DDRnet utilises xgboost model to explore genetic interactions with and amongst DDR genes, offering a complementary approach to CRISPR screen analyses. The xgboost model identifies interactions with a target gene, such as ATM, by predicting its z-scores based on those of other genes across all screens within the DDRcs. Through a training process, the xgboost model autonomously constructs an ensemble of regression trees with a select few important genes, which are considered to interact with the target gene (e.g. ATM). DDRnet applies this procedure to all genes in the Pendragon to infer genetic interactions with DDR genes.

The DDRnet web app offers two modes of network visualization: (1) gene query and (2) cluster. In gene query mode, users select a list of genes of interest and query all the genes interacting with these input genes. Users have the flexibility to adjust the network confidence by setting frequency and importance threshold. Higher frequency and importance yield more stringent analyses but result in fewer interacting genes. Additionally, users can choose from various display options to customize the network visualisation. In cluster mode, users can explore subsets of Pendragon genes, which have been pre-clustered offline. Adjusting the frequency threshold results in display of different gene clusters. However, changing the importance threshold does not affect the cluster display.

Since we only focused on finding interactions with DDR genes in the Pendragon, DDRnet does not encompass a complete genetic network of all gene pairs. If you cannot locate your genes of interest in the networks or if they only interact with few others, it is likely that these genes were not included in our analysis. The list of genes utilised in the DDRnet can be found in the “Genes” tab.