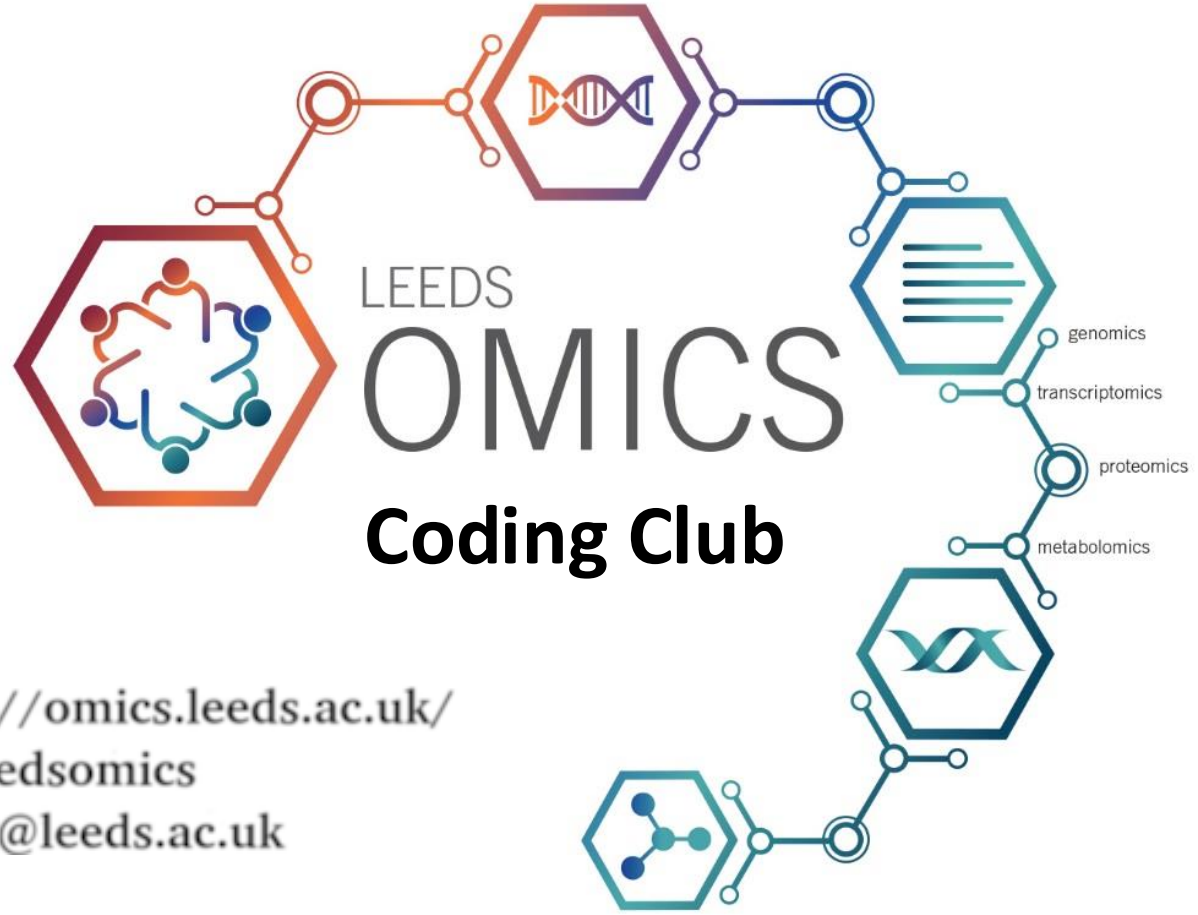

Coding Club

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