Capturing the experimental research history of signalling pathways in Drosophila melanogaster

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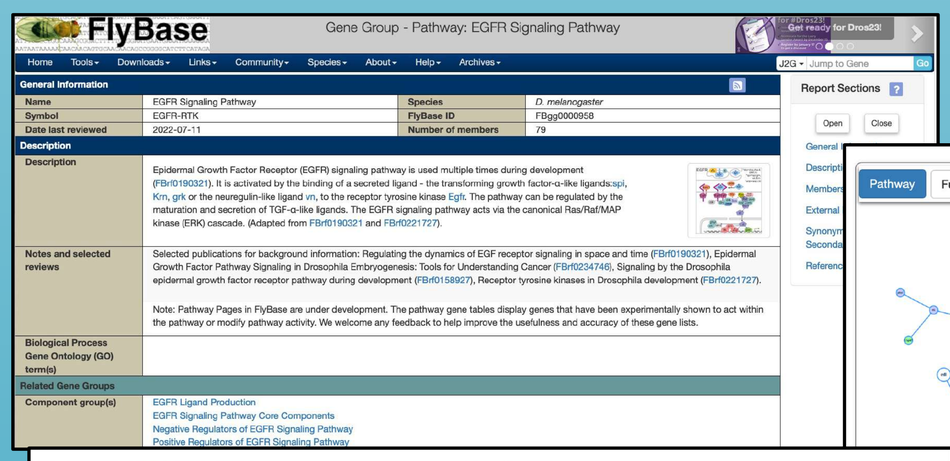
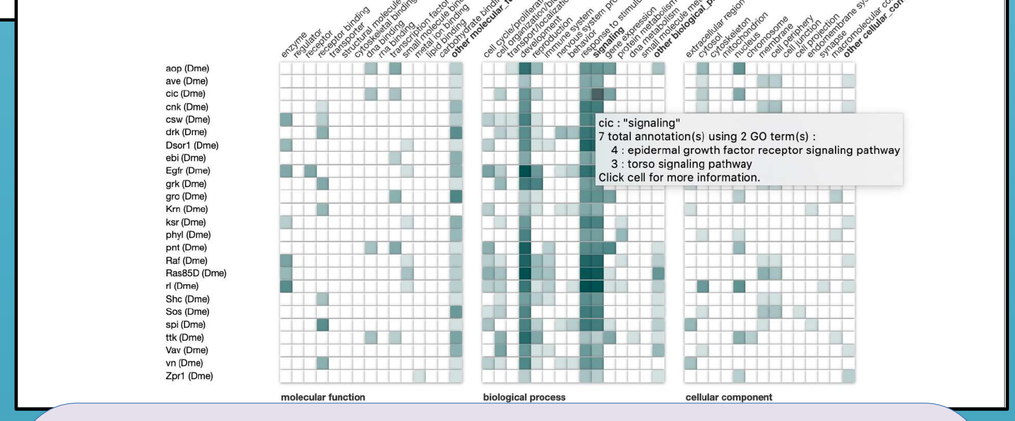
Evidence-weighted pathway curation as a representation of the experimental landscape





The FlyBase pathway resource

FlyBase provides a dedicated signalling pathway resource, where pathway members supported by experimental evidence are grouped according to their role in the pathway. A summary and a textbook representation (“thumbnail”) of the pathway and its most important members are provided.

