Base - Standards

- View Domains Information
- View Domain Variables Details

All Data Sta	andards 🏻 🏗	DataStandard4	■ DataStandard4/AE ×									
letadata	Variables											
Order ^	Name	P Label		P Des	cription	₹ Туре	7	Length 🖁 Format	Origin	₹ Role	▼ Core	
	1 STUDYID	Study Identifie	er	Unic	que identifier for a study.	CHAR		200	CRF	Identifier	Required	1
	2 DOMAIN	Domain Abbr	eviation	Two dom	-character abbreviation for the nain.	CHAR		200 AE	ASSIGNED	Identifier	Required	
	3 USUBJID	Unique Subje	ct Identifier	subj app	ntifier used to uniquely identify a ject across all studies for all lications or submissions involving product.	CHAR		200	DERIVED	Identifier	Required	
	4 AESEQ	Sequence Nu	mber	unio	uence Number given to ensure queness of subject records within nain. May be any valid number.	NUM a		8	ASSIGNED	Identifier	Required	
	5 AEGRPID	Group ID			d to tie together a block of related ords in a single domain for a subje			200	DERIVED	Identifier	Permissib	ole
					1 , , , , , , , , , , , , , , , , , , ,							
TA	Trial Arms				STUDYID, ARMCD, TAETORD							
TE	Trial Elemen	nts on/ Exclusion Criteria			STUDYID, ETCD STUDYID, IETESTCD							
TI TV	Trial Visits	on/ Exclusion Criteria			STUDYID, IETESTCD STUDYID, VISITNUM, ARMCD						(0
VS	Vital Signs				STUDYID, VISITNOM, ARMED STUDYID, USUBJID, VSTESTCD, VISITNUM, VST	DTREE V/STRTNII IN	4) ,

Knowledge Base – Controlled Terminology (CT)

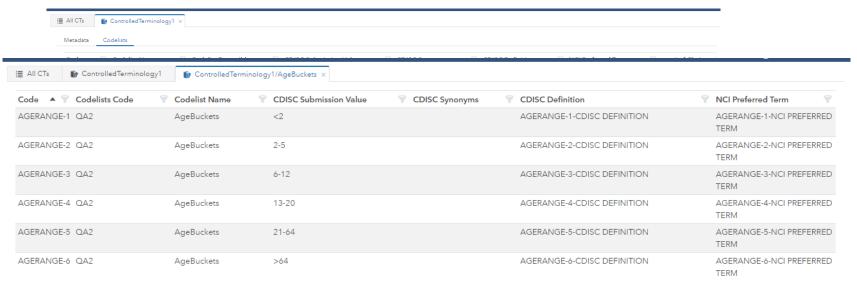
- Register Controlled Terminology by Importing
- View list of Registered Controlled Terminologies





Knowledge Base – Controlled Terminology (CT)

- View Codelists Information
- View Codelist Values



Standards Consortium Study Data Tabulation Model.



Knowledge Base – Mapping Collection (Under Development)

- Define Mapping Collections by Importing
- View list of defined Mapping Collections

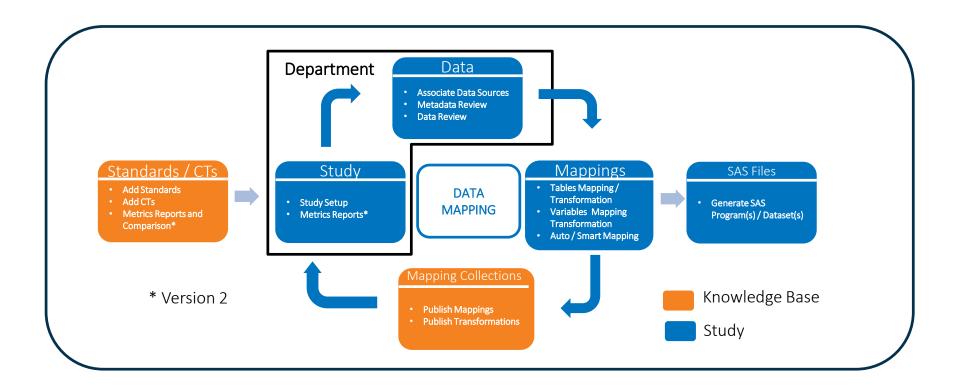


Knowledge Base – Mapping Collections (Under Development)

