



# Time to bring it all together

From data transfer to processing to full reporting under ICH M10  
based on the EBF Data Integrity Initiative (LCMS)

Presented at the 13<sup>th</sup> EBF Open Symposium  
E-environment/Data Integrity Workshop

## Data Integrity Workshop

13th EBF Open Symposium

### E-Environment; towards a vendor neutral bi-directional data transfer process

Gidion de Boer, Neil Loftus, Burkhard Schaefer (on behalf of the working group)

### Following the EBF 2019 workshop the White Paper was published in Bioanalysis

White Paper

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Bioanalysis

### Improving data integrity in regulated bioanalysis: proposal for a generic data transfer process for LC–MS from the European Bioanalysis Forum

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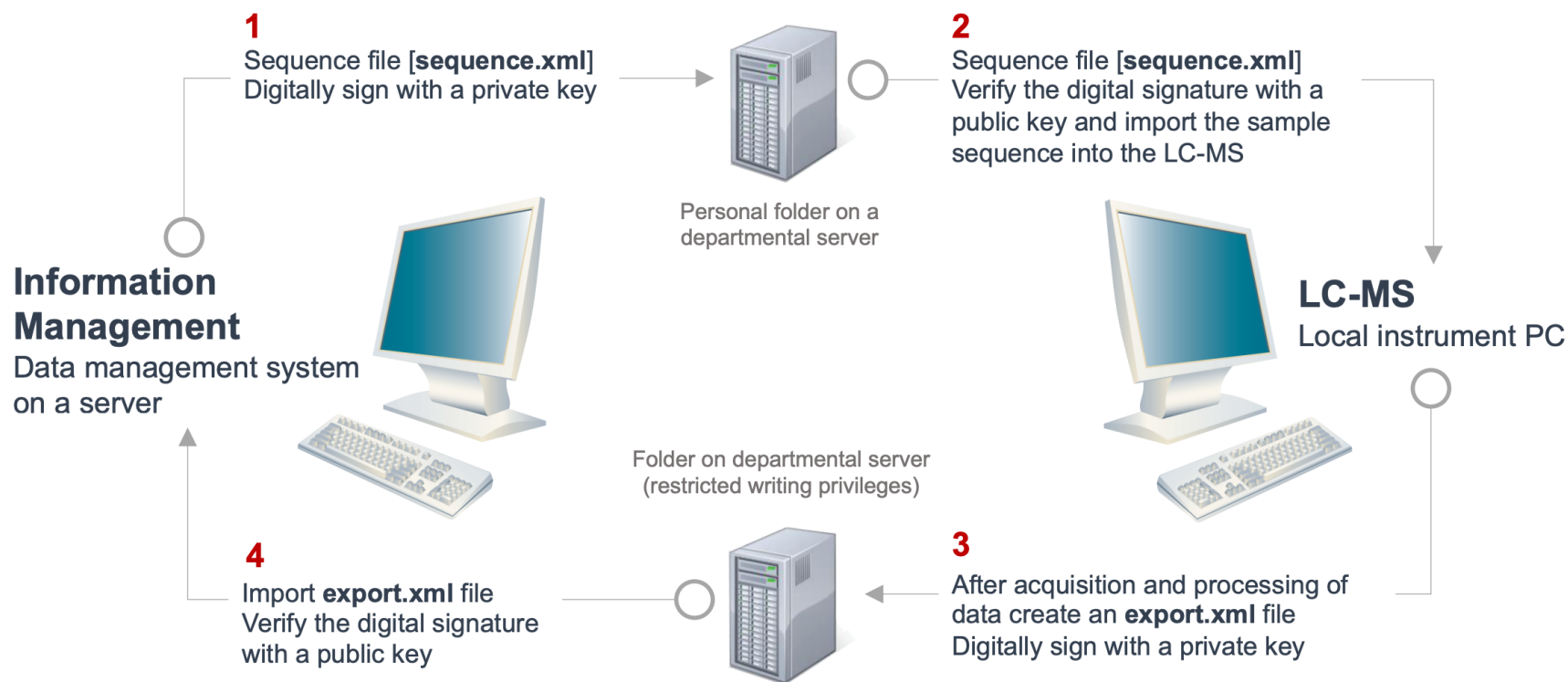
The White Paper was published online 22 July 2020 and highlighted the need to increase compliance related to data integrity (DI) in today's LC-MS workflows (**Bioanalysis (2020) 12(14), 1033–1038**)

# The scope: Data-Integrity for LIMS to/from LCMS workflow

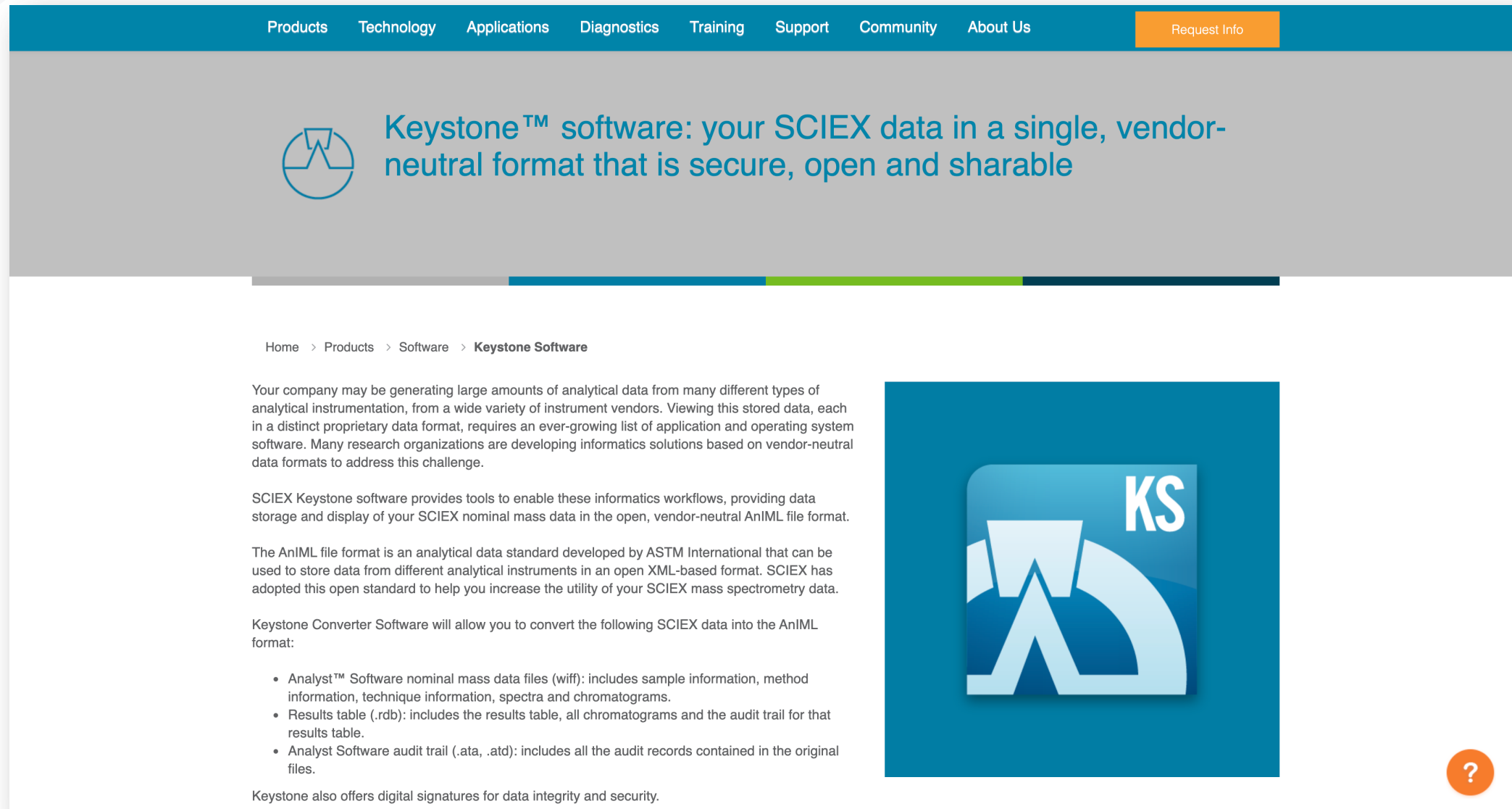
Presented at the 13<sup>th</sup> EBF Open Symposium  
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## A proposed way forward

