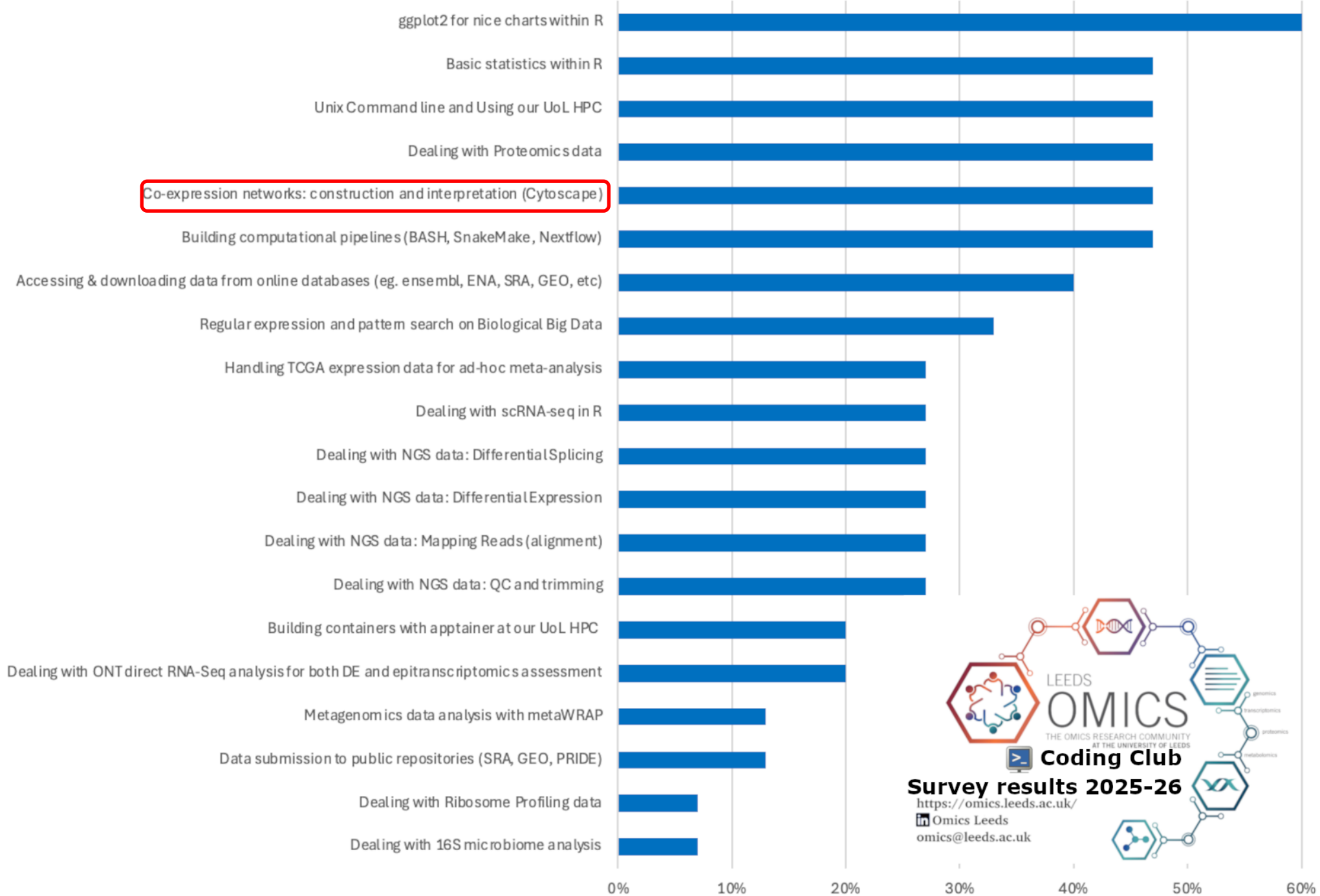


## Co-expression Networks: Construction and interpretation

Club Moderator(s): Elton Vasconcelos and Eilidh Ward

# Topics to be addressed on the 2025-26 season - Survey Result



**LEEDS OMICS**  