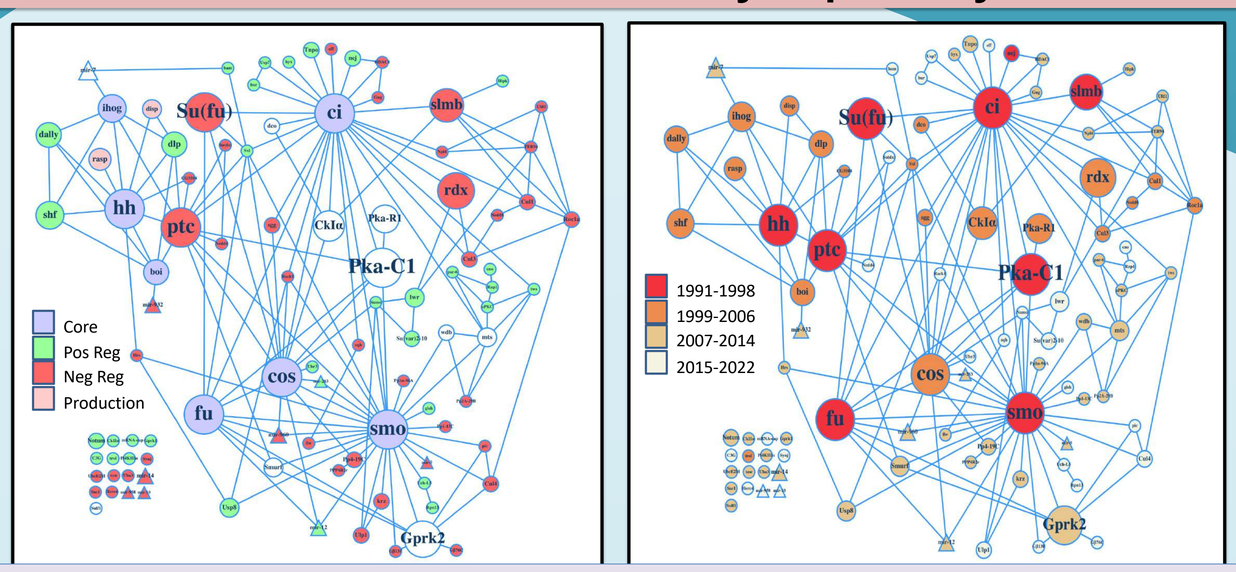
Interactive pathway networks

Accurate pathway membership assignment allows us to build network models using physical interaction data. In these networks, the size of each gene node is based on the amount of curated experimental evidence linking the gene to the pathway, and nodes are coloured based on the gene’s role in the pathway. The evidence-weighted curation model also have the advantage of showing the reproducibility of observations.

A starting point for scientific exploration of pathways

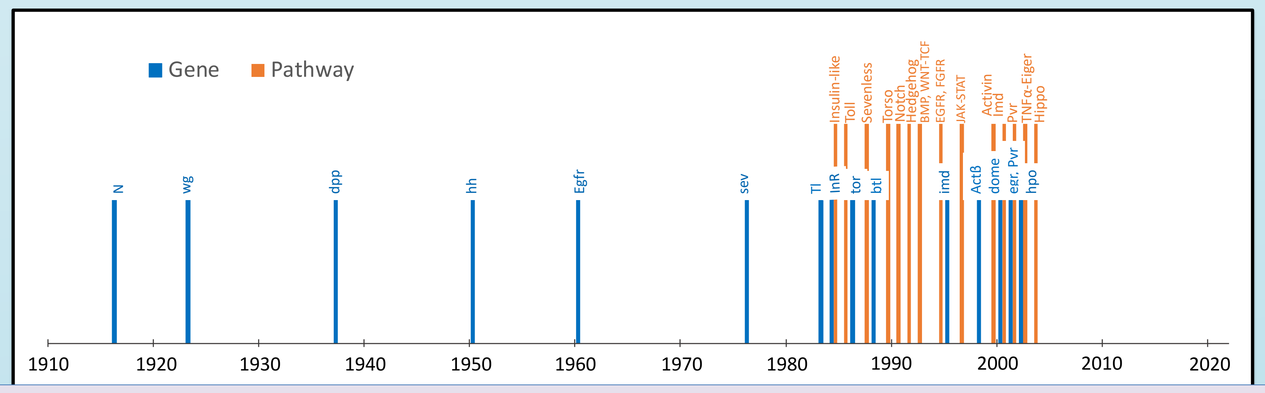
Member tables provide comprehensive details on various information available on pathway members in FlyBase. These tables can be exported and downloaded, or the gene lists can be fed into other tools in FlyBase. Pathway pages also include GO ribbon stacks, which are a graphical summaries of the GO annotations for each pathway member (darker colours indicate a larger number of unique GO terms). The terms that group under a particular cell can be seen by hovering over or clicking on the cell.