Replacing .txt files with digitally signed .xml files



# SCIEX: Data format comes to life



The screenshot shows the SCIEX website's product page for Keystone Software. The top navigation bar includes links for Products, Technology, Applications, Diagnostics, Training, Support, Community, and About Us, along with a Request Info button. The main header features the Keystone logo and the text: "Keystone™ software: your SCIEX data in a single, vendor-neutral format that is secure, open and sharable". Below this, a breadcrumb trail reads: Home > Products > Software > Keystone Software. The page content describes the challenges of managing analytical data from various vendors and introduces the AnIML file format as a solution. It lists the types of data that can be converted to AnIML: Analyst™ Software nominal mass data files (.wiff), Results table (.rdb), and Analyst Software audit trail (.ata, .atd). A large image of the Keystone Software icon (a stylized 'KS' with a mountain peak) is shown on the right. A small orange circle with a question mark is visible in the bottom right corner of the page.

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Keystone™ software: your SCIEX data in a single, vendor-neutral format that is secure, open and sharable

Home > Products > Software > Keystone Software

Your company may be generating large amounts of analytical data from many different types of analytical instrumentation, from a wide variety of instrument vendors. Viewing this stored data, each in a distinct proprietary data format, requires an ever-growing list of application and operating system software. Many research organizations are developing informatics solutions based on vendor-neutral data formats to address this challenge.

SCIEX Keystone software provides tools to enable these informatics workflows, providing data storage and display of your SCIEX nominal mass data in the open, vendor-neutral AnIML file format.

The AnIML file format is an analytical data standard developed by ASTM International that can be used to store data from different analytical instruments in an open XML-based format. SCIEX has adopted this open standard to help you increase the utility of your SCIEX mass spectrometry data.

Keystone Converter Software will allow you to convert the following SCIEX data into the AnIML format:

- Analyst™ Software nominal mass data files (.wiff): includes sample information, method information, technique information, spectra and chromatograms.
- Results table (.rdb): includes the results table, all chromatograms and the audit trail for that results table.
- Analyst Software audit trail (.ata, .atd): includes all the audit records contained in the original files.

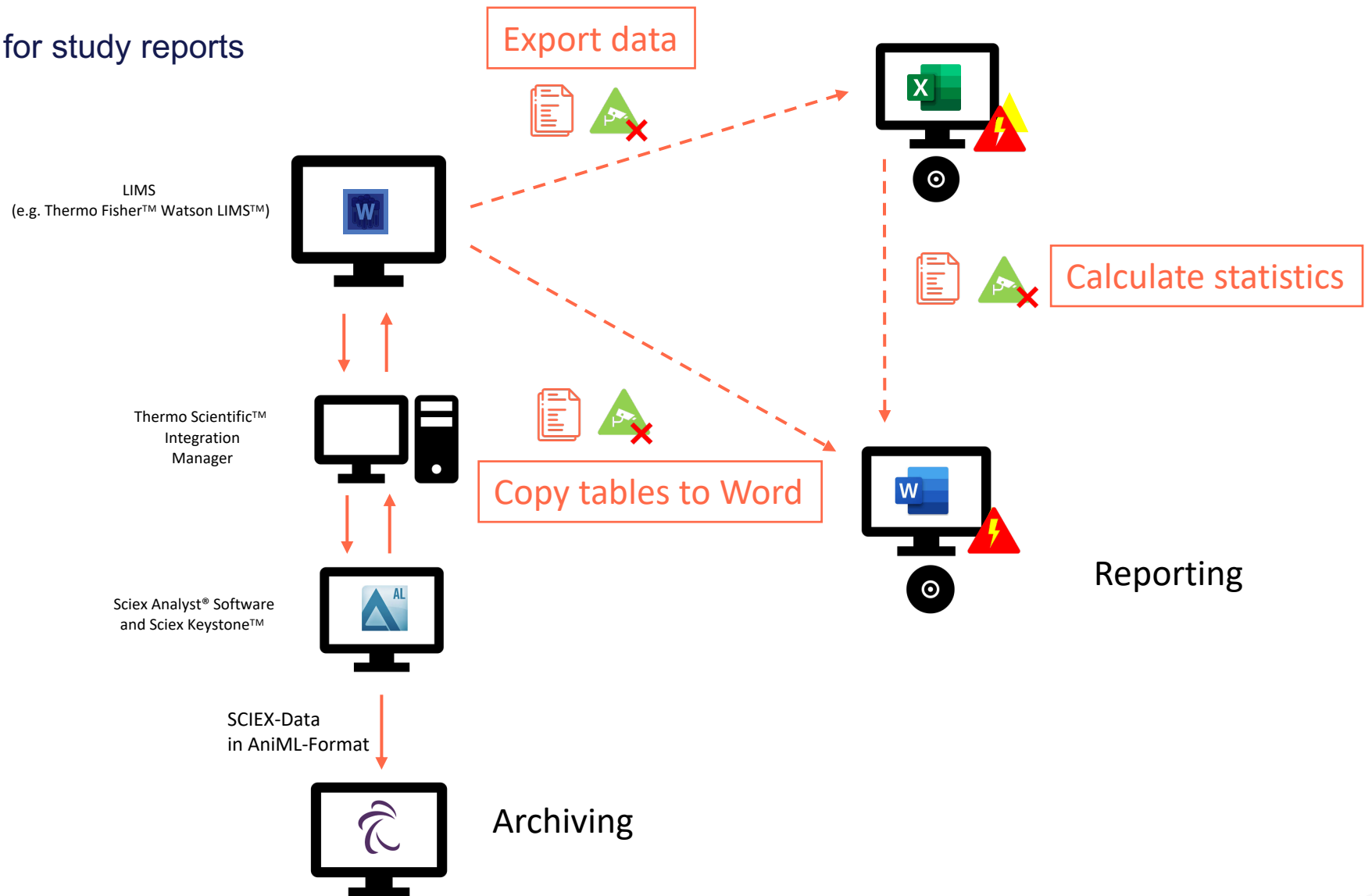
Keystone also offers digital signatures for data integrity and security.