THE OMICS RESEARCH COMMUNITY AT THE UNIVERSITY OF LEEDS

**Coding Club**  
Survey results 2025-26  
<https://omics.leeds.ac.uk/>  
Omics Leeds  
omics@leeds.ac.uk

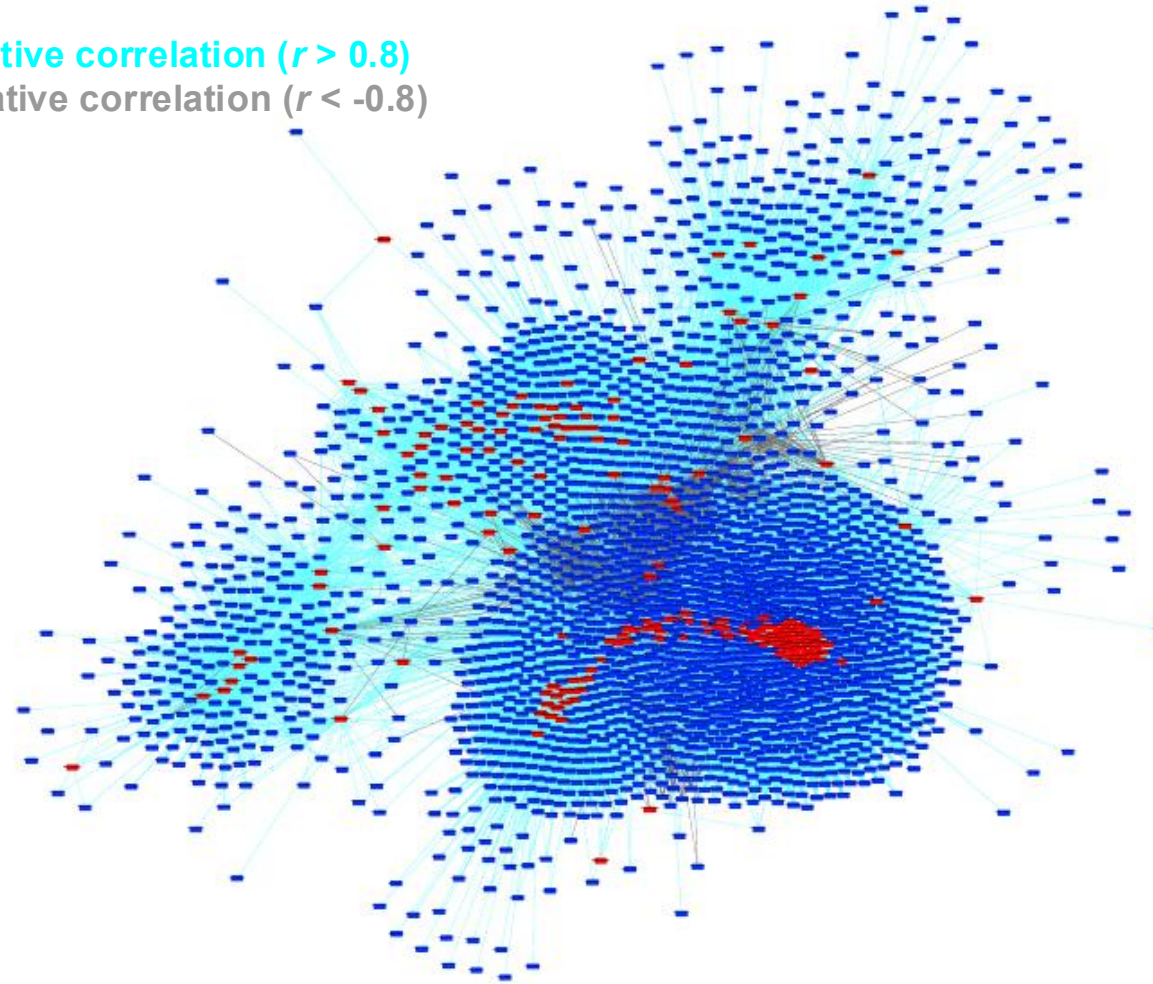
# Why building co-expression networks?