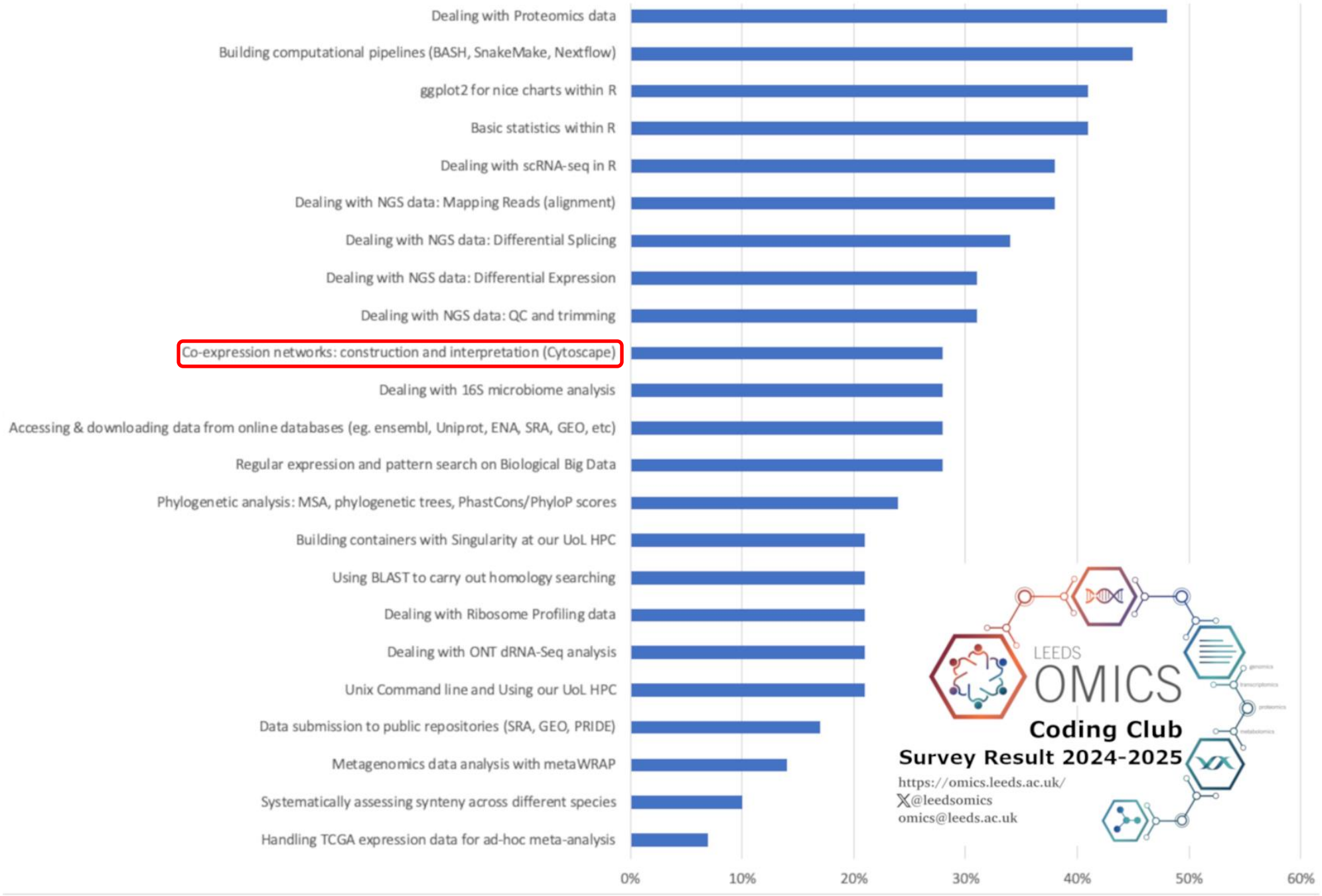
Co-expression Networks: Construction and interpretation

