

GlycoTF

GlycoTF is a web tool for exploration of transcriptional factors (TFs) of glycogenes and glycopathways in human. The TF-glycogene relationship is characterized by their single-cell transcriptome in the Tabula Sapiens dataset [1], specifically their mutual information (MI). Users are able to select glycogenes in glycopathways or use own glycogene set for customized analysis. Please refer to the publication for more information on the evaluation of MI [2]. Webtool is accessible at: <https://www.virtualglycome/glycotf>

TF-glycogene network

Glycogene (red), TF (blue)

Slider: adjust total nodes in network

Select gene set (glycopathways)

Query glycogenes

User-defined threshold

MI threshold for TF-glycogene (percentile). Only those **above** the threshold are included.

Glycogenes in pathway

Users can refine glycogene set by (de)selecting genes.

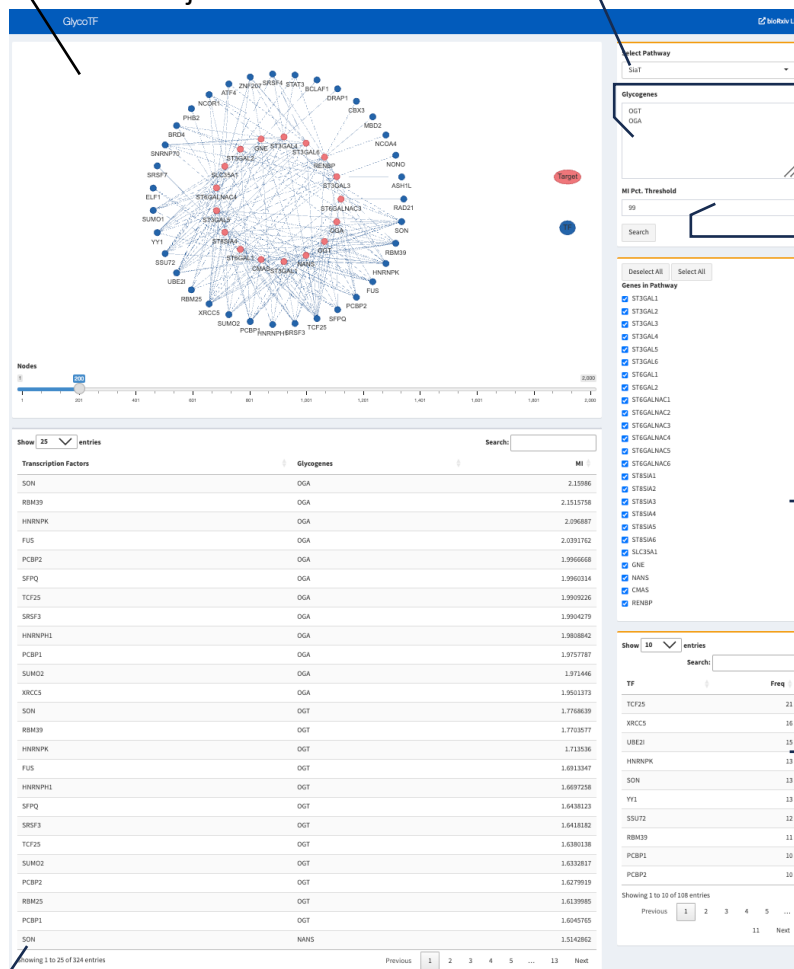
TF-Glycogene Frequency

For each TF, this table gives the number of glycogenes in the query set with MIs above the user-defined threshold.

Search: find TF in the table

TF-Glycogene Table

This table gives all TF-glycogenes with MIs above the user-defined threshold.
Search: find TF / glycogene in table



References:

1. Tabula Sapiens Consortium *et al.* (2022). The Tabula Sapiens: A multiple-organ, single-cell transcriptomic atlas of humans. *Science*, 376(6594), eabl4896.
2. P. Chrysinas, S. Venkatesan *et al.* (2023). Cell and tissue-specific glycosylation pathways informed by single-cell transcriptomics. *bioRxiv*, 559616.