**181 lincRNAs** (SmLINC)

**2359 SMPs**

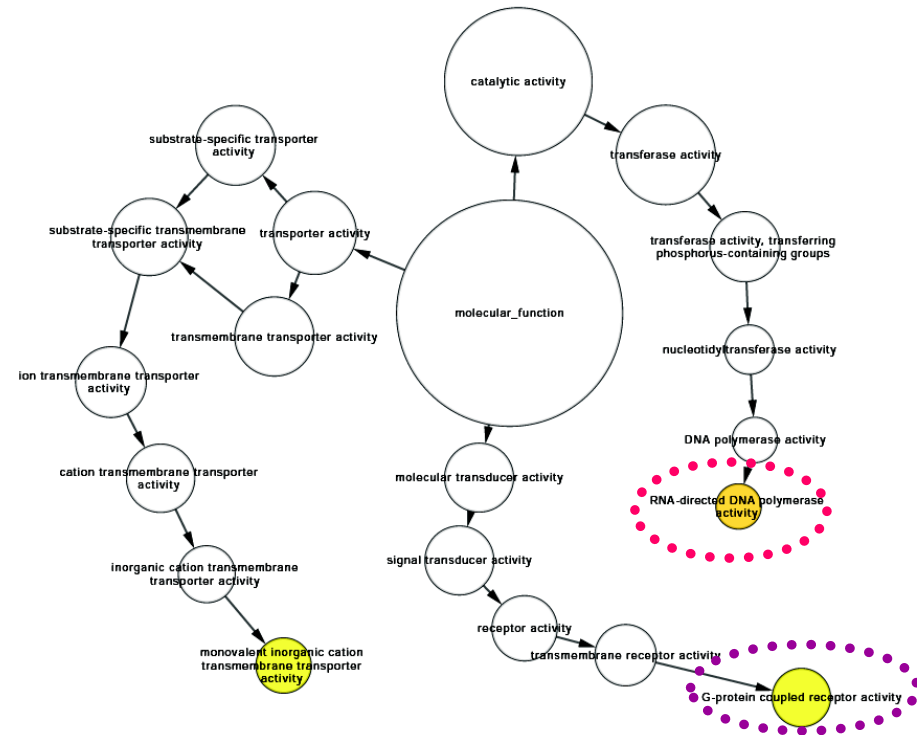
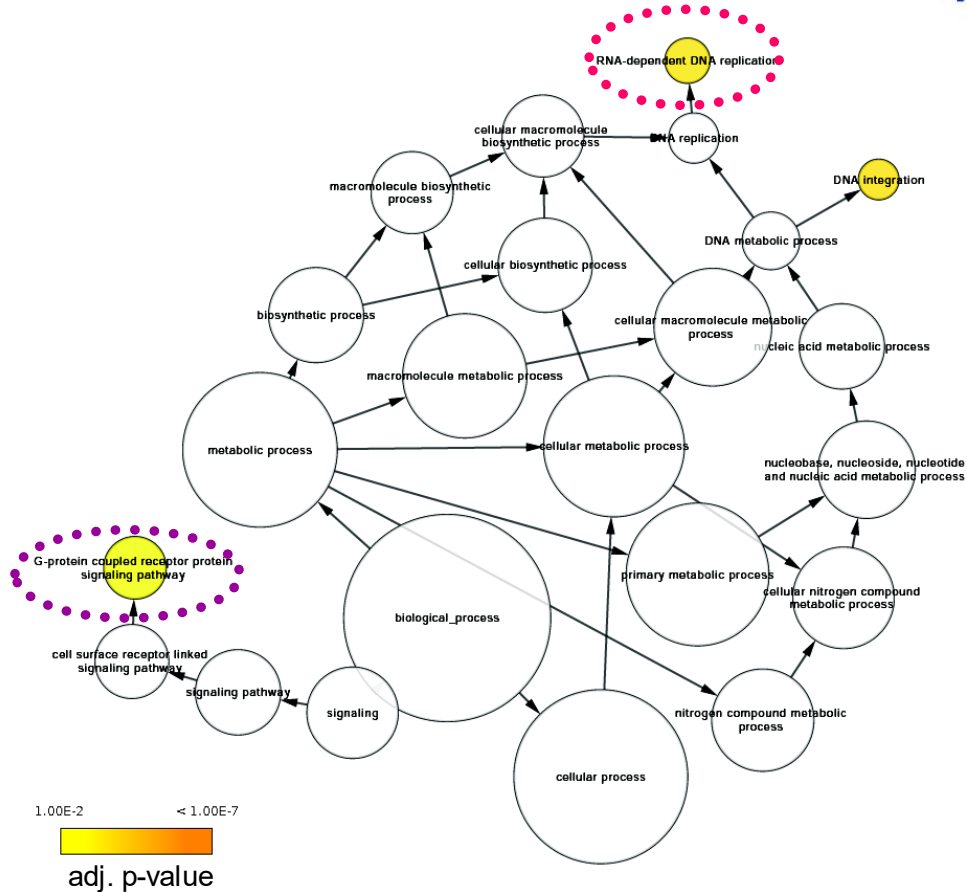
