## Glycoinformatics Consortium (GLIC) seminar series

**Special topic: Glycan Arrays**

<table>
<thead>
<tr>
<th>Date</th>
<th>Speaker(s)</th>
<th>Topic</th>
</tr>
</thead>
<tbody>
<tr>
<td>02/06/2023</td>
<td>René Ranzinger and Akul Mehta</td>
<td>Introduction into glycan arrays</td>
</tr>
<tr>
<td>02/13/2023</td>
<td>Yukie Akune</td>
<td>CarbArrayART for glycan microarray data storage, presentation and reporting</td>
</tr>
<tr>
<td>02/27/2023</td>
<td>Akul Mehta</td>
<td>Using GLAD for exploratory glycan microarray data analysis and visualization</td>
</tr>
<tr>
<td>03/06/2023</td>
<td>Zachary Klamer</td>
<td>Using CarboGrove to Guide Experimental Design and Data Interpretation</td>
</tr>
<tr>
<td>03/20/2023</td>
<td>René Ranzinger</td>
<td>The Glycan Array Data Repository</td>
</tr>
<tr>
<td>03/27/2023</td>
<td>Jon Lundstrøm</td>
<td>LectinOracle@glycowork: Lectin binding predictions &amp; glycan sequence analysis in Python</td>
</tr>
</tbody>
</table>

More information and registration: [https://glic.glycoinfo.org/seminar/](https://glic.glycoinfo.org/seminar/)
Using GLAD for Exploratory Glycan Microarray Data Analysis and Visualization

Akul Mehta
February 27, 2023
aymehta@bidmc.harvard.edu
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.
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.

Bioinformatics, Volume 35, Issue 18, Pages 3536–3537
GLAD - Overview

GLAD Workflow

1. Enter data from tab-delimited text files
   2a. Visualize data using bar charts
   2b. Add entire data from files into selections directly

3. Data manipulations
   - Save/Load
   - Normalize
   - Filter
   - Sort

Stage 1

Stage 2

4. Visualize multiple data selected in the selections using different visualizations

https://glycotoollkit.com/GLAD/
Important Links to Note:

• Main Page: https://glycotooldit.com/GLAD/

• Tool Page: https://www.glycotooldit.com/Tools/GLAD/

• Documentation: https://glycotooldit.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

Using CarboGrove to guide experimental design and data interpretation

Zachary Klamer
Van Andel Research Institute
Grand Rapids, MI, USA