CIFER

Carbohydrate

Informatics

Frequentist

Extraction

Repo

Our tool provides a flexible framework to study the glycan 2D structure and its substructure.

Why we need glycan?

Background: Glycan biologists want have a better understanding about the structure of glycan.

Glycan is synthesized by multiple glycosyltransferases and the order of the operation consists of a complex network. The glycosyltransferases are located in three sub compartment of Golgi. It’s like an assembly line, the glycosyltransferases compete with each other to modify the glycan within a limited time. There is no template for glycan to duplicate itself and the synthesize of glycan is a stochastic dynamic process. However, there is a recurrence of a group of specific glycan substructure which have specific biological meaning.

Currently: The tech for generating high–throughput glycan data is feasible. Scientists now are able to analyze glycan profiles or study the structure of a bunch of glycan at one time. However, the structure of glycan is so complicated and the pattern recognition across glycan profile is limited by the human mind.

Main goal: our tool is able to decompose the structure of glycan and represent it as a substructure vector. the substructures from a glycan dependency. is able to identify the meaningful glycan substructure through a comprehensive statistical augmentation in single glycan comparison or groups comparison. It could help

People want to st

Because of X, I know x y z

Feature ‘

Case

Decompose

We are looking for syntax of the glycan biology

Glycan share / unique substructure

Pul in out the all substructure

We are id mean glycan substru

Comprehensive

Explorative way to find out the shared motif, that might help more meaning

Where the glycan motif/what they do?

profile’s similarity with given glycan mass spectrum profile.

Our tools are able to detect

Quantify the glycan structure mutation,

Find the unique glycan model

Capture the enzyme function

View the cell line’s glycan from a substructure perspective.

Find the undergoing rule of the enzymes’ synthesize.

Help clustering the glycan profile.

An enrichment of the glycan structure analysis.

Find a flexible benchmark to

Help to distinguish/prioritize the enzyme’s function, profile difference across large dataset.

Capture the substructure signature which helps to link specific enzyme

link enzyme rule with glycan structure

The synthesize of the glycan goes through a network, thus in a glycan profile each glycan are dependent.

Our method contains

Our method are able to compare glycan

Different cell line

Cell line specific glycan profile analysis

Tissue specific glycan profile analysis

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