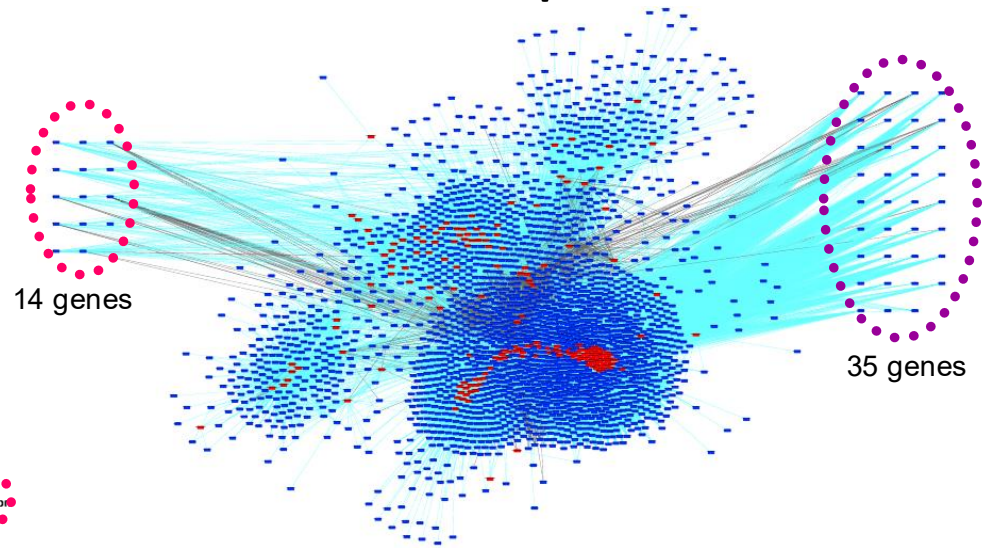
**Cyan Edges = positive correlation ( $r > 0.8$ )**