View Mapping Collection Information



Study Flow

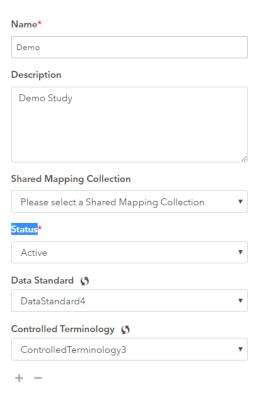






1. Metadata —

- Define study name and description
- Mapping Library
- Associate Standards
- Associate Controlled Terminologies

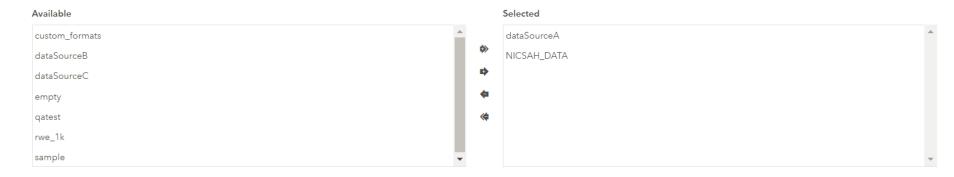






2. Data Sources –

• Associate Data Source(s) defined at Departments with study







3. Data Transform –

12 run;

- Provide ability to read non-SAS datasets and convert them into SAS datasets.
- Live SAS Session with ability to view log and output datasets

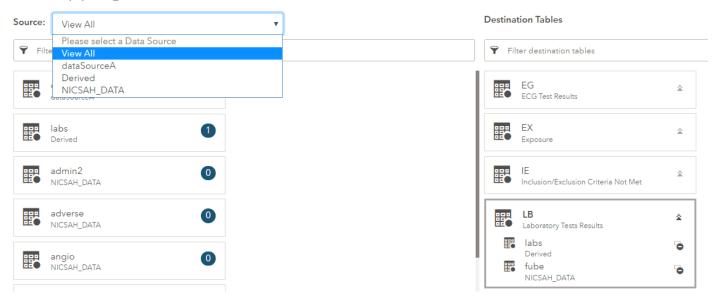






4. Tables –

- Provide ability to map Source datasets to Destination Domains.
- List all associated data sources
- Mapping count is maintained.



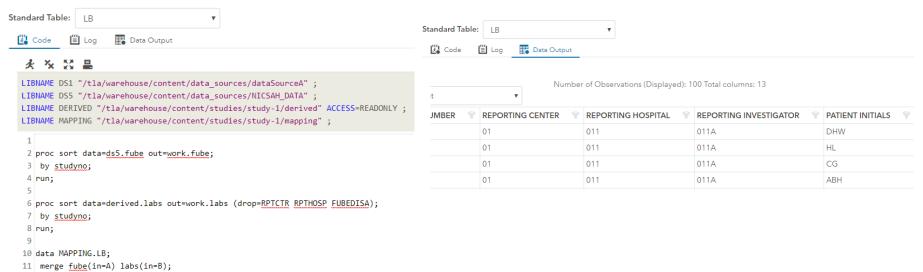




5. Tables Transform –

12 by studyno; 13 run; 14

- Provide ability to realign source datasets and derive datasets for better alignment for variable mapping.
- Live SAS Session with ability to view log and output datasets

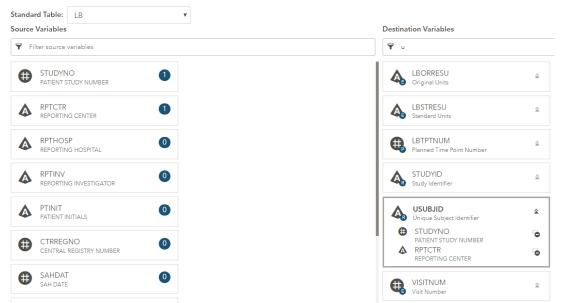






6. Variables –

- Provide ability to map Source variables to Destination Domain variables.
- List all associated data source tables variables per domain
- Mapping count is maintained







