

Comparing Gene Regulation Networks

A Research Internship supervised by Chris Needham and Netta Cohen and carried out by Karl Hopkinson-Turrell

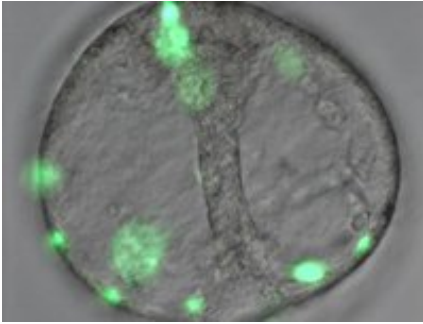


Fig 1. An urchin embryo expressing a gene that has been combined with a fluorescent protein

Gene regulation networks control the patterns of gene activation that differentiate cells from one another, causing two cells with the same DNA to perform different functions.

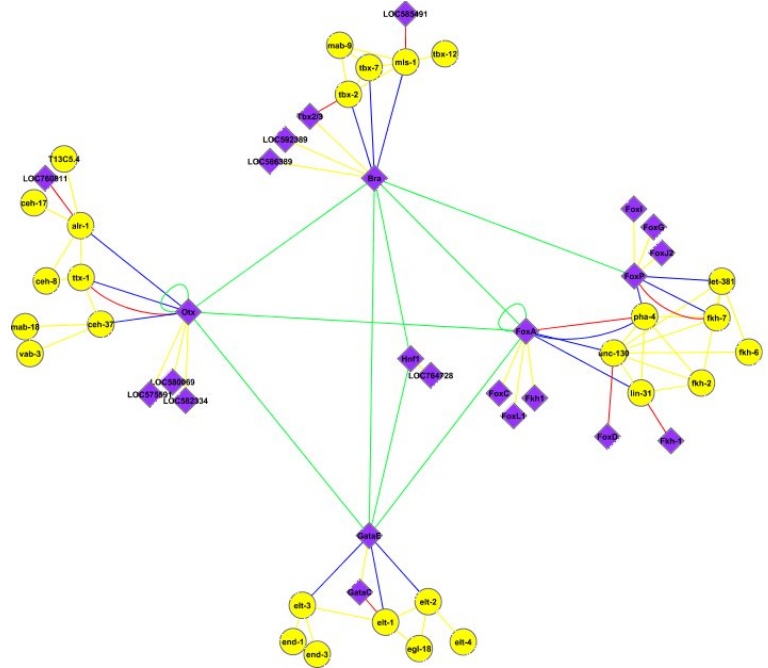


Fig 2. Graph representation of BLAST sequence similarities between Urchin and Eelegans genes

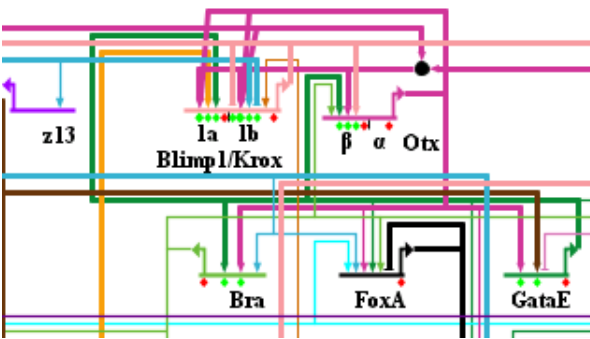


Fig 3. Biotapestry graph snippet showing the existing Urchin gene regulation subset used

Graph visualisation methods are explored to represent data in an informative way and existing regulation data is used to help establish the confidence of regulation prediction.

