Advancements in Data Review for Therapeutic Protein Glycosylation Monitoring with Deep Query Powered Dashboards

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Overview:

- Dashboards provide a comprehensive view of the glycosylation data, enabling users to easily observe trends.
- Designed for web access, allowing for seamless sharing among users.
- Automatically updated with new data to ensure the information remains current.
- Users can set up alarms to notify them if values fall outside the expected range.

Introduction

N-linked glycosylation is potentially the most prevalent and unquestionably among the most intricate post-translational modifications of proteins. As a critical quality attribute, its assessment and monitoring are essential. This requires comprehensive analyses across various molecular dimensions, namely intact protein, peptide analyses, and released glycan assays. Such analyses play a pivotal role in characterizing and quantifying glycosylation levels in therapeutic proteins. However, synthesizing the results of these analyses introduces complexity, as data are typically processed in isolation through disparate workflows, resulting in findings that are often confined to separate reports. Consolidating these diverse sets of data is imperative to obtain a holistic understanding of glycosylation for the examined proteins. The integration of data across these various analytical frameworks can enhance the accuracy and reliability of glycosylation assessment, ultimately contributing to the optimization of therapeutic protein development and quality assurance. This cohesive approach is vital for achieving comprehensive insights into protein glycosylation.
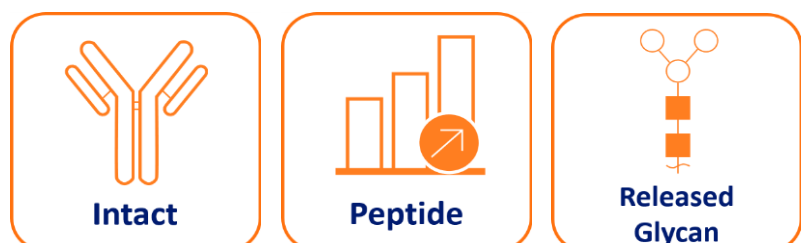
- Data is processed through workflows tailored to specific analyses.
- Information is presented in dynamic reports.
- All processed data is securely stored in a database.
- Data can be queried by filtering through metadata, allowing results from multiple analysis projects to be visualized in dashboards.
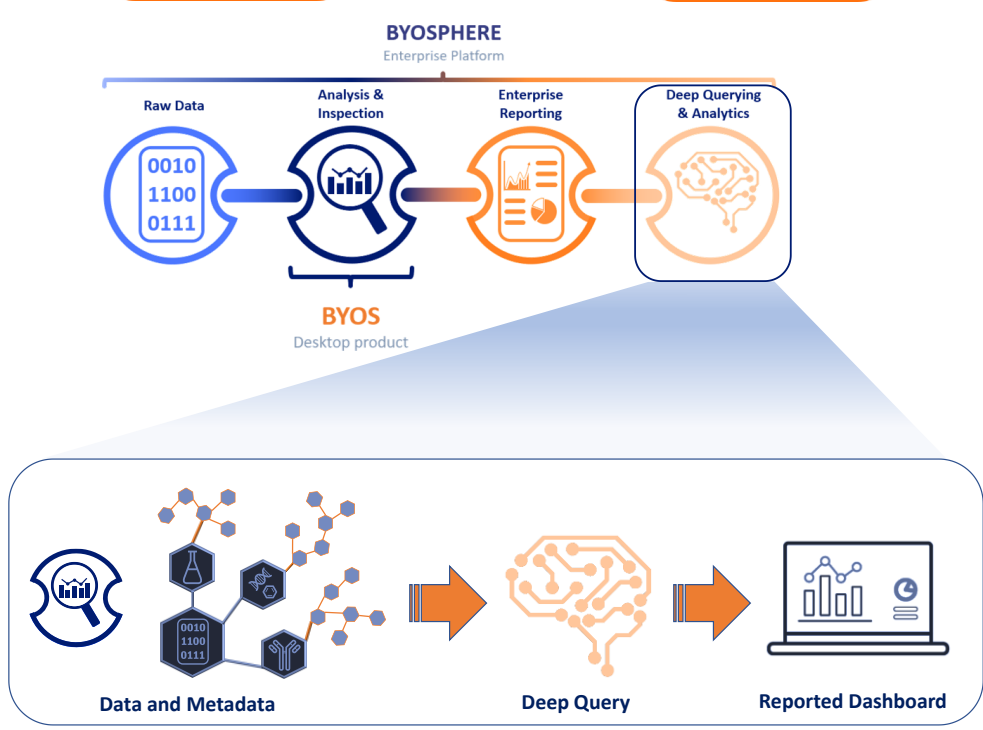
Glycosylation Dashboard Insights