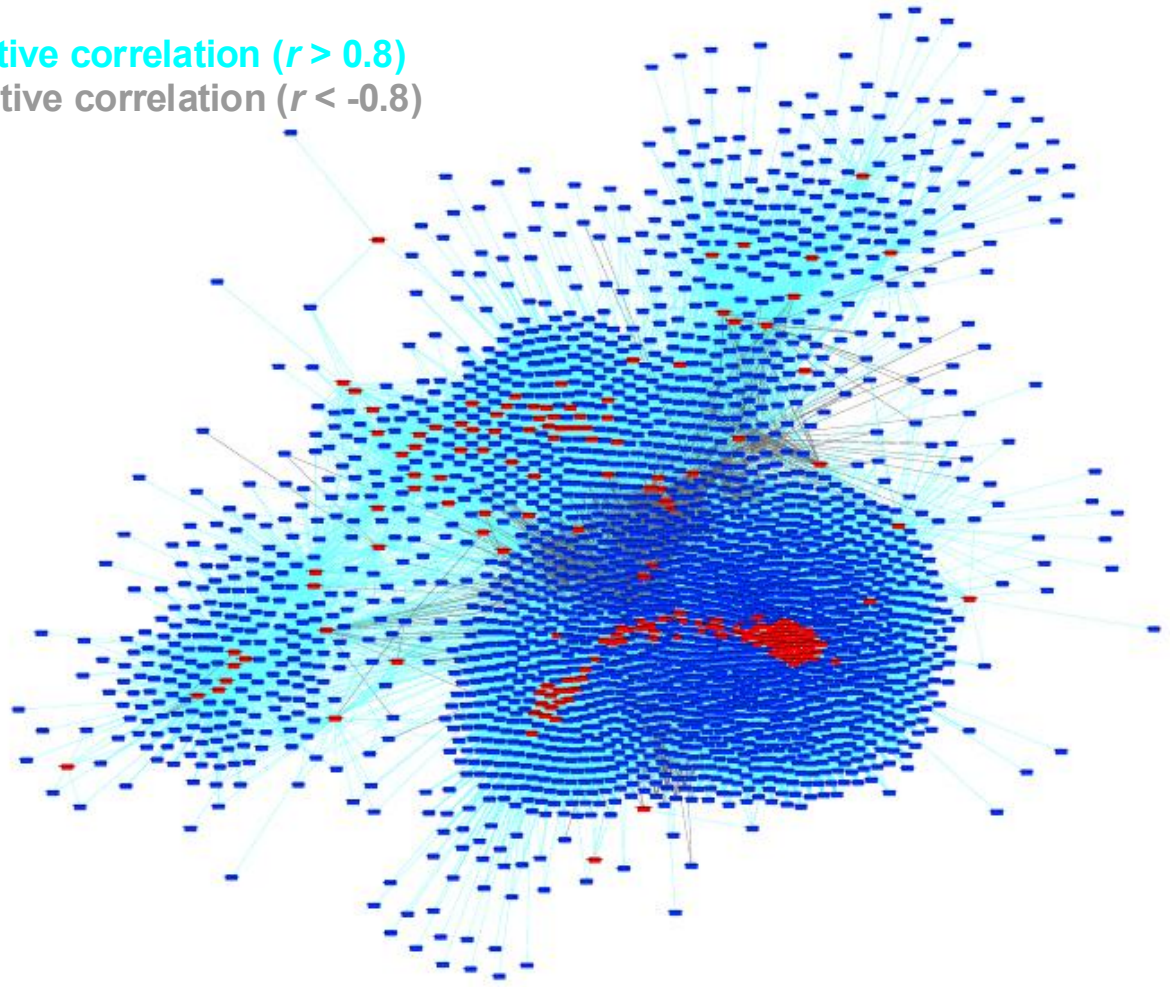
Club Moderator(s): Elton Vasconcelos and Eilidh Ward

Topics to be addressed during **2024-25** season - **Survey Result**



Why building co-expression networks?

