RPGeNet v2.0

Enhanced navigation through the retinitis pigmentosa interaction network

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INTRODUCTION

Retinitis pigmentosa (RP) is a heterogenous genetic visual disorder characterized by the death of photoreceptor cells leading to gradual loss of vision (as seen in the figure to your right). RP affects 1 in every 4000 people around the world. With over 270 genes known to be associated with the disorder, new bioinformatic tools are needed to assist in the research of the disorder.

RPGeNet was created for researchers to visualize the vast RP interaction network and to assist in narrowing down new potential candidate genes to explore. RPGeNet v2.0 has an updated database with a new database manager and new features to facilitate searches and navigation through the network.

DATA SOURCES

RPGeNet combines various sources to create its core network. The list of known driver genes of RP is retrieved from the RetNet database[1] and their aliases from HGNC [2]. Our Interaction data is gathered from two interaction databases: *BioGRID* (v3.4.60) [3] and *STRING* (v10.5) [4]; but also from text-mining articles that contain any of the known driver genes or are related to RP, retrieved by *PPaxe* [5]. The data is curated before creating the graph.
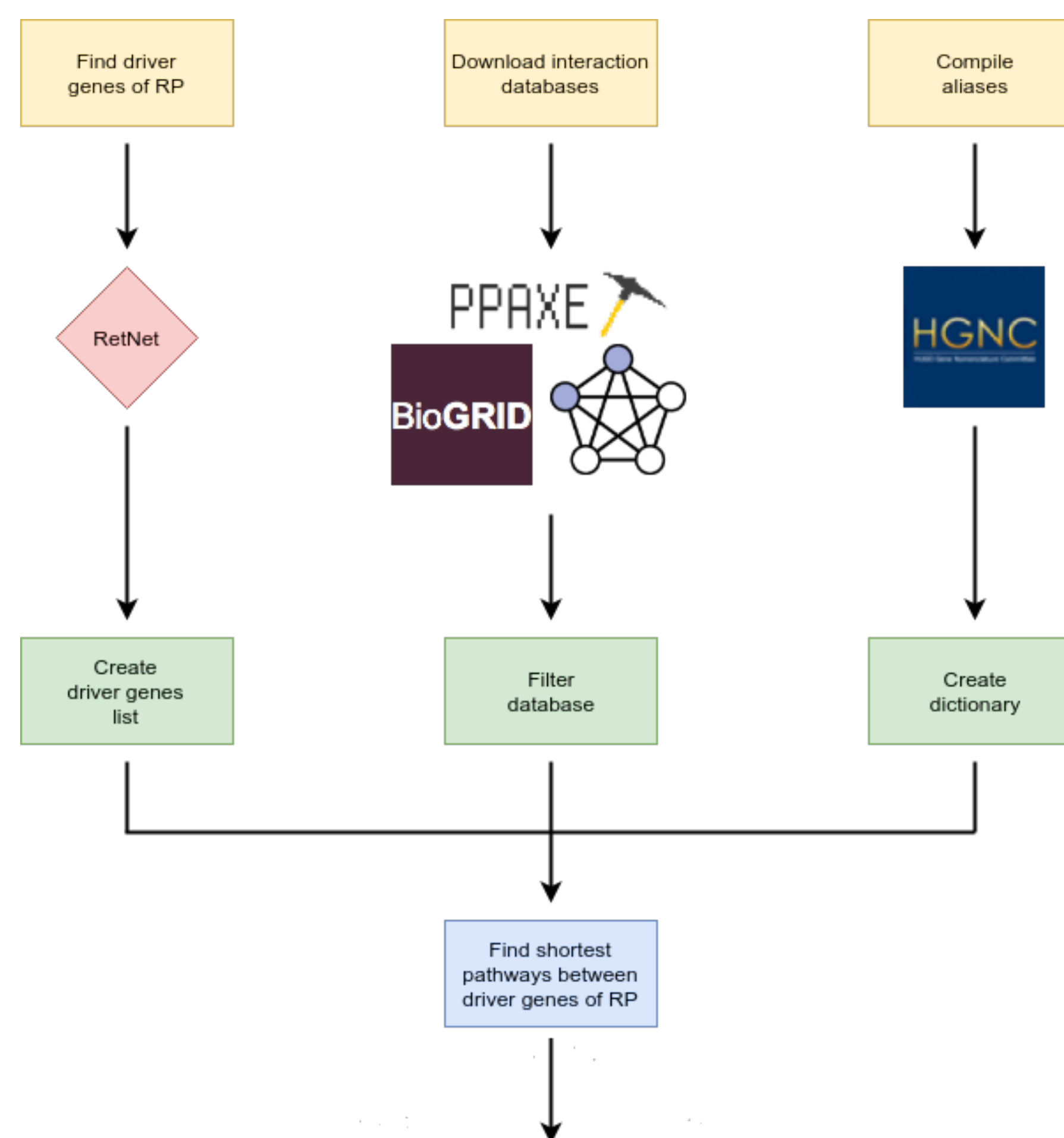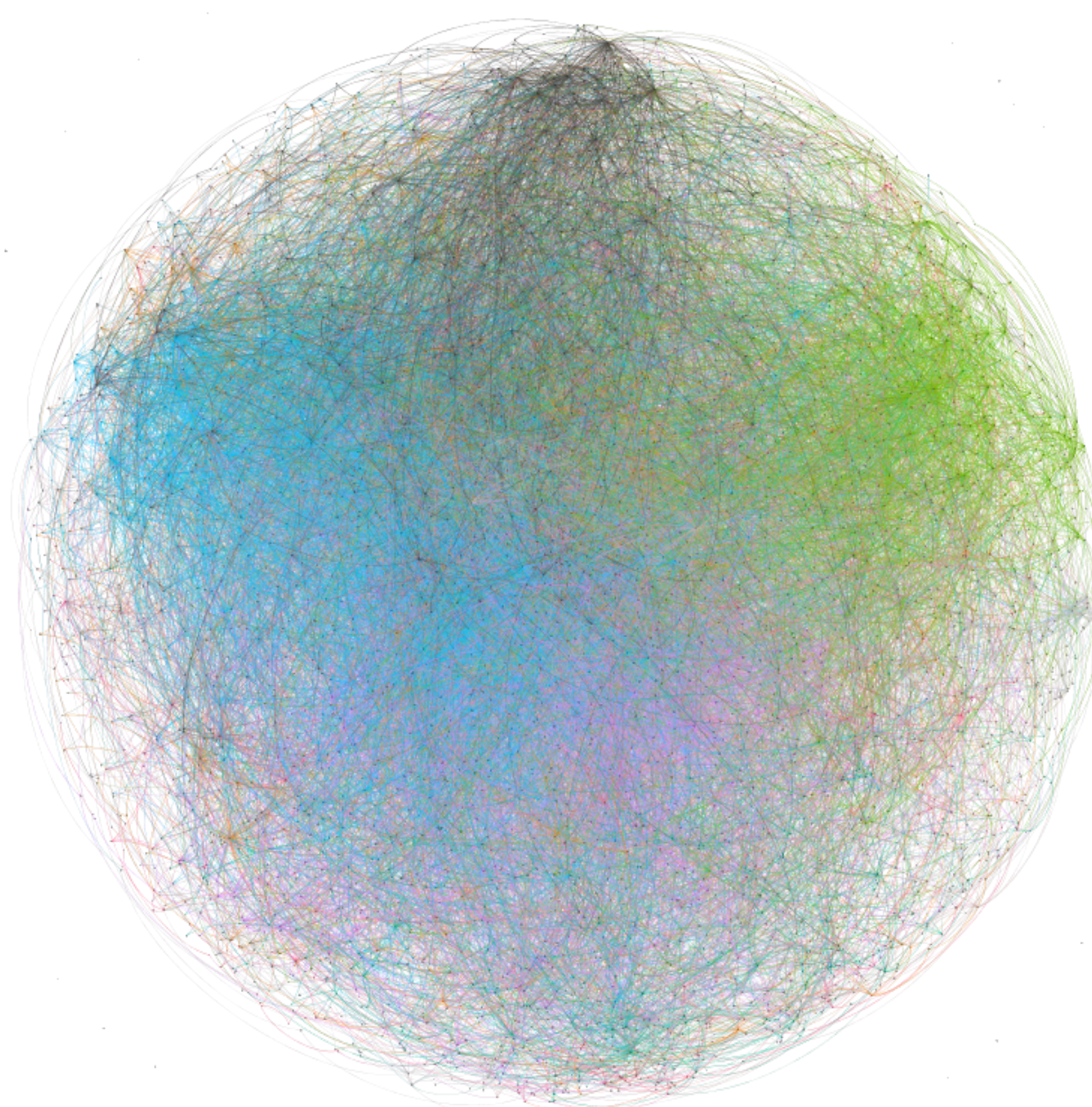
GRAPH