**Gray Edges = negative correlation ( $r < -0.8$ )**



Hypotheses generation on genes' functionality

■ Gene enrichment analysis on **2359 SMPs** from the co-expression network



# ■ TFS - Topological Filtering Strategy

## 1<sup>st</sup> step:

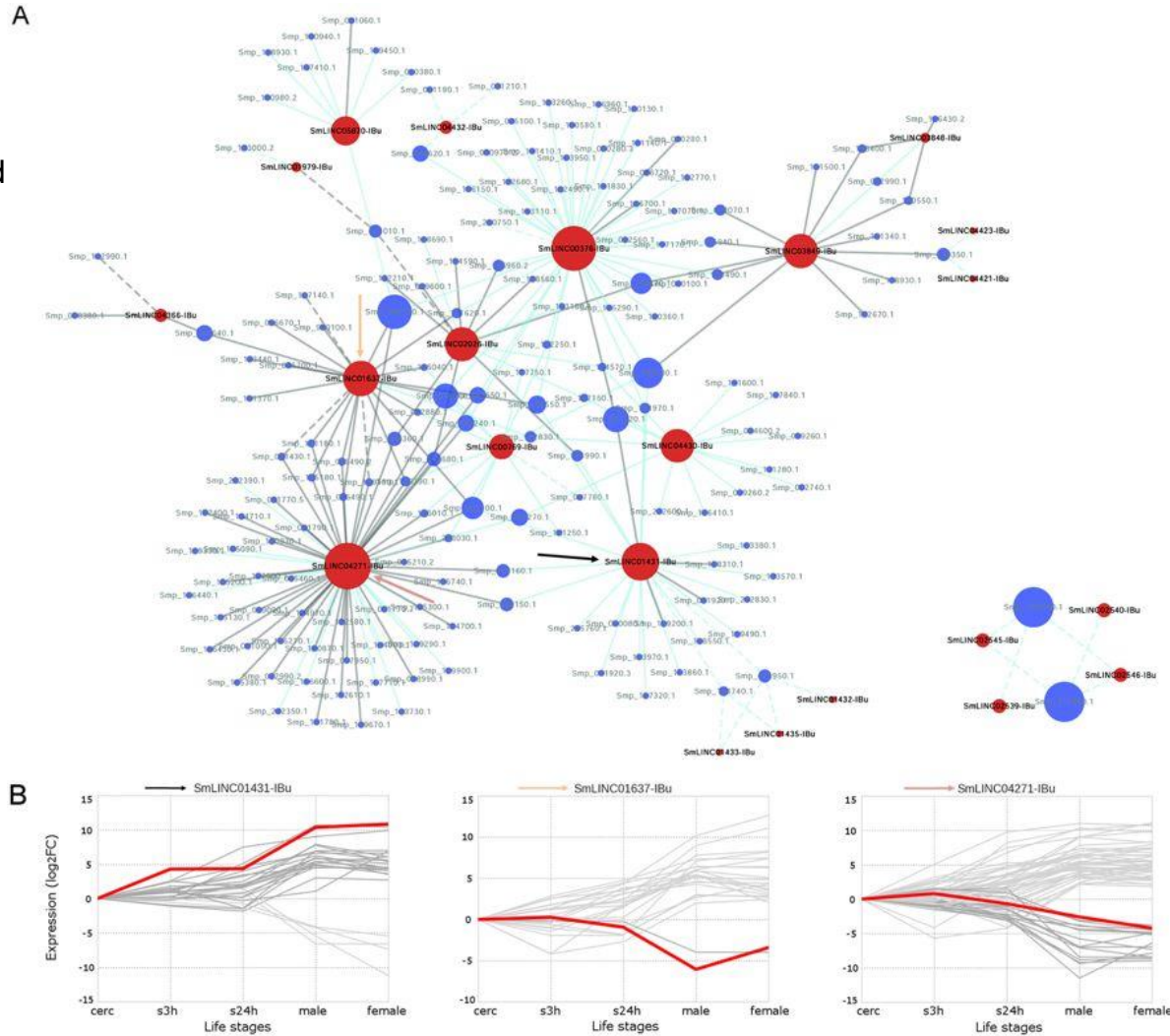
→ expression correlation among 5 life cycle stages ( $r > 0.5$  or  $r < -0.5$ )

## 2<sup>nd</sup> step:

→ correlated gene pairs are either neighbors or prone to form TFO-TTS structure (predicted by triplexator algorithm)

**89 lincRNAs** out of the 181 robust ones  
**237 SMPs**

## ■ Network view considering **betweenness centrality** metric:



## **Some useful terminologies**

Degree

Betweenness centrality

Closeness centrality

Clustering coefficient

Topological coefficient

# Important tools

- WGCNA

<https://web.archive.org/web/20230323144343/horvath.genetics.ucla.edu/html/CoexpressionNetwork/Rpackages/WGCNA/>

<https://bioinformaticsworkbook.org/tutorials/wgcna.html#gsc.tab=0>

- igraph

<https://r.igraph.org/>

- Cytoscape

<https://cytoscape.org/>

[https://manual.cytoscape.org/en/stable/Network\\_Analyzer.html](https://manual.cytoscape.org/en/stable/Network_Analyzer.html)

Bring your issues on!