KS

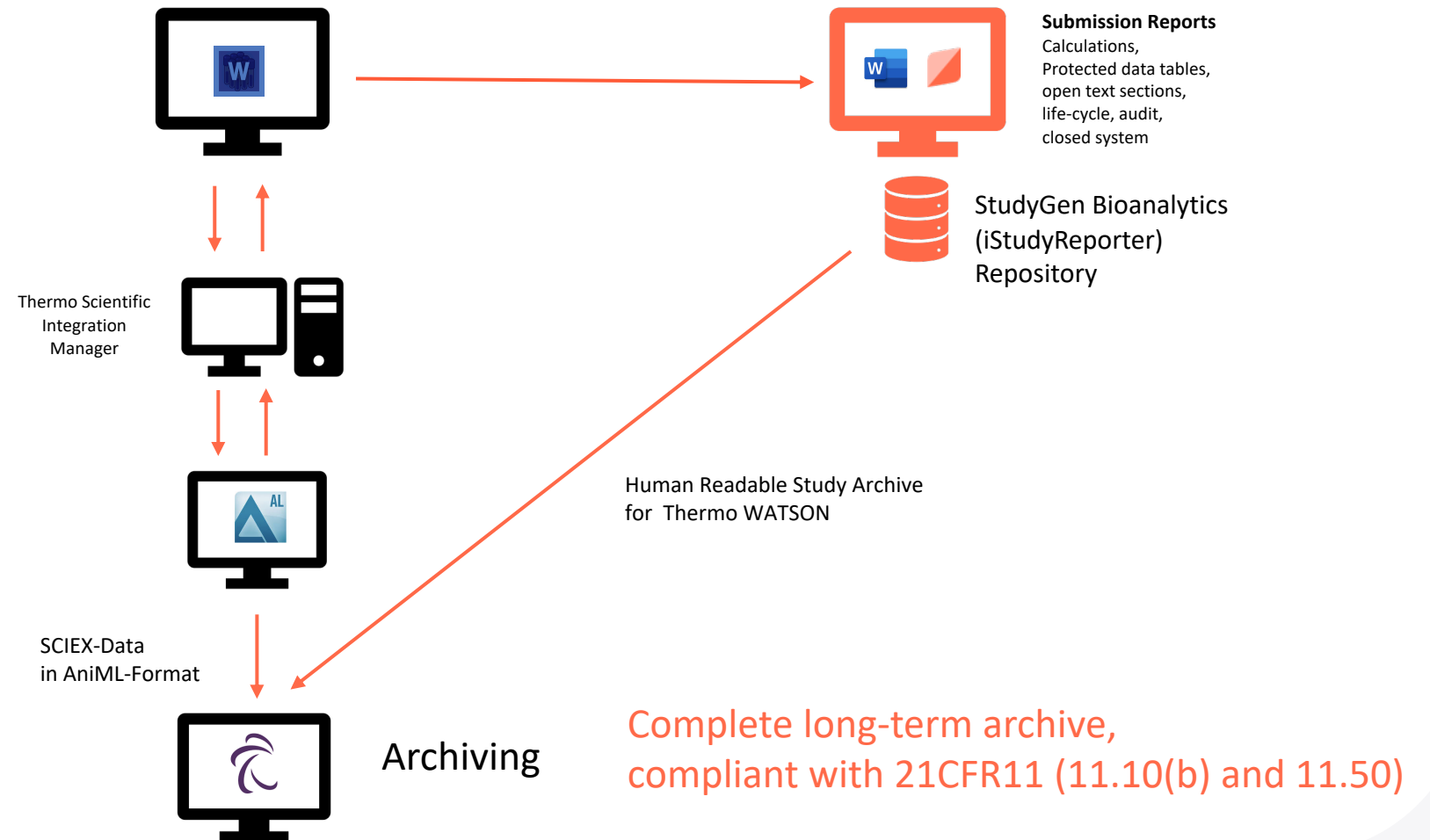
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# Reporting – still an open DI-issue in a LIMS scenario