Stacked Bar Chart - Glycan Distribution (Glycopeptide Analysis)
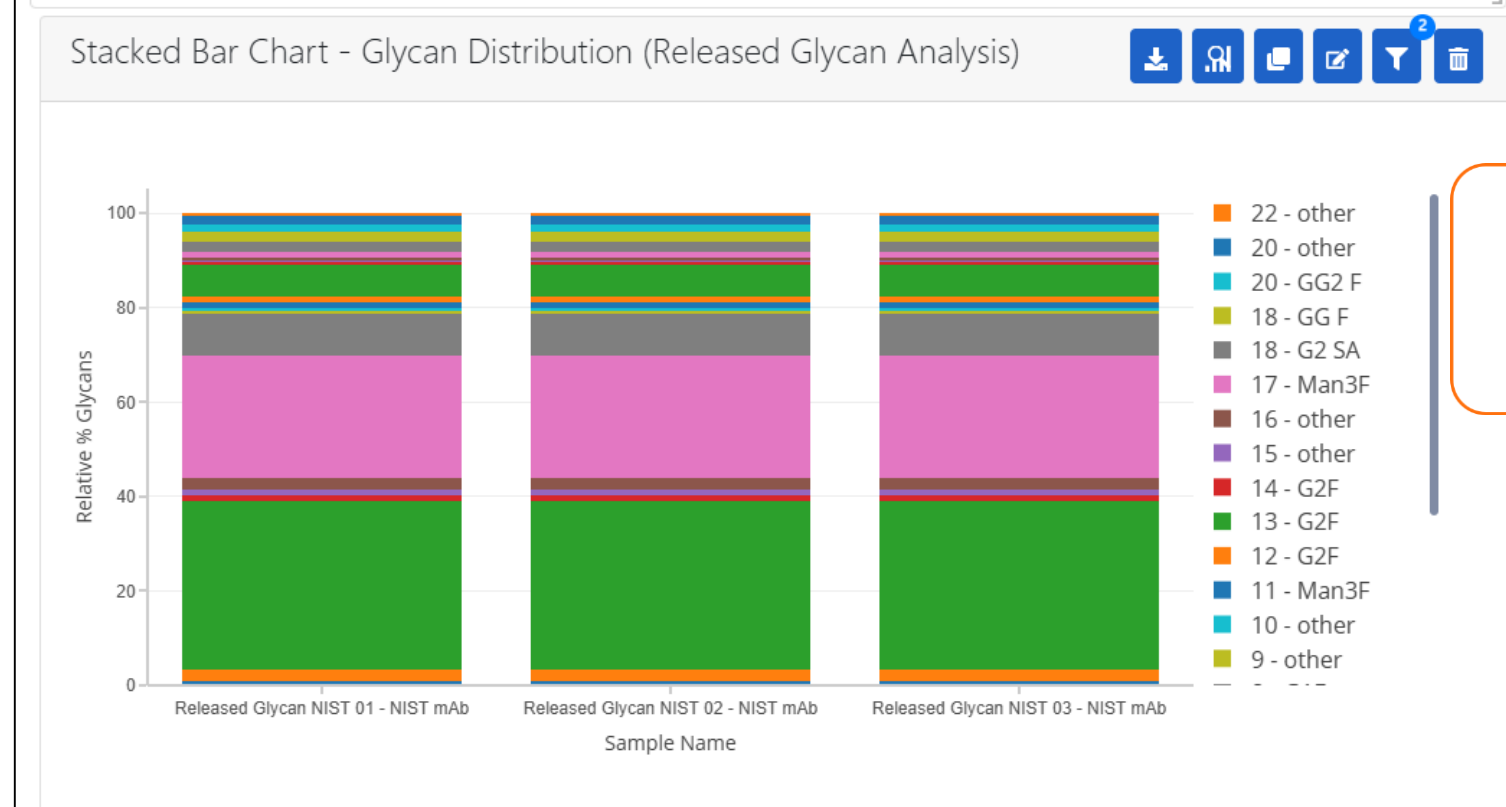