



# IO17 | Large Scale Bioinformatics for Immuno-Oncology

## Signaling pathways with Omnipath - solutions

**Francesca Finotello, Federica Eduati, and Pedro L. Fernandes**

**GTPB | The Gulbenkian Training Programme in Bioinformatics**  
Instituto Gulbenkian de Ciência, Oeiras, Portugal | Sept 19th-22nd, 2017

## 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:

```
op_subgraph <- induced_subgraph(op, V(op)[label %in% c("IFNG", "IFNGR1", "JAK1",  
                                                    "JAK2", "STAT1", "EGF", "EGFR",  
                                                    "PTEN", "AKT1", "NFKB1")])  
  
plot(op_subgraph)  
plot(op_subgraph, layout=layout_as_tree(op_subgraph, root=c(9,11)))
```

9. Find all shortest paths between AKT1 and NFKB1 using the function *all\_shortest\_paths*

### Solution:

```
sp_AKT1_NFKB1 <- all_shortest_paths(op, from=V(op)[label=="AKT1"],  
                                   to=V(op)[label=="NFKB1"])  
  
length(sp_AKT1_NFKB1$res)
```

```
## 22
```

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