## ■ Data-Integrity issues for study reports

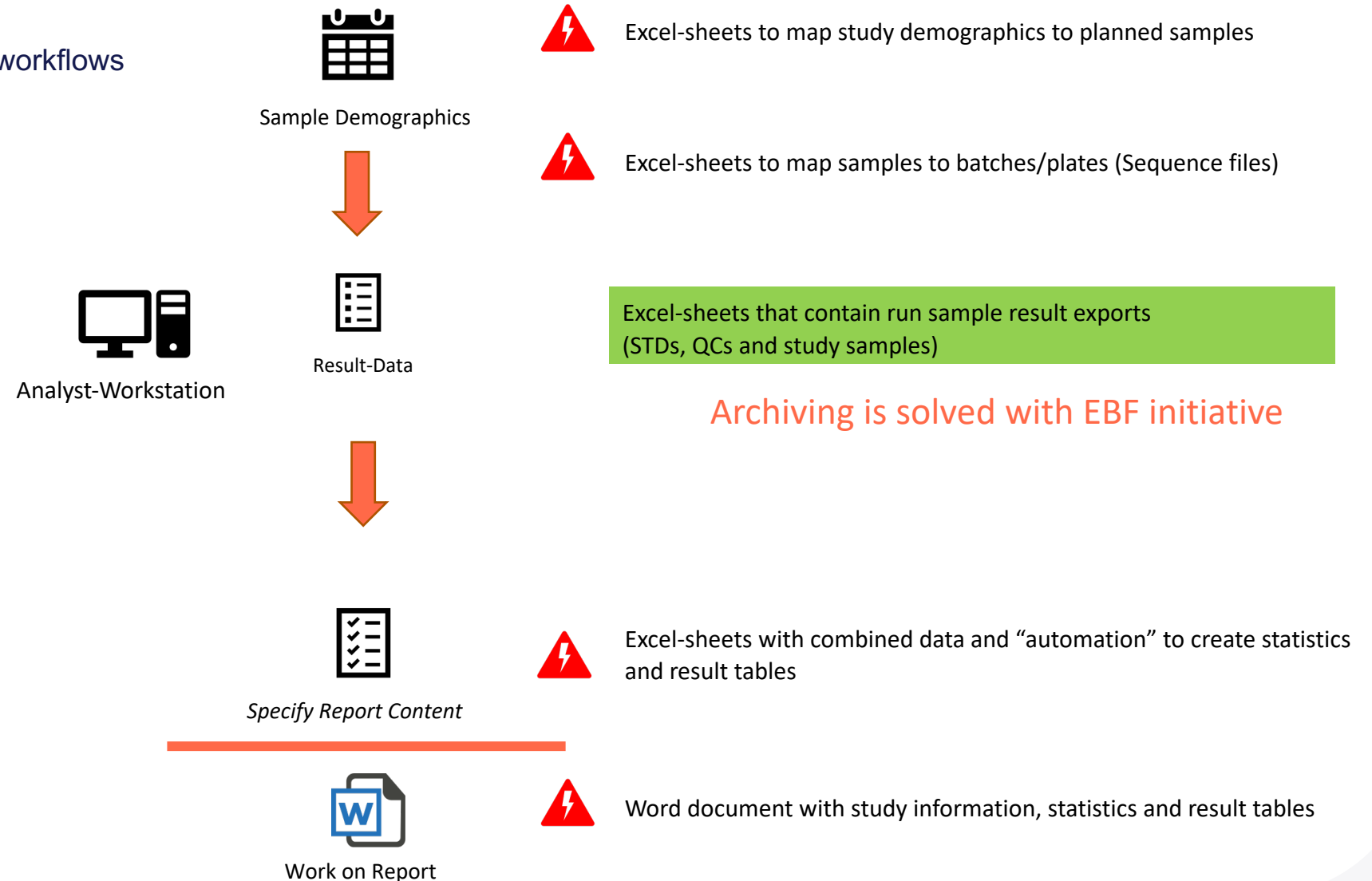


- Data-Integrity issues for study reports, solved e.g. with StudyGen (former iStudyReporter)



# Data Integrity issues in a none-LIMS scenario

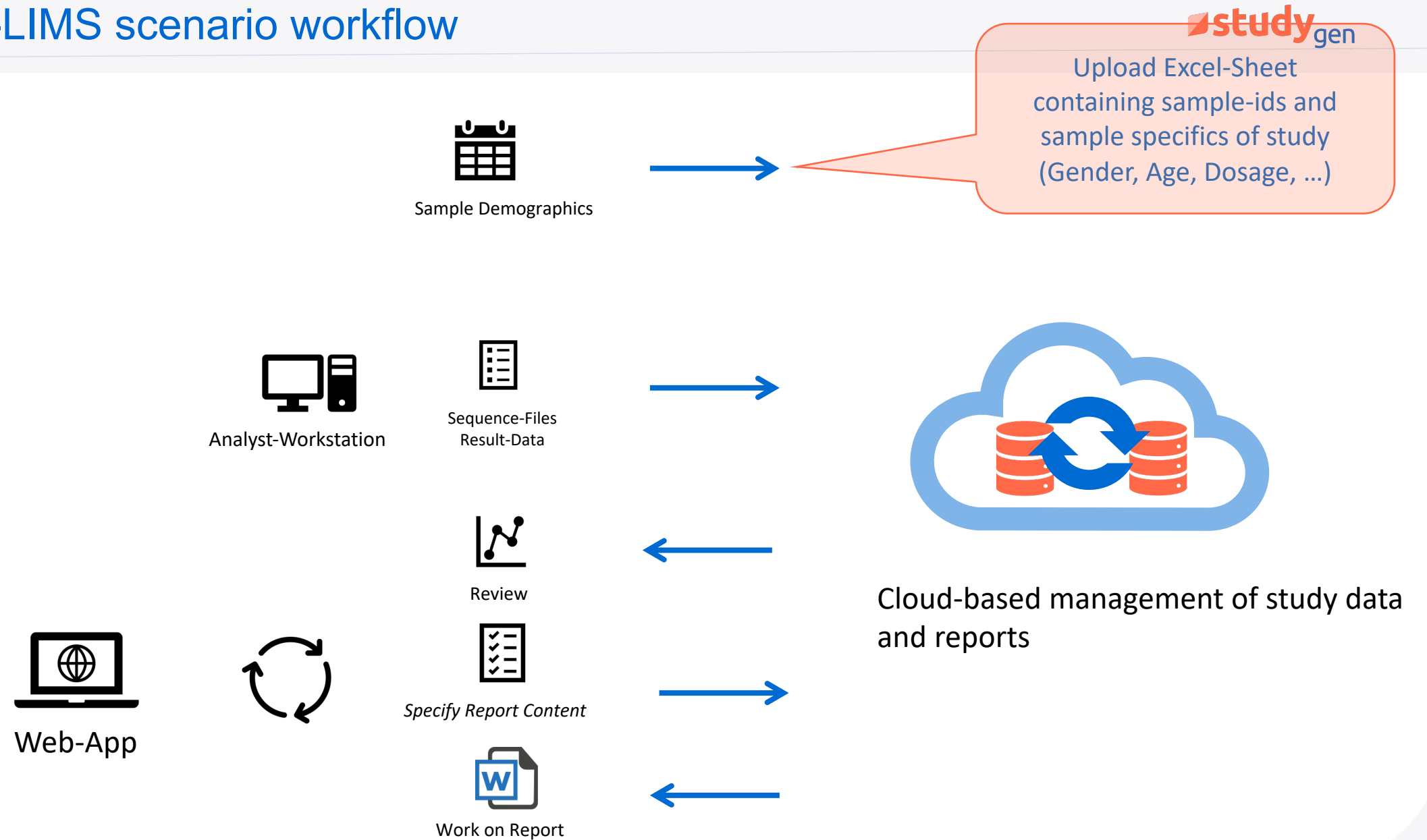
- Current state:
  - Word/Excel dominated workflows