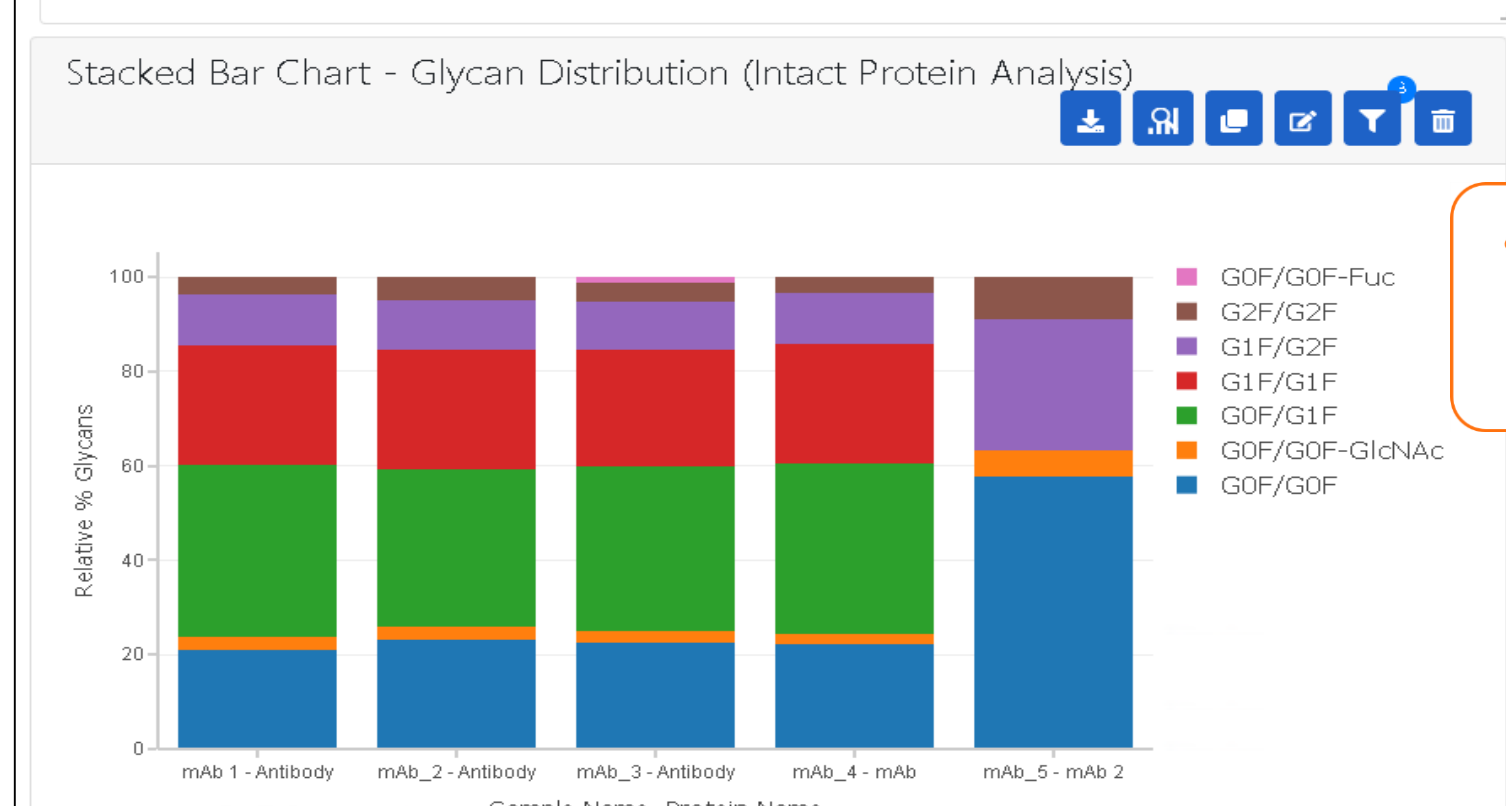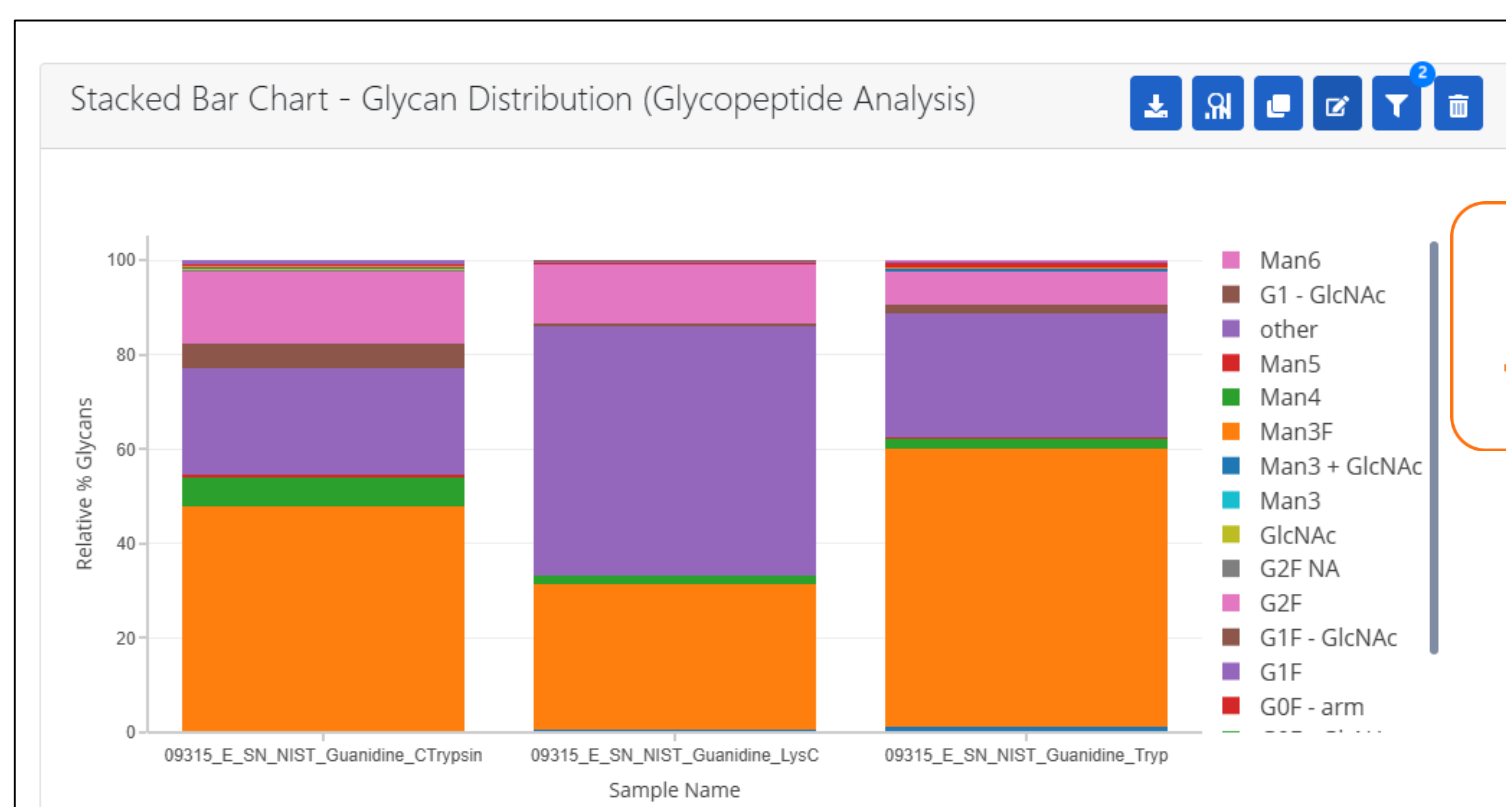
Folder	File Name	Sample Name
PTM	001.btgc	09315_E_SN_NIST_Guanidine_Tryp
PTM	002.btgc	09315_E_SN_NIST_Guanidine_LysC
PTM	003.btgc	09315_E_SN_NIST_Guanidine_CTrypsin