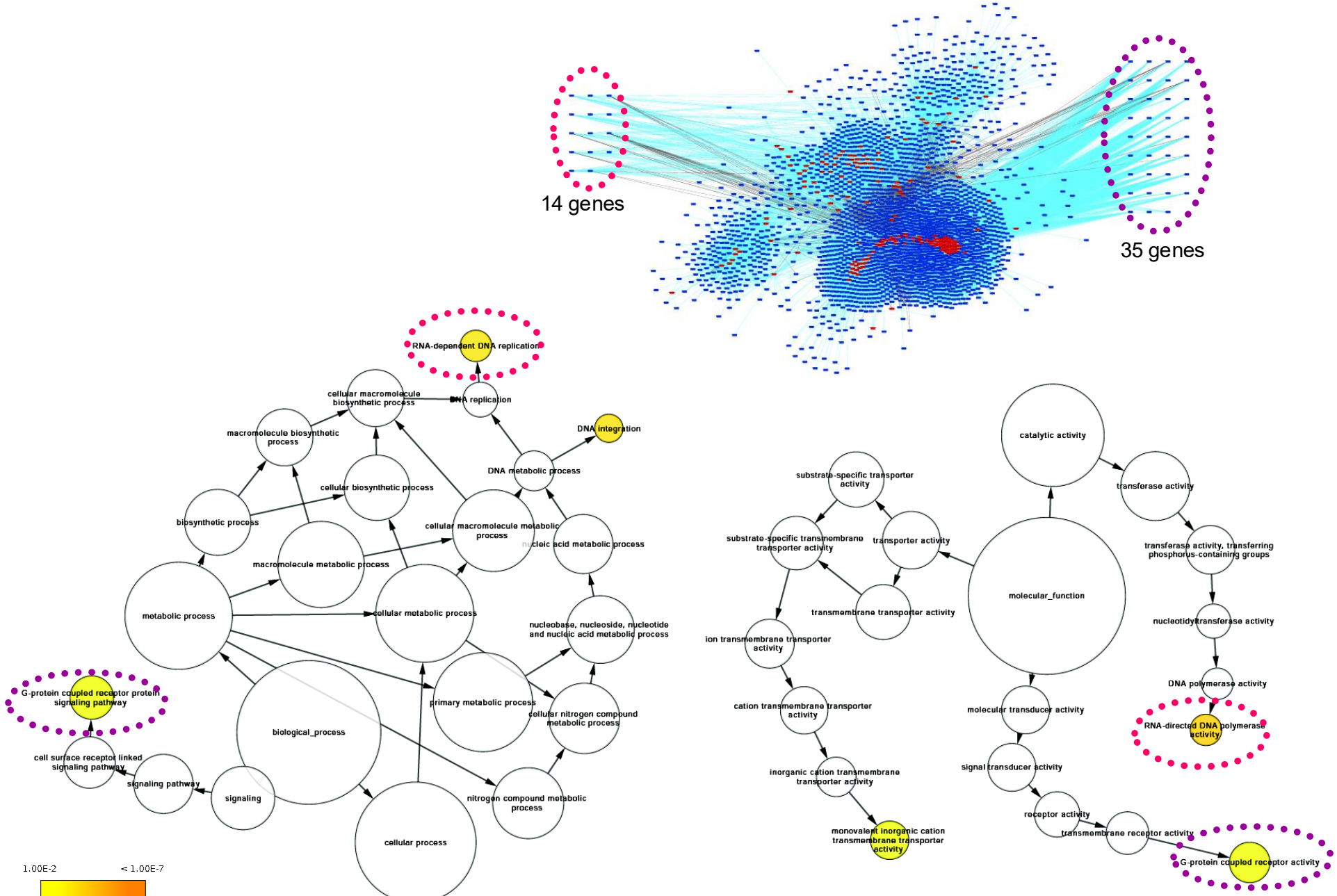
181 lincRNAs (SmLINC)
2359 SMPs
Cyan Edges = positive correlation ($r > 0.8$)
Gray Edges = negative correlation ($r < -0.8$)



Hypotheses generation on genes' functionality

Vasconcelos et al., 2017 (*Sci. Rep.)*

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



Vasconcelos et al., 2017 (*Sci. Rep.*)