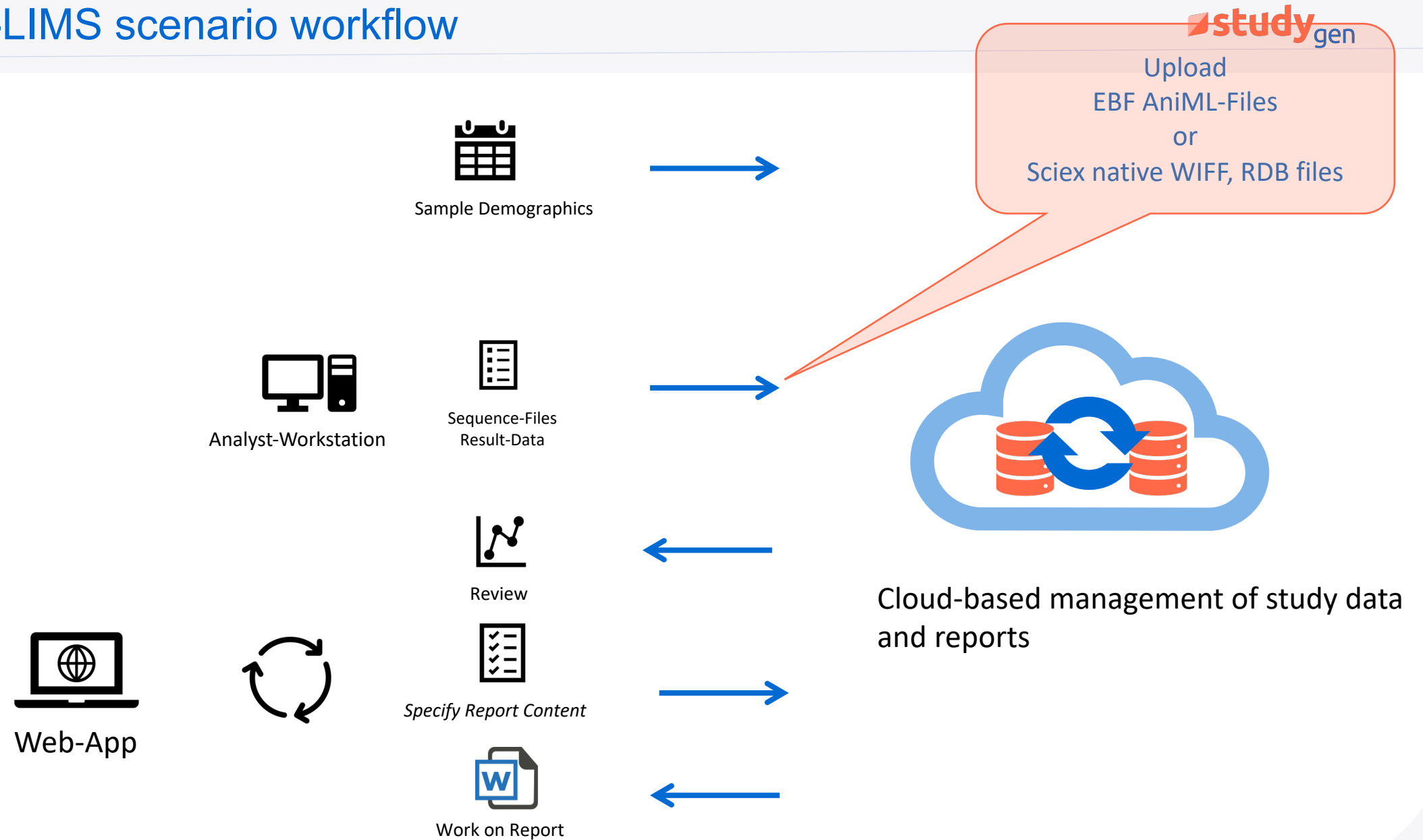
- Based on up to data application prototype
- Joint project of Idorsia (Susan Globig) and up to data initiated mid-2021
- Goals:
  - Introduce data integrity measures in a none-LIMS scenario
  - Introduce and support standardized workflows
  - Allow to instantly generate submission-ready bioanalytical reports without further QC measures
  - Incorporate ICH M10 requirements for reporting as they will come available
  - Provide a GLP compliant application
- Approach:
  - Take advantage of the features of the commercially available SCIEX data converter
  - Leverage and extend functionality of existing application
  - Use state-of-the-art cloud technology
  - Evaluate approaches for private and public cloud deployment
- Expectation:
  - Reduce the time and effort required to manually perform quality control of LCMS data
  - Reduce the time to create, review and submit bioanalytical reports



