

Glycoinformatics Consortium (GLIC) seminar series

Special topic: Glycan Arrays



02/06/2023	René Ranzinger and Akul Mehta	Introduction into glycan arrays
02/13/2023	Yukie Akune	CarbArrayART for glycan microarray data storage, presentation and reporting
02/27/2023	Akul Mehta	Using GLAD for exploratory glycan microarray data analysis and visualization
03/06/2023	Zachary Klamer	Using CarboGrove to Guide Experimental Design and Data Interpretation
03/20/2023	René Ranzinger	The Glycan Array Data Repository
03/27/2023	Jon Lundstrøm	LectinOracle@glycowork: Lectin binding predictions & glycan sequence analysis in Python



More information and registration: <https://glic.glycoinfo.org/seminar/>

GLIC Seminar Series – Glycan Arrays

Using GLAD for Exploratory
Glycan Microarray Data Analysis
and Visualization

Akul Mehta

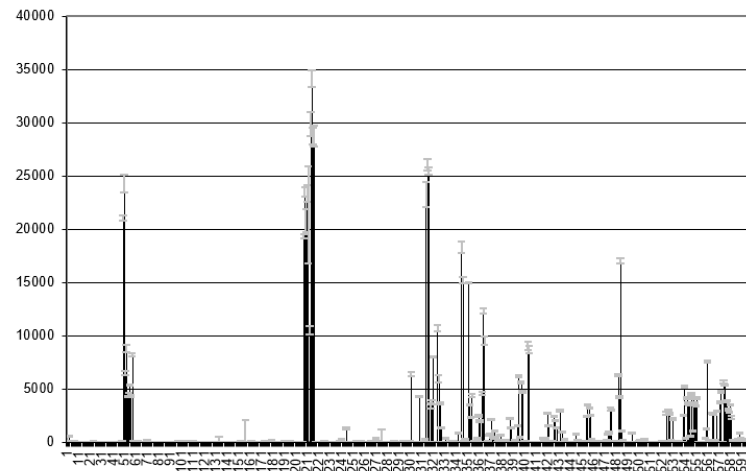
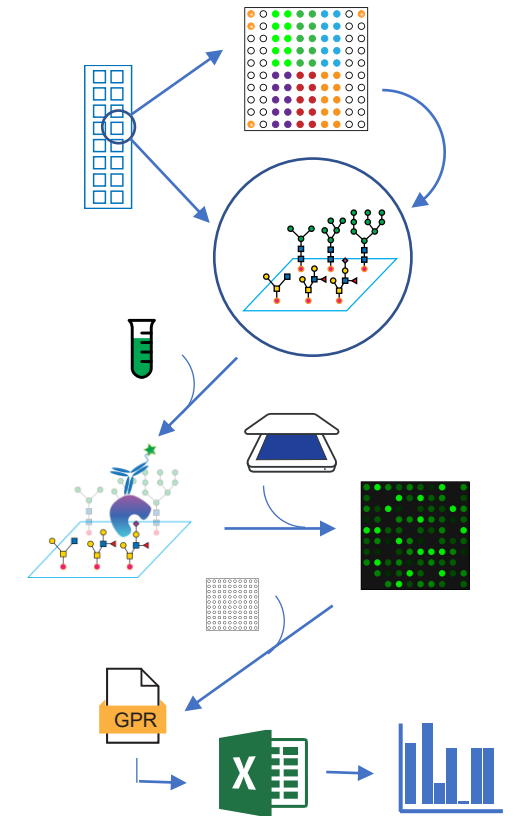
February 27, 2023