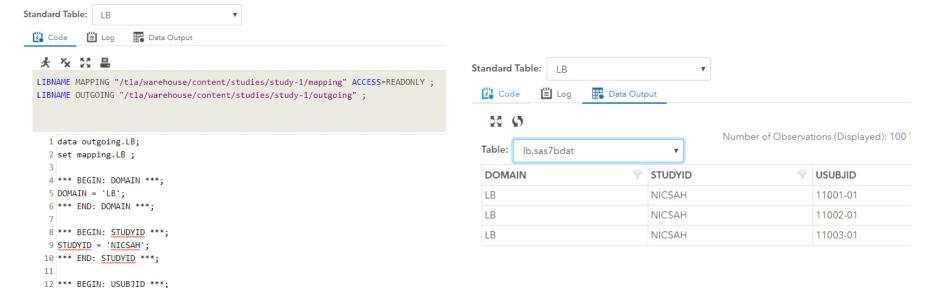
Variables Transform –

13 USUBJID = CATS(STUDYNO,"-", RPTCTR);

14 *** END: USUBJID ***:

15

- Provide ability to add any derivations/macro calls for Domain variables.
- Live SAS Session with ability to view log and final output Domain







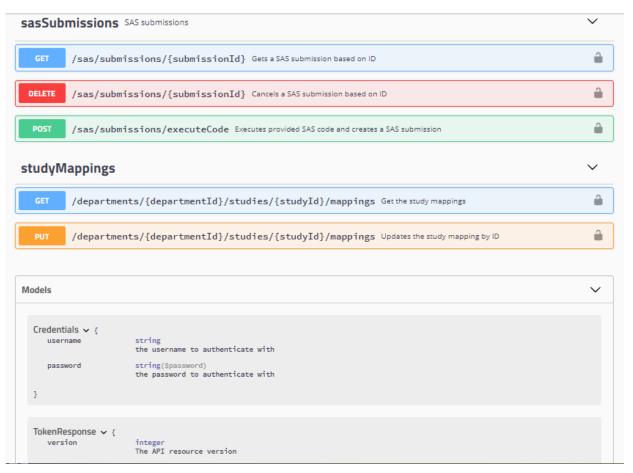
8. Export –

- Ability to export mapped domains.
- Ability to publish mapping to Library





REST APIs



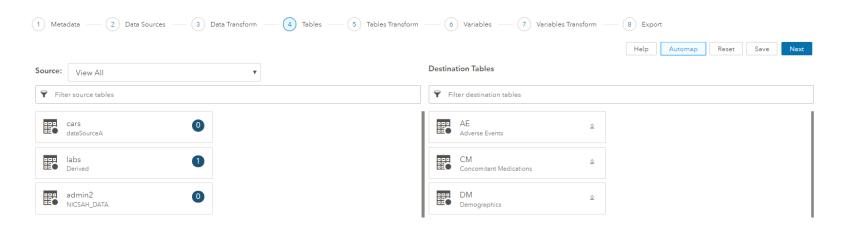


Study Mapping Process (Under Development)



4. Tables AutoMap –

 Provide ability to Automap Source datasets to Destination Domains based on previous mapping information available in published libraries



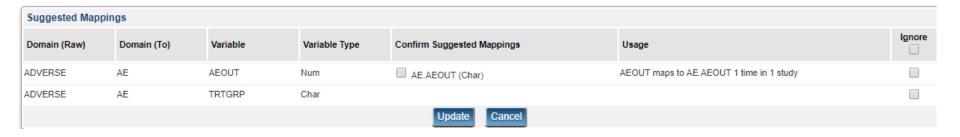


Study Mapping Process (Under Development)



4. Tables AutoMap –

- Smart Mapping function is under development for improvement & enhancement.
- The following screen shot was from previous version of Data Mapper.