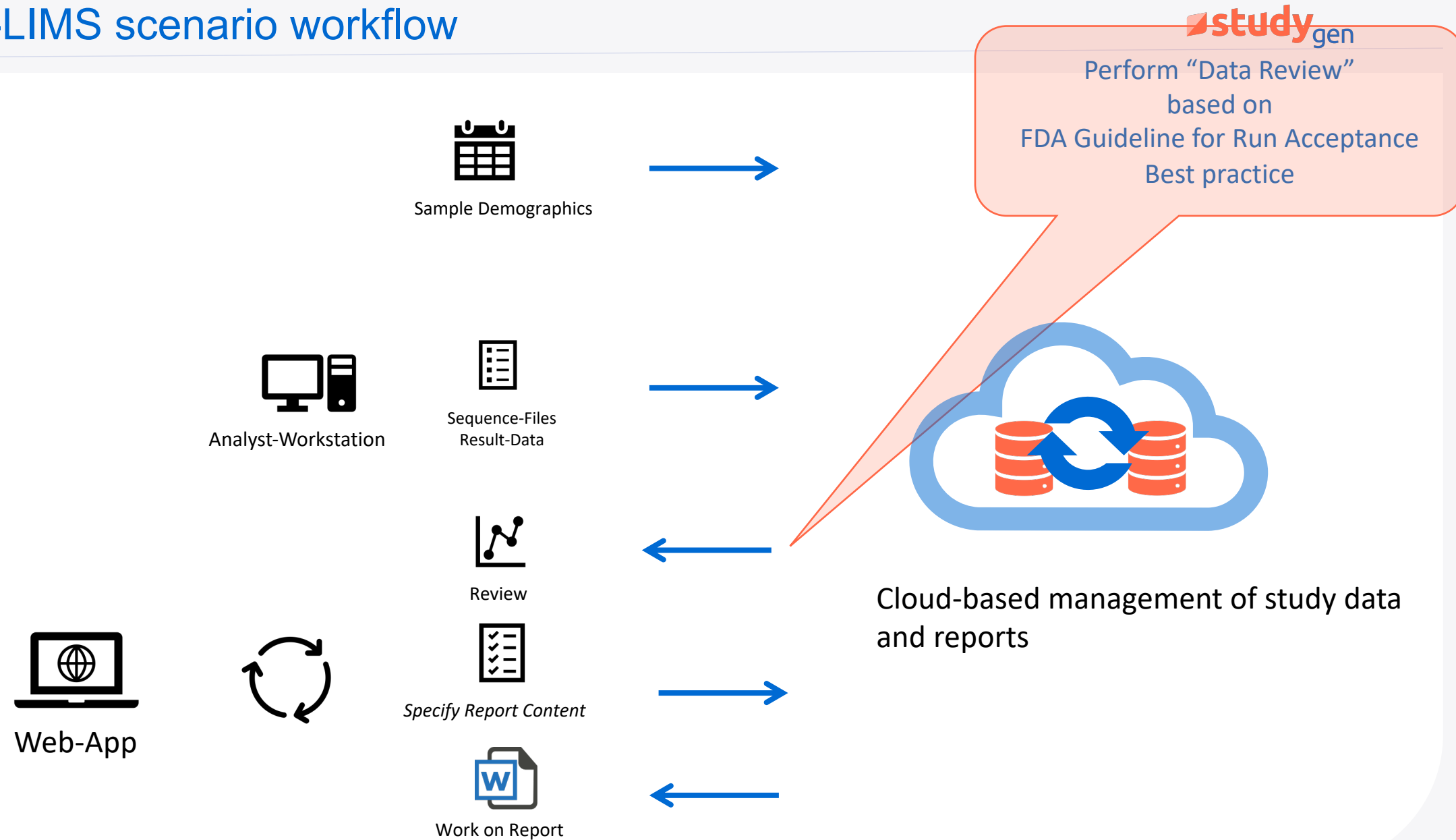
# None-LIMS scenario workflow



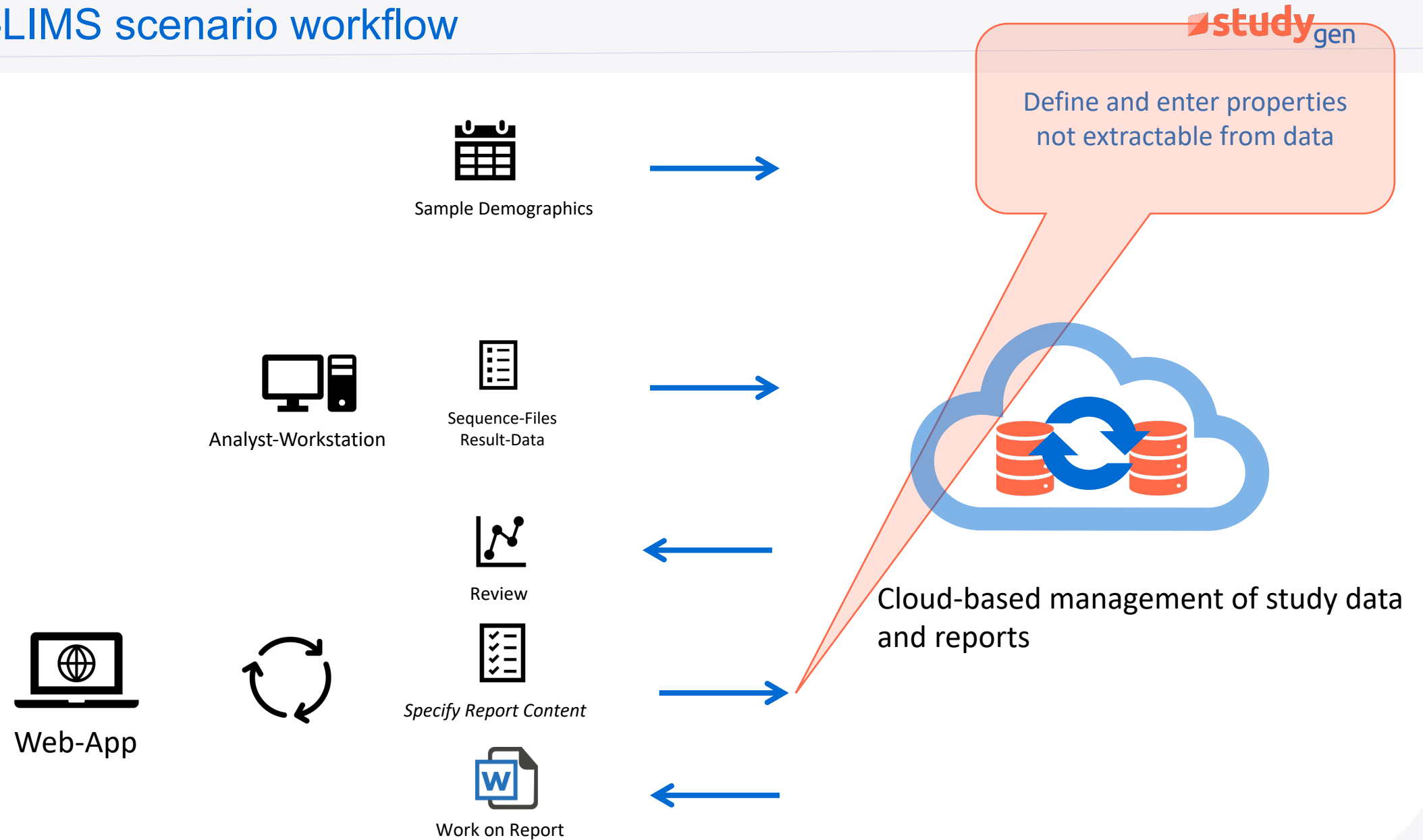
# None-LIMS scenario workflow



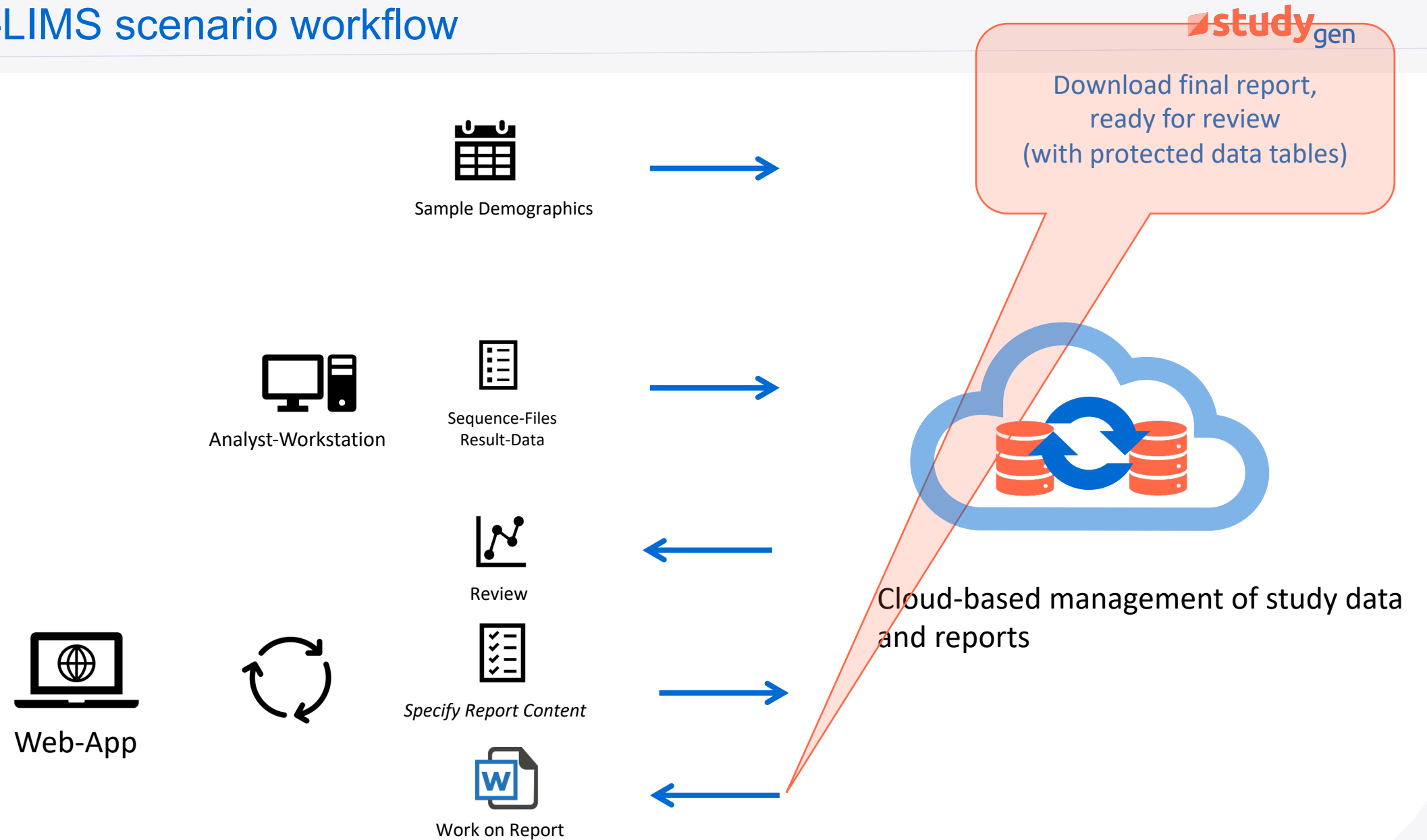
# None-LIMS scenario workflow



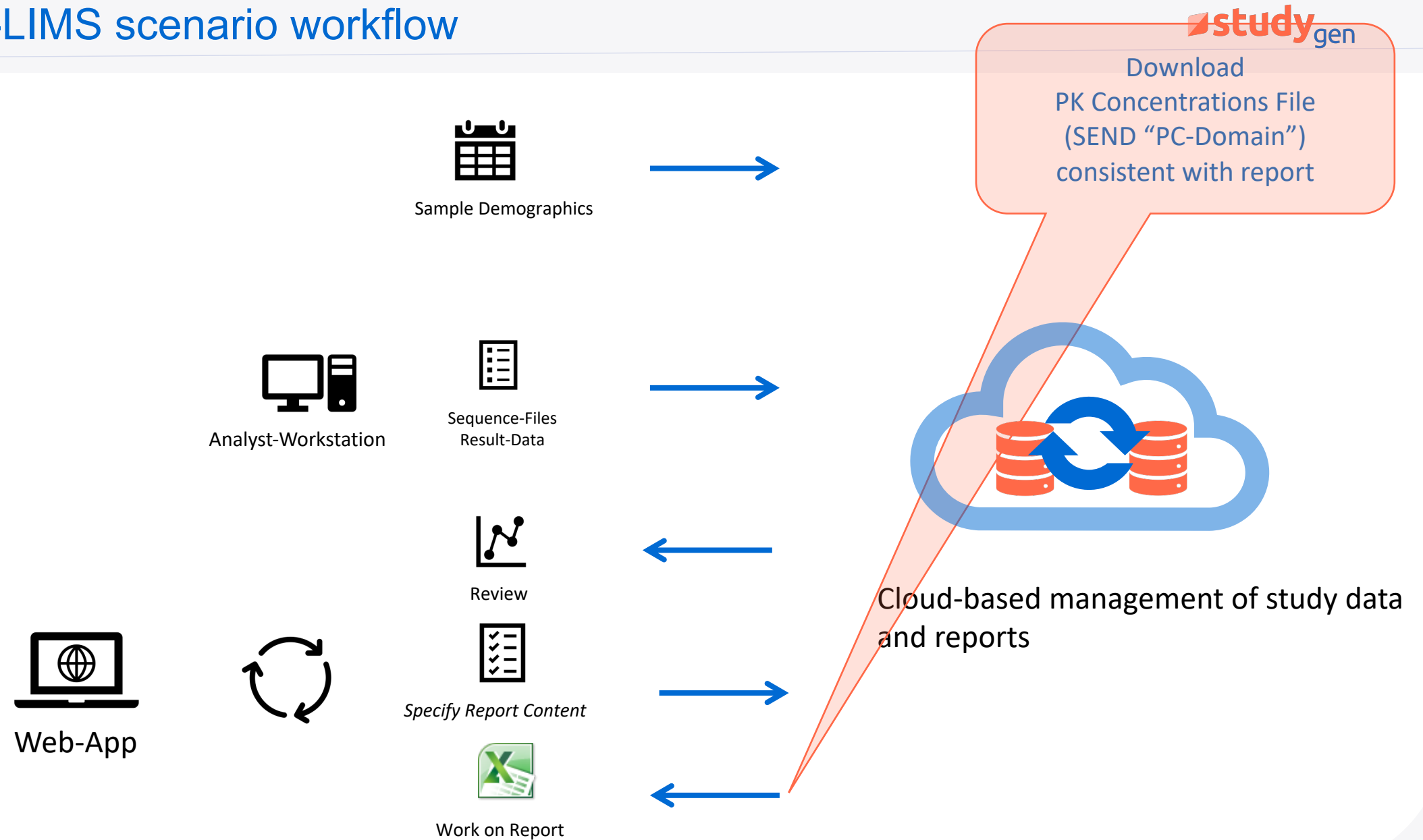
# None-LIMS scenario workflow



# None-LIMS scenario workflow



# None-LIMS scenario workflow



# Technological and workflow challenges

- Technological challenges
  - Selection of technology for efficient implementation
    - Rejected container approach
    - Serverless architecture
  - Transfer/Migration of existing software modules and algorithms
    - No one-to-one migration of current solution
    - Modularization and migration to serverless architecture
  - Initial feasibility study by up to data in 2021, to leverage future proof technologies

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and



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Investition in unsere Zukunft  
Europäischer Fonds  
für regionale Entwicklung

- Open workflow challenges
  - Setup of specific workflows to support
    - Re-assay decisions
    - Incurred sample reanalysis

# Regulatory Challenges

- Build „compliant“ bioanalytical reports
  - Best practice based on reports of existing clients
  - Take available guidelines into account
    - FDA
      - Bioanalytical Method Validation, Guidance for Industry (May 2018)
      - Bioanalytical Methods Template, Guidance for Industry, Tech. Specifications Document (Sep 2019)
    - EMA
      - Guideline on bioanalytical method validation (Feb 2012)
    - ICH (draft)
      - Bioanalytical Method Validation M10 (draft, Feb 2019)