Data.Protein Accession Name	Glycan Short Name	09315_E_SN_NIST_Guanidine_CTryp sin	09315_E_SN_NIST_Guanidine_L ysC	09315_E_SN_NIS T_Guanidine_Tr yp
NIST HC	AGly	0.2	0.5	1.1
NIST HC	G0F	47.7	31.0	59.0
NIST HC	G0F - GlcNAc	6.4	1.7	2.4
NIST HC	G0F - arm	0.5		0.0
NIST HC	G1 - GlcNAc		0.0	0.1
NIST HC	G1F	22.5	52.7	26.1
NIST HC	G1F - GlcNAc	5.2	0.7	2.1
NIST HC	G2F	15.2	12.5	7.0
NIST HC	G2F NA	0.5		
NIST HC	GlcNAc	0.1		0.0
NIST HC	Man3	0.1		0.1
NIST HC	Man3 + GlcNAc	0.2	0.1	0.5
NIST HC	Man3F	0.4		0.3
NIST HC	Man4	0.0		
NIST HC	Man5	0.3	0.5	0.9
NIST HC	Man6			0.0
NIST HC	other	0.7	0.2	0.3

Stacked Bar Chart - Glycan Distribution (Intact Protein Analysis)

Search: 5 records...

Folder	File Name	Sample Name
Intact	Intact_001.ntms	mAb 1
Intact	Intact_002.ntms	mAb_2
Intact	Intact_003.ntms	mAb_3
Intact	Intact_004.ntms	mAb_4
Intact	Intact_005.ntms	mAb_5

Data.Delta Mass Name	mAb 1	mAb_2	mAb_3	mAb_4	mAb_5
G0F/G0F	21.1	23.3	22.5	22.1	57.7
G0F/G0F-Fuc			1.3		
G0F/G0F-GlcNAc	2.5	2.6	2.6	2.4	5.6
G0F/G1F	36.5	33.3	34.7	35.9	
G1F/G1F	25.3	25.5	24.9	25.4	
G1F/G2F	10.8	10.5	10.1	10.7	27.8
G2F/G2F	3.8	4.9	3.9	3.5	9.0

Stacked Bar Chart - Glycan Distribution (Released Glycan Analysis)

Search: 3 records...

Folder	File Name	Sample Name
SH DB Projects	Released Glycan NIST 01.bmap	NIST mAb
SH DB Projects	Released Glycan NIST 02.bmap	NIST mAb
SH DB Projects	Released Glycan NIST 03.bmap	NIST mAb

Data.Peak #	Released Glycan Short Name	Released Glycan NIST 01	Released Glycan NIST 02	Released Glycan NIST 03
2	G0 - GlcNAc	0.8	0.8	0.8
3	G0F - GlcNAc	2.6	2.6	2.6
4	G0F	35.7	35.7	35.7
5	G1F - GlcNAc	1.2	1.2	1.2
5	Man5	1.2	1.2	1.2
6	G1F - GlcNAc	2.6	2.6	2.6
7	G1F	25.8	25.8	25.8
8	G1F	9.1	9.1	9.1
11	Man3F	1.1	1.1	1.1
12	G2F	1.2	1.2	1.2
13	G2F	6.8	6.8	6.8
14	G2F	0.5	0.5	0.5
17	Man3F	1.2	1.2	1.2
18	G2 SA	2.1	2.1	2.1
18	GG F	2.1	2.1	2.1
20	GG2 F	1.7	1.7	1.7
20	other	1.7	1.7	1.7