Annotations illuminate the history of pathway research



The history of experimental characterization of the Hedgehog pathway

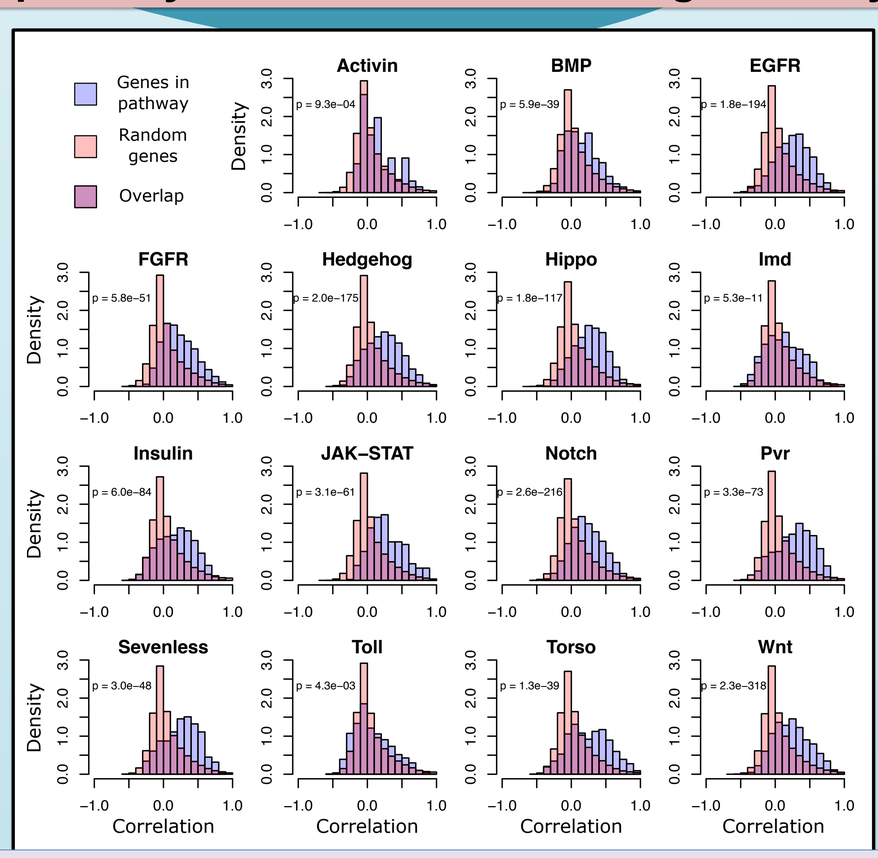
Left: Node colour is a function of the role of a gene in the pathway. **Right**: node colour is a function of the publication year of the first research paper that has been used to annotate that gene to the pathway. It can clearly be seen that core members and key regulators of the pathway were often the first to be characterized. This analysis also shows that ongoing research on this pathway is still very active, considering how many new members have been linked to the pathway for the first time in the last decade.



Timeline of research on defining members and their pathways

The publication years of the first research papers in FlyBase associated with the defining members of pathways, and of the first research papers associated with the pathways themselves. In many cases, what is considered the defining member of the pathway was described by observable mutant phenotype long before molecular techniques allowed the pathway to be characterized.

Accurate pathway member lists fuel biological analyses



Co-expression patterns among genes within pathways

For each pathway, the distribution of correlation values between the mRNA expression profiles of all pairs of genes is displayed and compared to the same distribution for a set of random genes of the same size as the pathway. The p-value displayed is from a t-test for a difference in the mean between the two distributions.

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