The *RPGeNet* network is built upon a skeleton graph composed of all the shortest pathways between the driver genes of RP. From the skeleton, levels are built upon, which include new genes that connect with genes in the skeleton, further expanding the network.
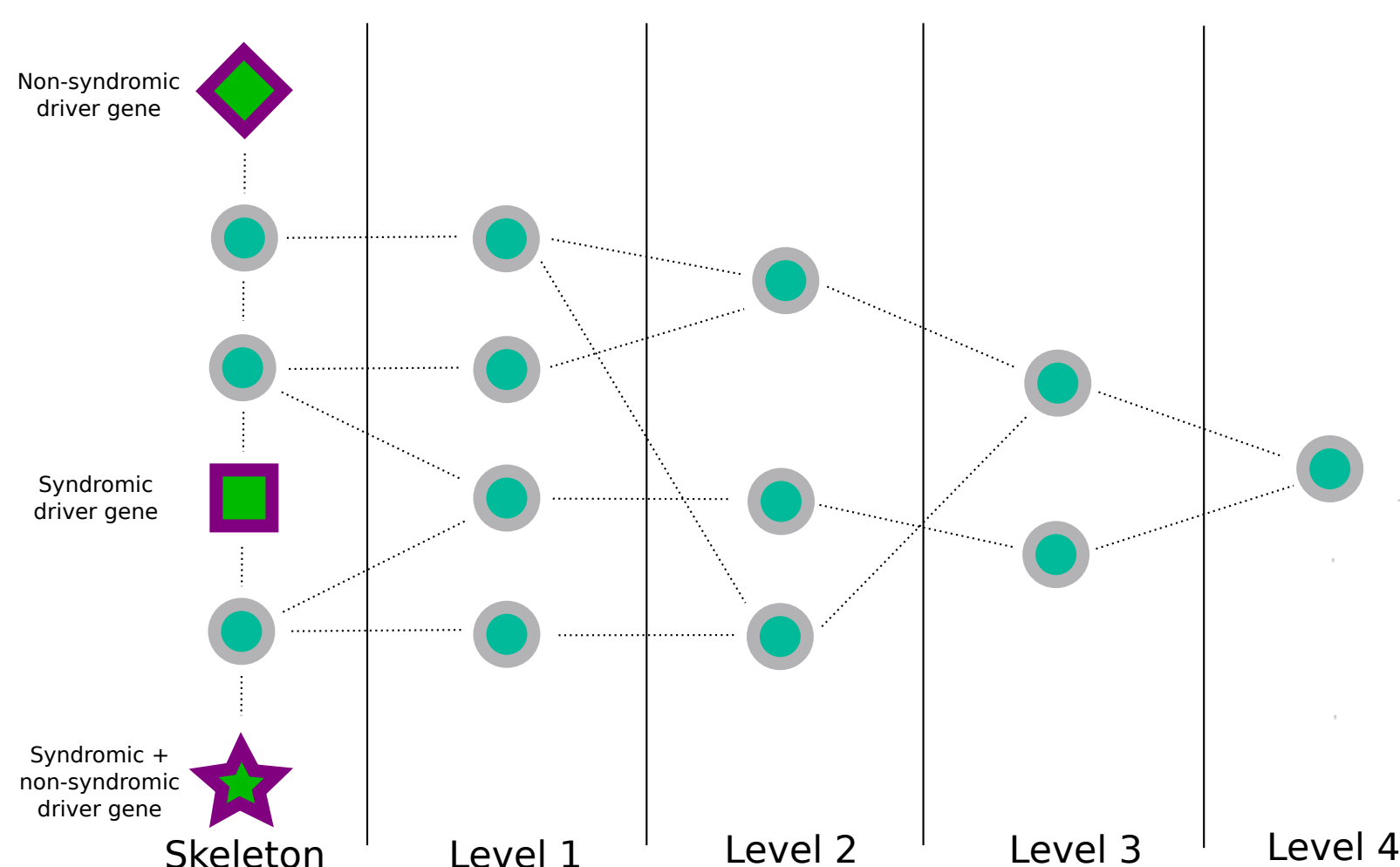
