Ready to Optimize KPIs with Xbiom? **CROSS** Use Xbiom's Metadata Technology to Speed up SDTM Cycles!

CONVERT EDC RAW CLINICAL DATA WITH LOW CODE INTO CRITICAL STUDY DECISIONS

Time to Create SDTMs	Fourteen Days Instead of MonthsIntegrated Standard Compliance ChecksHalf the Normal Team SizeThirty percent 				$\begin{array}{c} & & \\$				() ↑	
SDTM Compliance				Data	Data		Data		Data Data	
Number of Programmers to SDTMs				Ingestion System to load various sources	Aggregation Categorize, organize and		Intelligence Standardize raw data structure		Wor Valida conclu	
Study SDTM Expenses			and structures of raw data		index raw data		and values		maked	
POWERFUL VISUAL AND USER FRIENDLY INTERFACE FOR ALL TYPES OF USERS										
Statistical Programming Director		Statis	Statistical Programmer		Translational Scie		entist Stud		dy Statist	
								•		

Statistical Programming Director	Statistical Programmer
Manage Projects with Automation and Standards	Manage Submission Process with Low-Code Programming
	● • • >
 ✓ One SCE integrate tool for all Submission Deliverables ✓ Reduce Time and Budget per Clinical Study 	 ✓ Reduce writing SAS programs and macros ✓ Faster SDTMs, Define.xml and SDRG ✓ Auto Generate SDTM Mapping Specifications

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Monitor Safety Data Issues with Early Alerts



- ✓ Faster Ingestion, Curation and Harmonization
- User Interface to create SAP \checkmark Cohorts

Explore with Pre-defined Templates

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ILL	IJ

- Reduce Time to Tables, Lists \checkmark and Figures
- Drill down from summary to \checkmark patient level detail