      - .... expected to change
  - Enable configuration of templates
- Interpret applicable GxP regulations in a serverless architecture
  - e.g. how to interpret “Installation Qualification” or “multi tenant”
- Implications of “Software as a Service” (SaaS) for a regulated laboratory
  - e.g. how to define “control of data” or validate application updates
  - What does “disaster recovery” mean in an “AWS Availability Zone”



# Where are we now?

- Prototype is implemented
  - AWS-based, serverless architecture
- Initial Report templates are setup
  - IS-Analysis based on raw data
  - Bioanalytical Study Report
- Development of regulatory framework supported by
  - Bob McDowall
  - Practical experience of Idorsia („Cloud-first approach“, see <https://aws.amazon.com/solutions/case-studies/idorsia-case-study/>)

StudyGen

Selected Study Demo Study

Home

norbert.bittner@intolifescience.com

▼ Samples

▼ Data

▼ Reports

Drag a column head

File Name

Q

▶ Sample Report

▶ BA-17.053\_Bat

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▶ ISTD-Report

Create Filter

Summary Sample Report

Table \_table\_number\_ Summary of

Information	Data
Analyte	
Matrix	Matrix
Anticoagulant K2 EDTA	Anticoagulant K2 EDTA
Detector	
Extraction Technique Solid Phase Extraction	Extraction Technique
Sample Volume	
Calibration Curve Concentration Range	1.00 to 800 ng/mL
Quality Control (QC) Samples Concentrations	2.00 / 50.0 / 800 / 10
Regression Type	Weighted Linear(1/cc
Quantitation Method	Peak Area Ratio
Calibration Standards	Bias range -6.6 to 6.1 CV range 1.5 to 6.6 %
Quality Control Samples	Bias range to -10.6 to CV range to 1.7 to 6.