Building the network with a shortest path skeleton, creates a network that is focused around RP. This can facilitate the discovery of new candidate genes of RP by looking at genes within the lower levels close to skeleton.
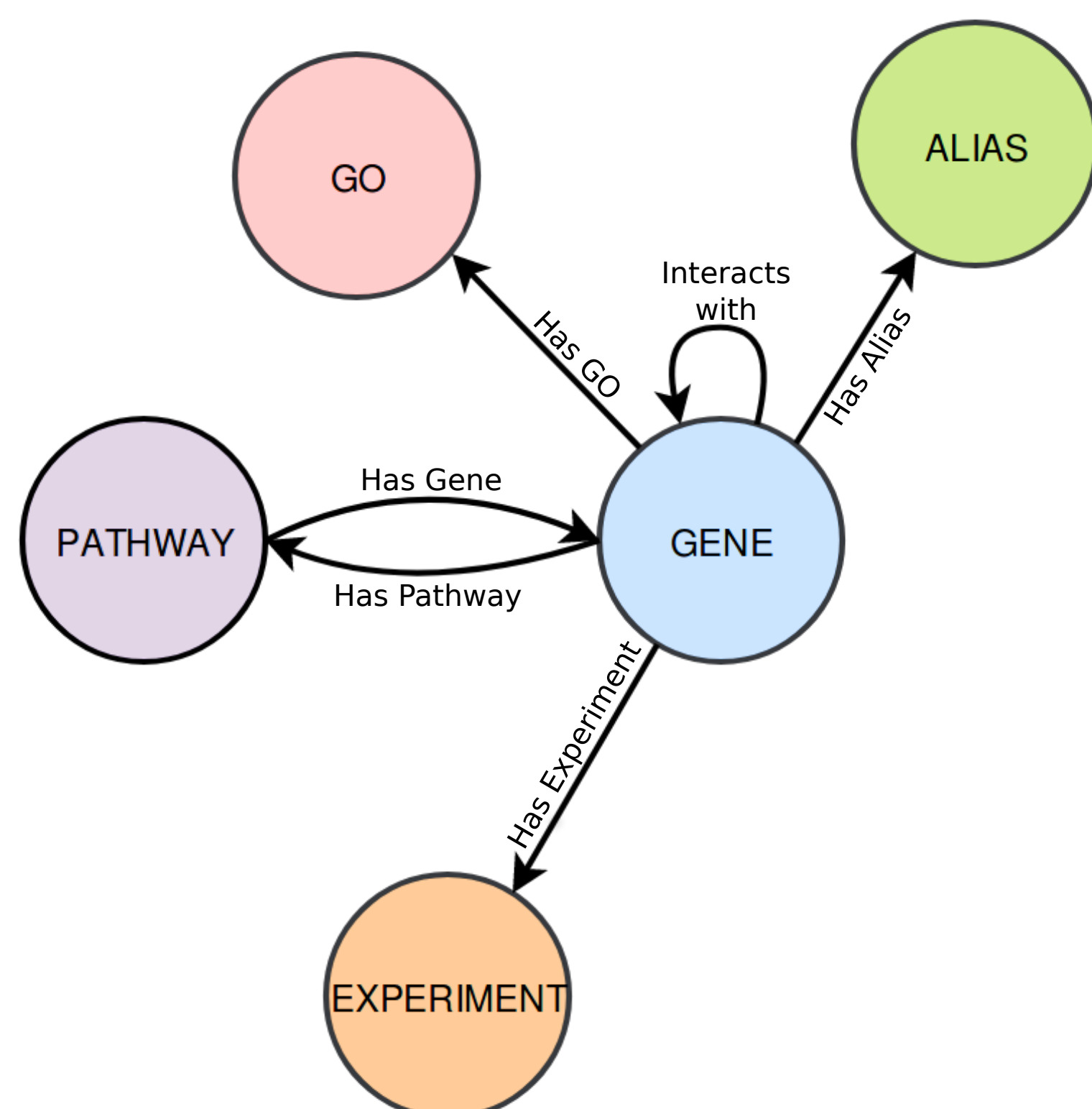
DATABASE MANAGER