Contact Us: ask@pointcross.com



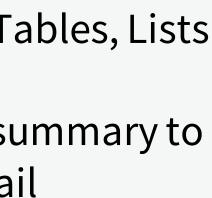


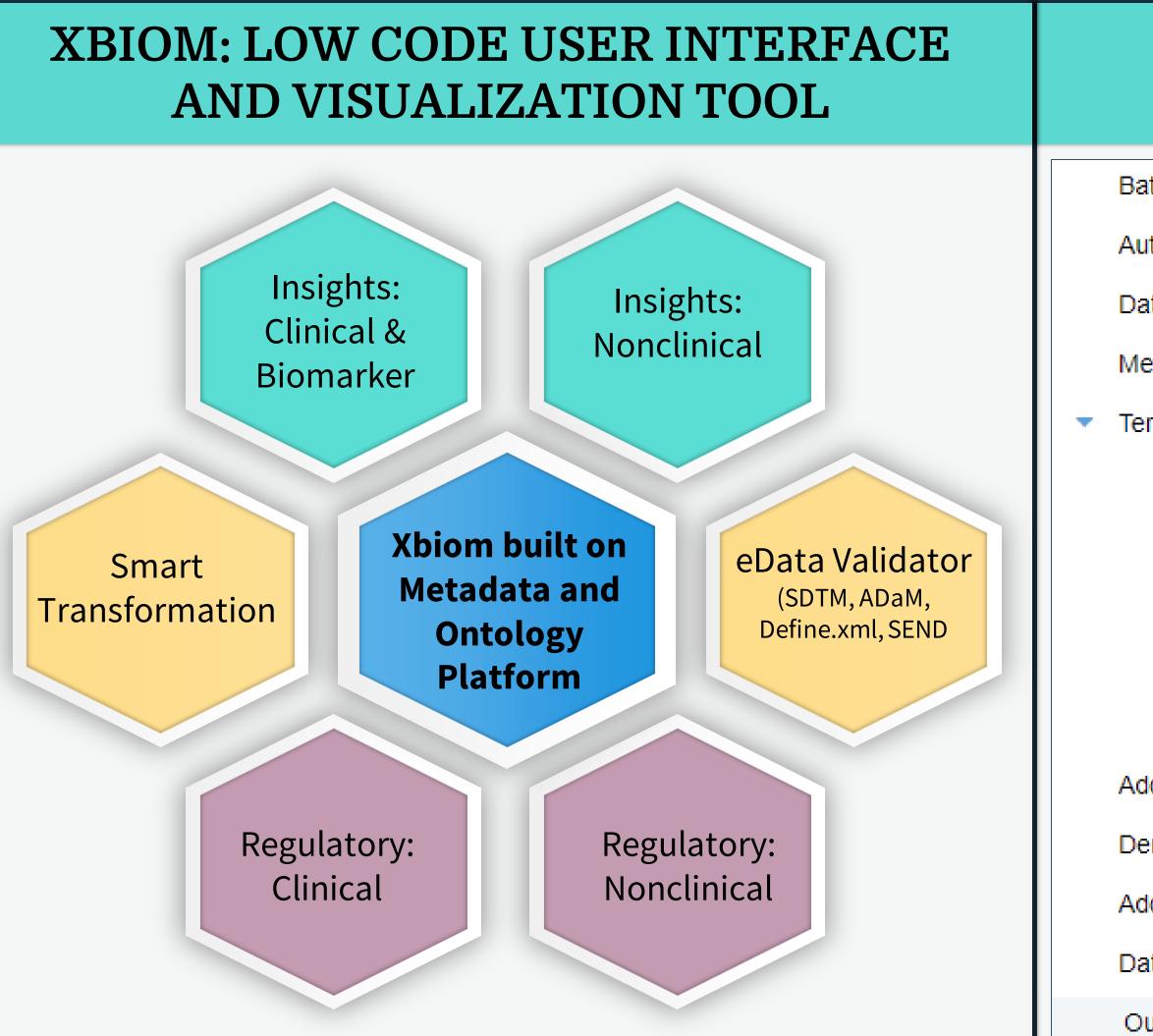
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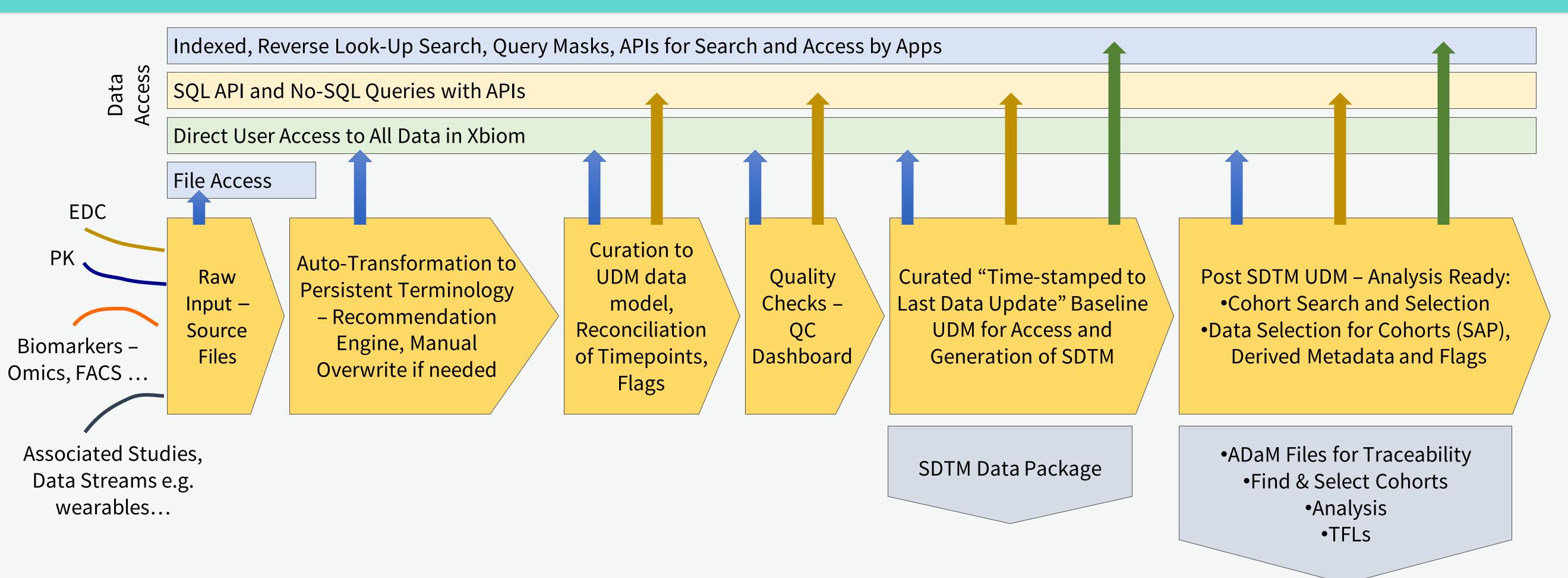








DATA CURATION AND STANDARDIZATION STAGES TO SDTM AND BEYOND



SMART TRANSFORMATION SECTION - APPLIES THE 80/20 PRINCIPLE

	Batch Details	Batch Details: Provide input (source) and output (targ
	Auto Generate	Auto Generate: Used if STUDYID, DOMAIN, SEQ (Sequ automatically generated by system.
	 Metadata Mappings Terminology Normalization Controlled Terminology 	Scripts for any Transformations: 3 sections (Datase Additional Transformations, Additional Scripts) are pr custom scripts in SQL, Python or PySpark languages for for any data derivations or corrections.
	MedDRA NCBI Gene Info UniProt mirBase	Metadata Mappings: Used to map source data struct domains and columns. System recommends mapping sets and users' previous decisions. User can approve o recommended mappings.
	HMDB Additional Transformations Derivations Additional Scripts	Terminology Normalization: Used to map the source terms. External dictionaries like MedDRA, NCBI Gene I mirBase, HMDB also supported. System recommends terms based on Xbiom global CT and loaded external can approve or modify the recommended mappings.
	Data Updates Output	Derivations: to derives the data, if missed to collect in Data Updates: To perform custom data updates.

Leader in SEND Automation Tool for Top Pharma/CROs such as Roche, Sanofi, Bayer and Ipsen.

put (target model and CT) Q (Sequence) values to be

(Dataset Transformations, ts) are provided to write any guages for file processing or

ta structure to target model mappings based on training pprove or modify the

e source terms to target 3I Gene Info, UniProt, nmends mappings to target external dictionaries. User

collect in source systems.

