

IO17 | Large Scale Bioinformatics for Immuno-Oncology

Signaling pathways with Omnipath - solutions

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Subgraph with nodes on interest

8. Extract the subgraph defined by vertices:

```
"IFNG", "IFNGR1", "JAK1", "JAK2", "STAT1", "EGF", "EGFR", "PIK3CA", "PTEN", "PIK3CA", "AKT1", "NFKB1"
```

Solution:

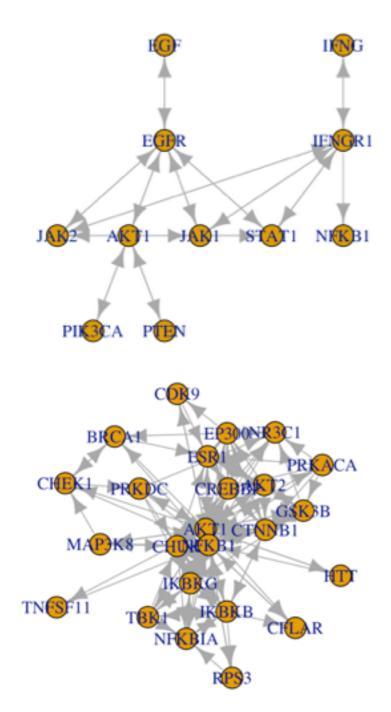
9. Find all shortest paths between AKT1 ad NFKB1 using the function all_shortest_paths

Solution:

```
op_subgraph_2<-induced_subgraph(op, unlist(sp_AKT1_NFKB1$res))
plot(op_subgraph_2)</pre>
```

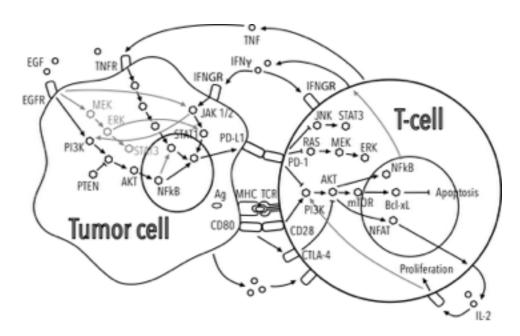
Important observations

subgraph defined by vertices:
"IFNG", "IFNGR1", "JAK1", "JAK2", "STAT1", "EGF",
"EGFR", "PIK3CA", "PTEN", "PIK3CA", "AKT1", "NFKB1"



Take-home messages:

- databases are a valuable resource for studying signaling pathways
- however... they contain all known interactions between pathways components
 - there is limited knowledge about context/cell-type specific pathways



 modeling approaches optimised fitting models to data can help to find functional interactions in specific context/cell-type

all shortest paths between AKT1 ad NFKB1