RPGeNet now uses *neo4j* [6] as our database manager. *neo4j* is a graph based database manager that uses the property graph model to store and access the network data using a set of graph functions.

Property graph model uses relevant relationships between nodes (elements where data of entity is stored) to efficiently navigate through huge datasets.

As seen in the figure to the left, *RPGeNet* contains different node types that connect to each other through relevant relationships. Theis speeds up the retrieval of information allowing for new types of queries too.

WEB SERVER

Thanks to our new database manager, *RPGeNet* now can provide three types of queries. The main query is the *NetExplorer*, where users are able to visualize graphically their genes of interests within the network along with intervening nodes
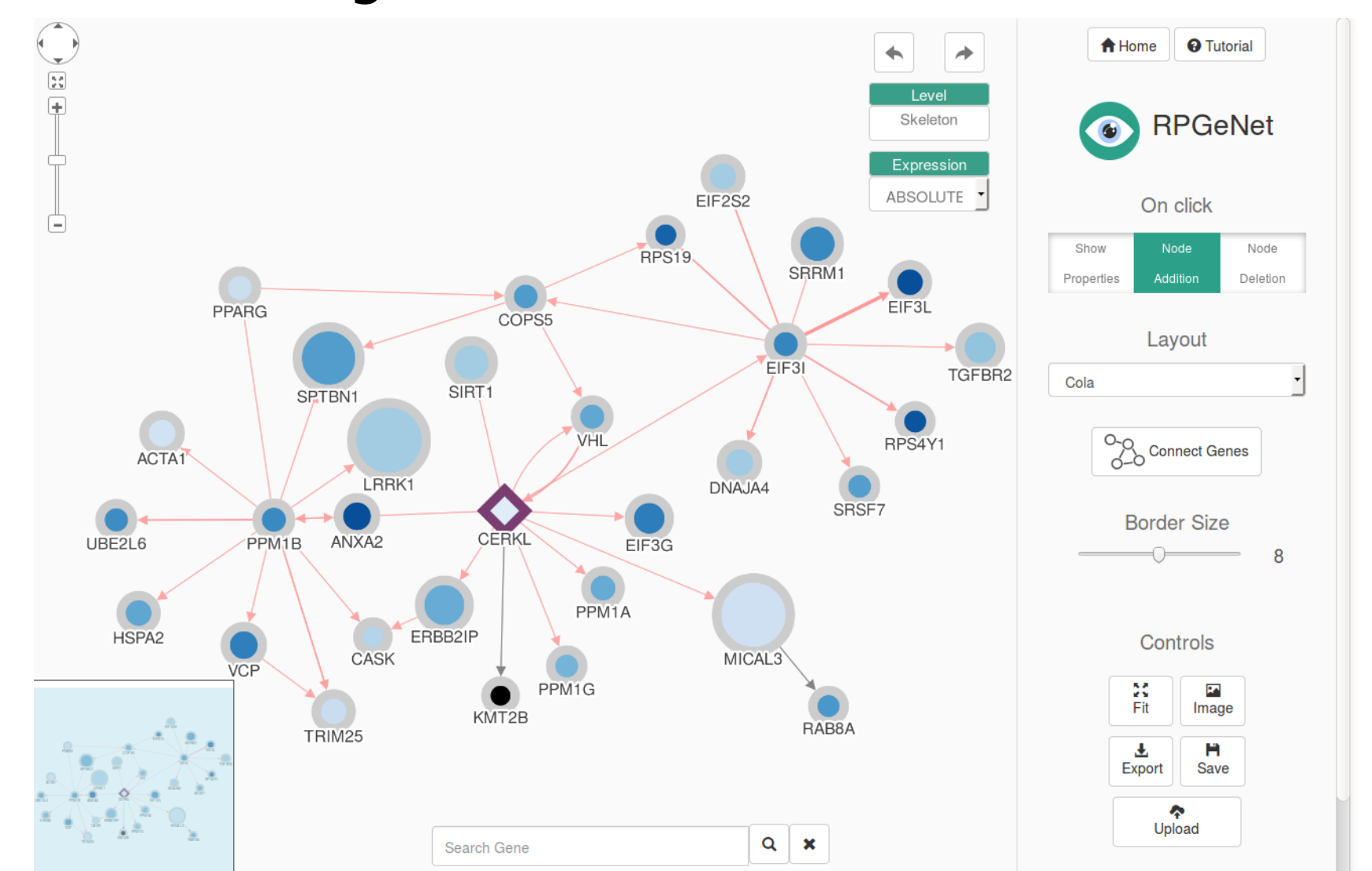
The second and third queries facilitate users to find the shortest path between two genes of interest (follows panels) or between a gene of interest outside the skeleton built upon the driver genes and an unspecified driver gene or skeleton. In both cases is a list of all the shortest pathways.
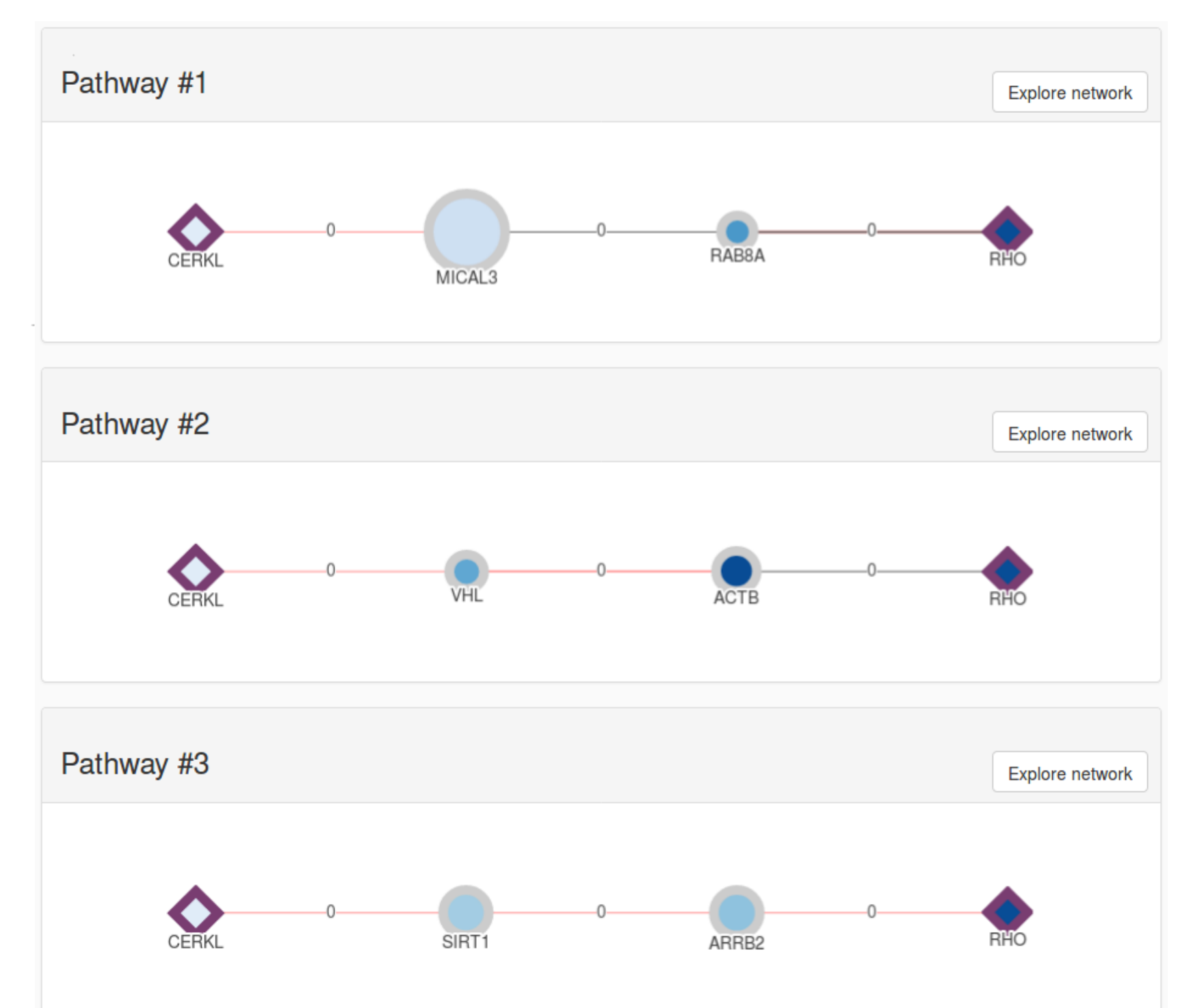
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email: rarenas.compgen@gmail.com
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