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Background

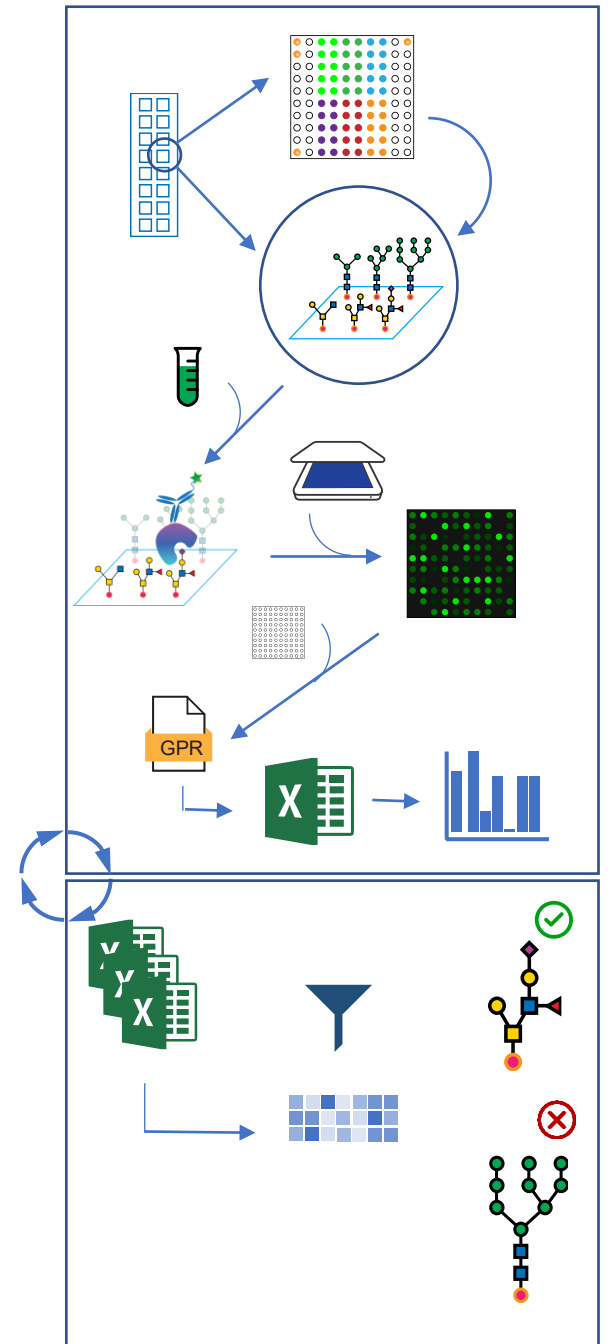
- Glycan array data is usually processed using Excel or other statistical software to produce individual data files.
- Issue:
 - Difficult to visualize structures.
 - Difficult to compare data from multiple experiments.
 - Filtering and sorting functionality is limited.

Chart Number	Structure on Masterlist	Average RFU	StDev	% CV
1	Gala-Sp8	15	6	38
2	Glca-Sp8	64	35	55
3	Mana-Sp8	583	66	11
4	GalNAca-Sp8	9	15	162
5	GalNAca-Sp15	34	22	65
6	Fuca-Sp8	21	20	97
7	Fuca-Sp9	38	27	70
8	Rhaa-Sp8	15	18	119
9	Neu5Aca-Sp8	13	9	73
10	Neu5Aca-Sp11	1	11	878
11	Neu5Acb-Sp8	6	9	145
12	Galb-Sp8	33	13	40
13	Glc-Sp8	7	5	67
14	Manb-Sp8	18	18	102
15	GalNAcb-Sp8	20	11	54
16	GlcNAcb-Sp0	16	7	41
17	GlcNAcb-Sp8	12	22	180
18	GlcN(Gc)b-Sp8	9	19	207
19	Galb1-4GlcNAcb1-6(Galb1-4GlcNAcb1-3)GalNAca-Sp8	21	9	45
20	Galb1-4GlcNAcb1-6(Galb1-4GlcNAcb1-3)GalNAc-Sp14	5	7	123