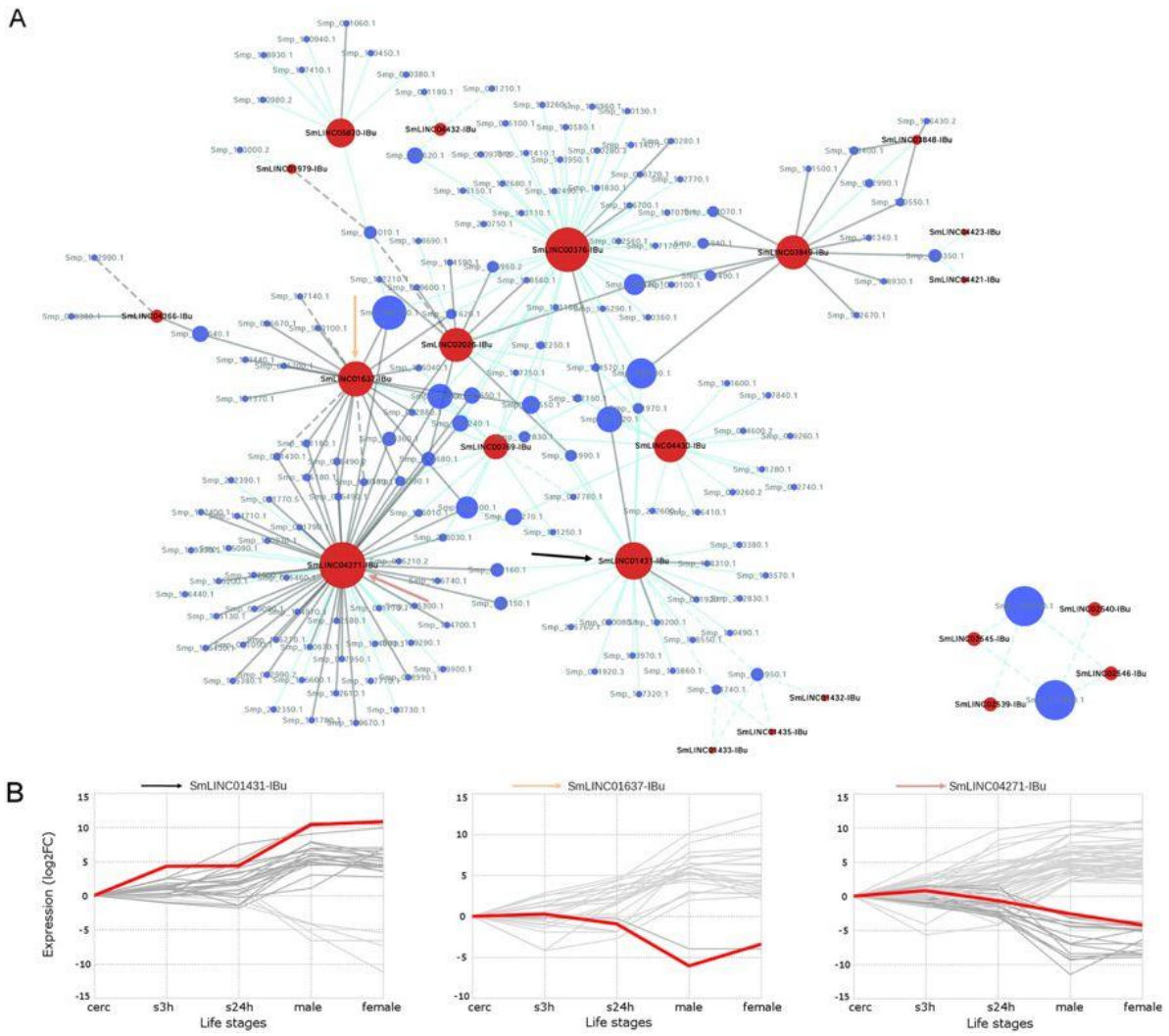
TFS - Topological Filtering Strategy

1st step:
→ expression correlation among 5 life cycle stages ($r > 0.5$ or $r < -0.5$)

2nd 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:



Vasconcelos et al., 2017 (*Sci. Rep.)*

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

Bring your issues on!