Mapping Types

MAPPING TYPE	DESCRIPTION	SOURCE			DESTINATION		
TABLES	1-1 MATCH (Top Similarity Value)	DATASET			DOMAIN		
VARIABLE (AUTOMAP)	1-1 MATCH (Top Similarity Value)	DATASET	VARIABLE		DOMAIN	VARIABLE	
VARIABLE (SMART MAP)	1-3 MATCH (>0.25 Similarity)	DATASET	VARIABLE		DOMAIN	VARIABLE	
CONTROLLED TERMS	1-1 MATCH (Top Similarity Value)	DATASET	VARIABLE	VALUE	CONTROLLED T	ERM	VALUE

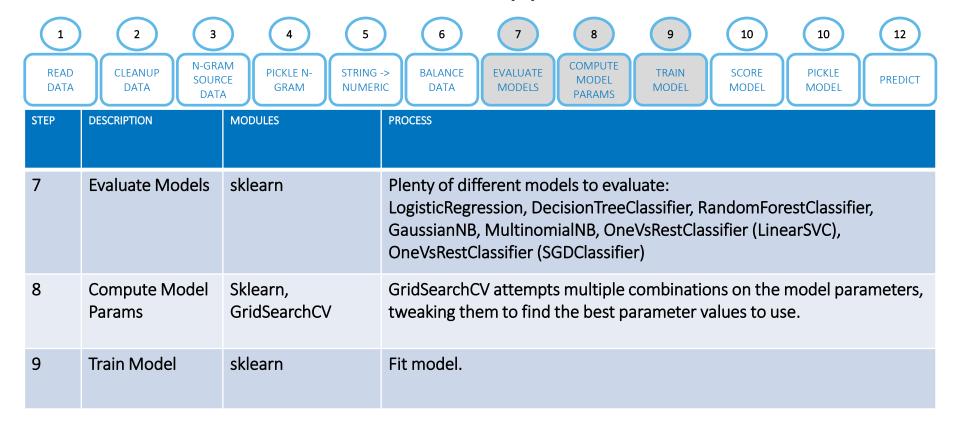


1 READ DATA	CLEANUP DATA ON THE SOUR DATA	CE PICKLE N- STRING GRAM NUMER	II MODEL II PREDICT
STEP	DESCRIPTION	MODULES	PROCESS
1	Read Data	Pandas Dataframe	Read data into Pandas Dataframe – A tabular data structure in Python
2	Cleanup Data	Pandas Dataframe	Drop NaN Records, convert to lower case, combine columns, filter categories based on MIN count.
3	n-gram Data	NGRAM	n-gram data using character n-gram with limit of 2. This gives us more data to work with when comparing similarity in variable names.



READ DATA	CLEANUP DATA N-GRA SOUR DAT	CE PICKLE N- STRING	MODEL NO. 11. PREDICT
STEP	DESCRIPTION	MODULES	PROCESS
4	Pickle n-gram	Pickle	n-gram pair of (Source, Destination) value and pickle it. The pickle file is the python data object after serialization, and is an efficient way to store and use any python object data.
5	String to Numeric Value conversion	TfidfVectorizer, MinMaxScaler	Generate Dictionary with TF-IDF values and re-scale it using MinMaxScaler. For machine learning to work, the values must be numeric between 0 and 1.
6	Balance Data	SMOTETomek	Balance data to handle under-sampling and over-sampling. If the data we have is skewing our results, we want to normalize closer to 0.5.







READ DATA	CLEANUP DATA N-GRA SOUR DATA	CE PICKLE N- STRING -	MODEL
STEP	DESCRIPTION	MODULES	PROCESS
10	Score Model	sklearn.metrics	Classification_report — Precision, Recall, F1 Score. This tells us how much data was relevant to the suggested mappings, and gives a value on how accurate the model thinks the mapping is.
11	Pickle Model	Pickle	Save the trained model in pickle file.
12	Predict	sklearn	Predict based on trained model. With user interaction with the predicted mapping (Supervised Machine Learning), the model will become smarter and more accurate over time.





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