Regeneration and tissue renewal are essential processes of adult animals that must be tightly controlled, since its dysfunction leads to common illness as degenerative diseases or cancer. Planarians are emerging as a model organism to study regeneration as an animal mainly due to the presence of a population of adult pluripotent stem cells, called neoblasts, a cell type able to produce all of the cellular lineages that conform these worms. However, the little available data of protein-protein interactions hinders the advances in understanding the mechanisms underlying its regenerating capabilities.

We have developed a protocol to predict protein-protein interactions using sequence homology data and a reference Human interactome. This methodology was applied on ten Schmidtea mediterranea transcriptomic sequence datasets and it has been automated to integrate future transcriptomic data for this species. We projected each network into a graph-based database manager, as interactions data can be queried much efficiently on such type of databases. On top of that we have deployed a web application, called PlanNET, to explore the multiplicity of networks and the associated sequence annotations.

PlanNET is available at https://compgen.bio.ub.edu/PlanNET