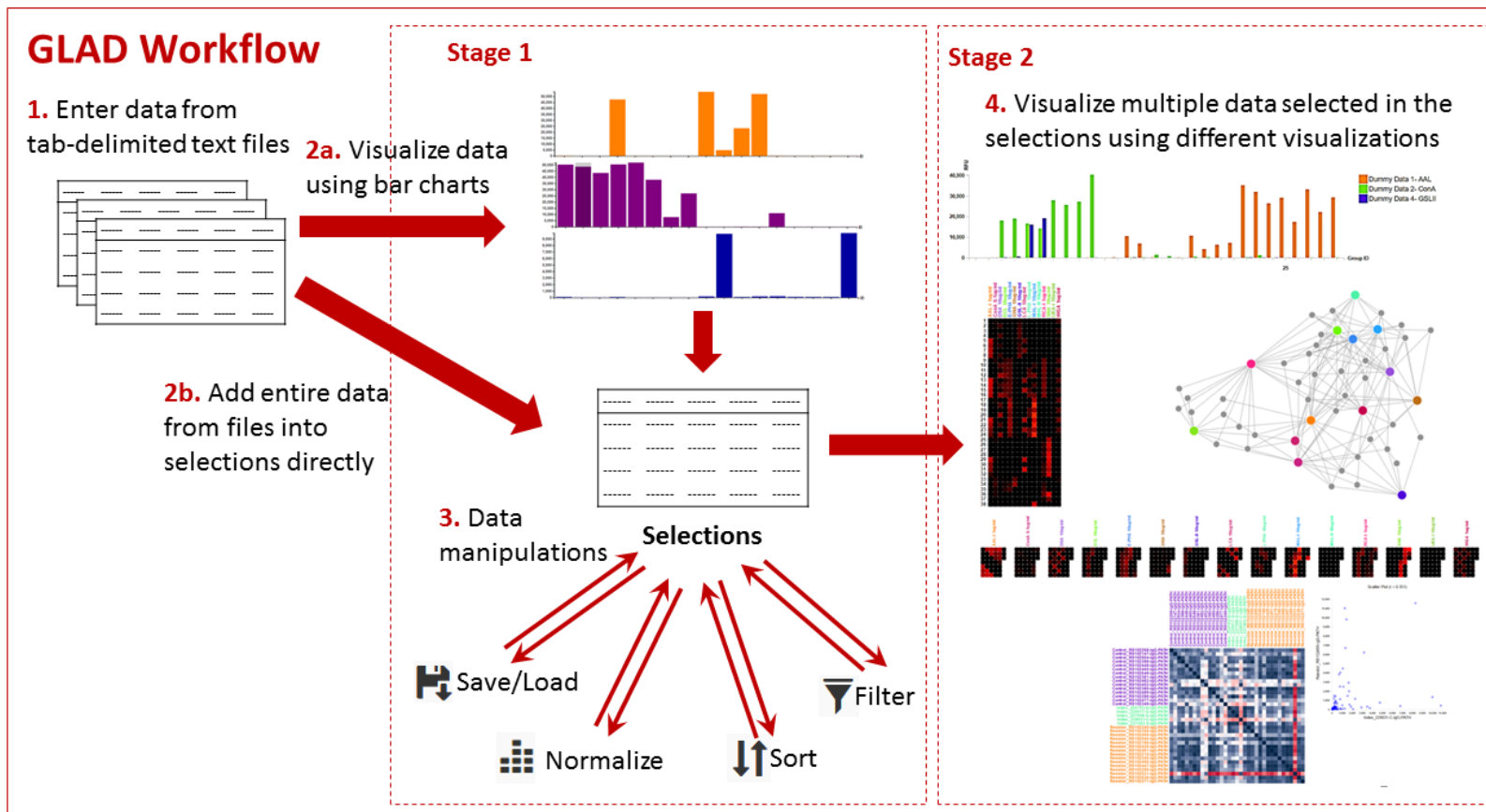


GLAD - Introduction

- GLAD – Glycan Array Dashboard
- Created to make visualization and comparison of microarray data simpler.
- Problems it solves
 - Helps visualize glycan structures alongside data.
 - Useful when trying to compare results from multiple experiments/samples.
 - Data mining functions to help filter and sort data.
- No data is uploaded to any server (privacy friendly) – everything is done on your computer, in your own browser.



GLAD - Overview



Important Links to Note:

- Main Page: <https://glycotookit.com/GLAD/>
- Tool Page: <https://www.glycotookit.com/Tools/GLAD/>
- Documentation: <https://glycotookit.com/GLAD/documentation>
- Publication: [*Bioinformatics*, Volume 35, Issue 18, 3536–3537](#)
 - Please cite if you use it for your data

Live Demo

What we will see in demo...

- Data for 4 lectins (in brackets the known binder):
 - AAL (Fucose) ▲
 - ConA (Mannose) ●
 - GNL (Mannose) ●
 - SNA (Sialic Acid/Neu5Ac) ◆
 - MAL-II (Sialic Acid/Neu5Ac) ◆
- Each lectin has data for 2 concentrations : 1 ug/ml and 10 ug/ml
- Using this data we will try to verify the known binding patterns for these lectins.

Next Event – March 06, 2023



Zachary Klamer

Van Andel Research Institute

Grand Rapids, MI, USA

Using CarboGrove to guide experimental design and data interpretation