Add Samples

Add Files

Generate Report

## Internal Standard Report

Analyte

30 % Mean IS	14312
170 % Mean IS	81099

### Calibration Standards

Sequence#	Sample Name	IS Response	Result
2	Cal1	48900	ok
3	Cal2	48700	ok
4	Cal3	47200	ok
5	Cal4	49500	ok
6	Cal5	49700	ok
7	Cal6	49200	ok
8	Cal7	32500	ok
9	Cal8	46900	ok

### Quality Controls

Sequence#	Sample Name	IS Response	Result
12	QCL_1	49200	ok
22	QCM_1	53400	ok
32	QCH_1	45900	ok
46	QCL_2	49800	ok
56	QCM_2	45600	ok
66	QCH_2	50700	ok
80	QCL_3	52100	ok
90	QCM_3	49100	ok
100	QCH_3	42200	ok
114	QCL_4	49300	ok
124	QCM_4	43500	ok
127	QCH_4	50700	ok

### Subjects

Sequence#	Sample Name	IS Response	Result
13	BA-17.053_109	41000	ok
14	BA-17.053_110	33600	ok
15	BA-17.053_111	53800	ok
16	BA-17.053_112	51500	ok
17	BA-17.053_113	74400	ok
18	BA-17.053_114	46900	ok
19	BA-17.053_115	48000	ok
20	BA-17.053_116	47400	ok
21	BA-17.053_117	44500	ok

Sequence#	Sample Name	IS Response	Result
23	BA-17.053_118	49400	ok
24	BA-17.053_119	47200	ok
25	BA-17.053_120	50100	ok
26	BA-17.053_121	39700	ok
27	BA-17.053_122	47300	ok

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**Table 3** Equations describing the calibration curves of [REDACTED]

batch	range	weighting factor	equation	r <sup>2</sup>
1	500 - 200000 ng/mL	1/x <sup>2</sup>	y = 0.00013 x + 0.00246	1.00
2	500 - 200000 ng/mL	1/x <sup>2</sup>	y = 0.000132 x + -0.00448	0.999
3	1.00 - 1000 ng/mL	1/x <sup>2</sup>	y = 0.00886 x + 0.00106	0.996
4	1.00 - 1000 ng/mL	1/x <sup>2</sup>	y = 0.00859 x + -0.000483	0.999
5	1.00 - 1000 ng/mL	1/x <sup>2</sup>	y = 0.0106 x + 0.00313	0.998

**Table 4** Summary of [REDACTED] calibration samples in Mouse plasma in the 500-200000 ng/mL range

Batch	500 ng/mL		1000 ng/mL		5000 ng/mL		20400 ng/mL		50000 ng/mL		100000 ng/mL		160000 ng/mL		200000 ng/mL	
	Conc	%RD	Conc	%RD	Conc	%RD	Conc	%RD	Conc	%RD	Conc	%RD	Conc	%RD	Conc	%RD
1	493	-1.4	1030	3.0	4990	-0.2	20400	2.0	49300	-1.4	102000	2.0	156000	-2.5	197000	-1.5
2	478	-4.4	1100	10.0	4840	-3.2	18900	-5.5	51000	2.0	98400	-1.6	165000	3.1	201000	0.5
N	2		2		2		2		2		2		2		2	
Mean	486		1070		4920		19700		50200		100000		161000		199000	
SD																
%CV																
%RD																

**Table 5** Summary of [REDACTED] calibration samples in Mouse plasma in the 1.00-1000 ng/mL range

Batch	1.00 ng/mL		2.00 ng/mL		5.00 ng/mL		25.0 ng/mL		100 ng/mL		400 ng/mL		800 ng/mL		1000 ng/mL	
	Conc	%RD	Conc	%RD	Conc	%RD	Conc	%RD	Conc	%RD	Conc	%RD	Conc	%RD	Conc	%RD
5	1.02	2.0	1.83	-8.5	5.42	8.4	26.4	5.6	102	2.0	397	-0.8	760	-5.0	955	-4.5
4	0.961	-3.9	2.15	7.5	*6.04	*20.8	26.0	4.0	99.5	-0.5	398	-0.5	786	-1.8	952	-4.8
3	0.965	-3.5	2.02	1.0	5.66	13.2	27.2	8.8	98.5	-1.5	367	-8.3	804	0.5	895	-10.5
N	3		3		2		3		3		3		3		3	
Mean	0.982		2.00		5.54		26.5		100		387		783		934	
SD	0.0269		0.131				0.499		1.47		14.4		18.1		27.6	
%CV	2.7		6.6				1.9		1.5		3.7		2.3		3.0	
%RD	-1.8		0.0				6.1		0.0		-3.2		-2.1		-6.6	

**Table 6** Summary of [REDACTED] QC samples in Mouse plasma in the 2.00-800 ng/mL range

Batch	Rep	2.00 ng/mL		50.0 ng/mL		800 ng/mL	
		Conc	%RD	Conc	%RD	Conc	%RD
5	1	1.89	-5.5	49.4	-1.2	788	-1.5
	2	1.70	-15.0	46.2	-7.6	778	-2.8
	3	*1.66	*-17.0	47.9	-4.2	741	-7.4
N	2			3		3	
Mean		1.80		47.8		769	
SD				1.6		24.8	
%CV				3.3		3.2	
%RD				-4.3		-3.9	
4	1	2.02	1.0	49.8	-0.4	770	-3.8
	2	1.88	-6.0	48.3	-3.4	796	-0.5
	3	1.99	-0.5	54.1	8.2	775	-3.1

## Coming up next

- Develop deployment strategy for “private and public” cloud that meets GLP requirements
- Test phase with other use-cases (Immunogenicity, Biomarker, ...) and testers (Pharma, CROs) planned for Q1/2022
- Go-live of Idorsia planned for Q2/2022

# Summary

- EBF initiative solves DI issues in data transfer from/to LCMS and other devices
  - Focus on LIMS
  - Long-Term archiving in vendor neutral format
- Challenge remains for none-LIMS scenario
  - Data processing is major issue here, otherwise solved with LIMS
  - EBF initiative builds a foundation to bring it all together
    - Leverage “secure” raw data files
    - Build cloud-based technology
    - Provide upcoming regulatory framework
    - Leverage available guidelines on content of reports for this environment (ICH M10)

# Acknowledgements

## ■ Acknowledgements

- Idorsia
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  - Lars Schröder
  - Henry Springer
- into Life Science
  - Jay Cheruvelil
  - Shehroze Malik
  - Usman Chaudhary

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