Dynamic Dashboards
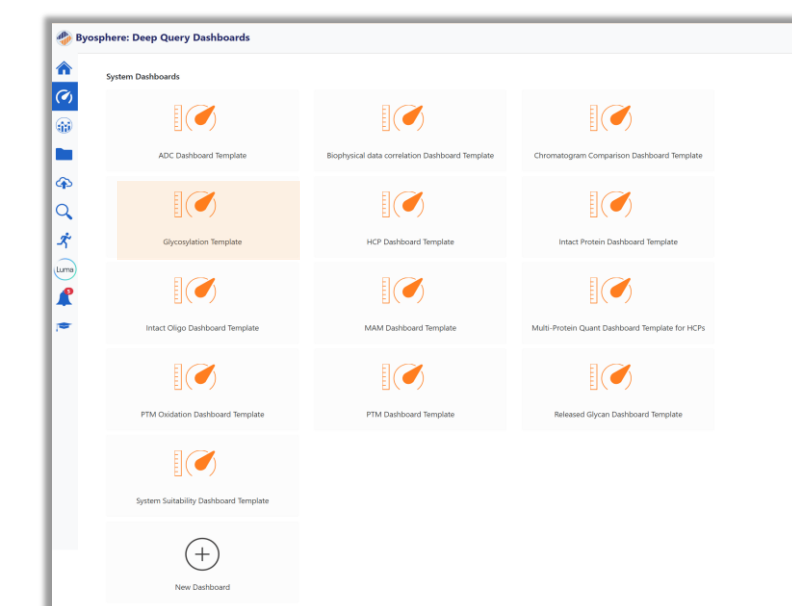
- Dashboard Templates provide a user with an option to use prebuilt visualization
- Querying commonly queried data
- Necessary calculations already included
- User can change in Global Filter what data is queried to show results for their own data
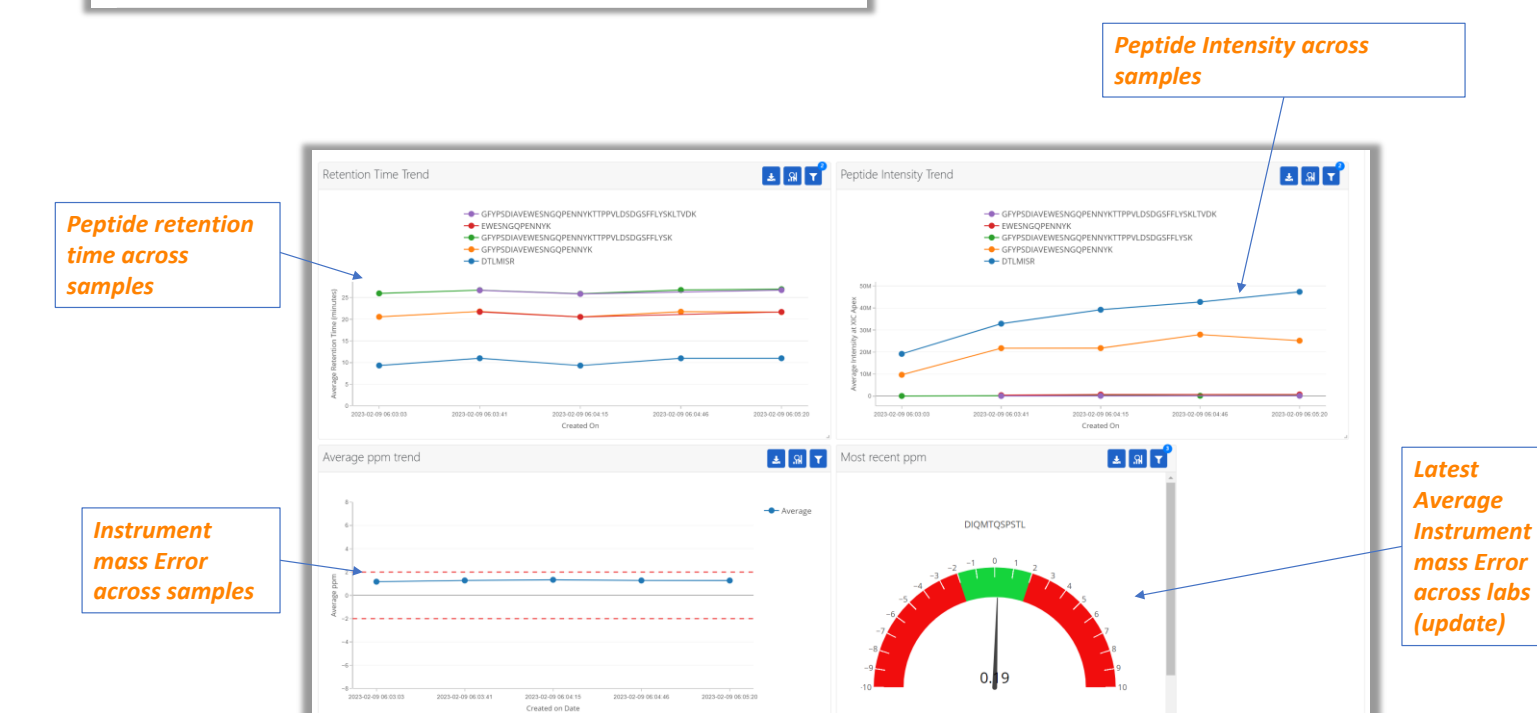
- Example System suitability template
- Monitoring specific attributes
- Observing trends
  - Visual tools to allow monitoring of system performance, and instantly see outliers

Boston/Characterization/AntiXRX/JSmith_PHRM123_NR-Intact
Location/Assay/Project/Analyst_Molecule_workflow
Boston/Characterization/AntiXRX/JSmith_PHRM123_NR-Intact

In the realm of data analysis, metadata plays a pivotal role as it is essentially data about the data. By utilizing metadata, users can effectively identify and precisely pinpoint specific data for queries within deep query powered dashboards.

Summary

- Protein Metrics' Byosphere software platform provides automated dashboards that empower users to conduct inquiries across multiple projects utilizing metadata for precise data selection.
- This innovative approach allows the outcomes of these data queries to be visualized through charts and tables available within the Byosphere web client.
- Here we showcased a comprehensive dashboard that captures results from all three levels of glycan analysis—intact, peptide, and released glycan.
- This tool is designed to facilitate instant access to complex and actionable data for any user within an organization, thereby enhancing the ability to make informed decisions efficiently.

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