

## BoolNet Inference (E-GEOD-18494, GSE47533 and GSE41491)

### Integrated analysis of microRNA and mRNA expression and association with HIF binding in MCF-7 cells under hypoxia (GSE47533)

Camps C, Saini HK, Mole DR, Choudhry H et al. Integrated analysis of microRNA and mRNA expression and association with HIF binding reveals the complexity of microRNA expression regulation under hypoxia. Mol Cancer 2014 Feb 11;13:28. PMID: 24517586

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE47533>

### Expression profiling of hypoxic HepG2 hepatoma, U87 glioma, and MDA-MB231 breast cancer cells: time course (E-GEOD-18494)

<https://www.ebi.ac.uk/arrayexpress/experiments/E-GEOD-18494/>

### Hypoxia transcriptomic time-series data in three different cancer cell lines (GSE41491)

Tumour hypoxia exhibits a highly dynamic spatial and temporal distribution and is associated with increased malignancy and poor prognosis.

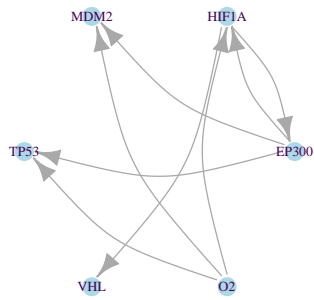
<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE41491>

Exponentially growing prostate (DU145), colon (HT29) and breast (MCF7) carcinoma cells were seeded on glass dishes in McCoy, DMEM or RPMI media, respectively with 10% FCS.

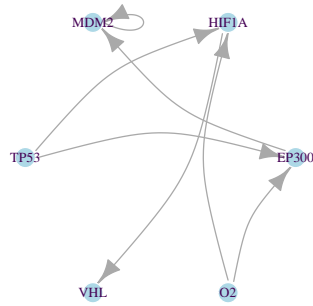
### Network inference:

```
# MDA-MB231 breast cancer - 4 time-points
par(mfrow = c(1,3))
plot(breast_MDA.1.p, vertex.label.color="#440154ff", vertex.color="lightblue", vertex.frame.color="white",
     main="MDA-MB231 breast\n 4 steps, replicate 1")
plot(breast_MDA.2.p, vertex.label.color="#440154ff", vertex.color="lightblue", vertex.frame.color="white",
     main="MDA-MB231 breast\n 4 steps, replicate 2")
plot(breast_MDA.3.p, vertex.label.color="#440154ff", vertex.color="lightblue", vertex.frame.color="white",
     main="MDA-MB231 breast\n 4 steps, replicate 3")
```

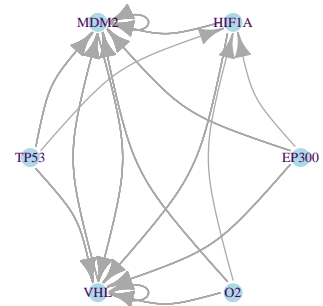
MDA-MB231 breast  
4 steps, replicate 1



MDA-MB231 breast  
4 steps, replicate 2



MDA-MB231 breast  
4 steps, replicate 3



```
# MCF7 breast cancer - 4 time-points
```

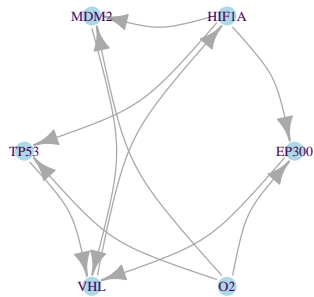
```
par(mfrow = c(1,3))
```

```
plot(breast_MCF7.1.p, vertex.label.color="#440154ff", vertex.color="lightblue", vertex.frame.color="white",  
     main="MCF7 breast\n 4 steps, replicate 1")
```

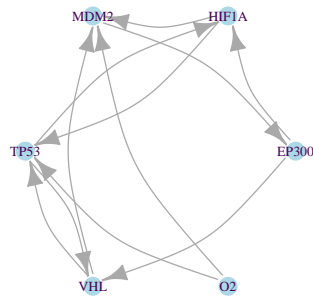
```
plot(breast_MCF7.2.p, vertex.label.color="#440154ff", vertex.color="lightblue", vertex.frame.color="white",  
     main="MCF7 breast\n 4 steps, replicate 2")
```

```
plot(breast_MCF7.3.p, vertex.label.color="#440154ff", vertex.color="lightblue", vertex.frame.color="white",  
     main="MCF7 breast\n 4 steps, replicate 3")
```

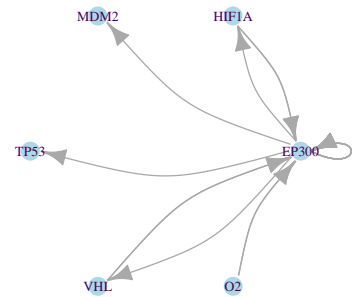
MCF7 breast  
4 steps, replicate 1



MCF7 breast  
4 steps, replicate 2



MCF7 breast  
4 steps, replicate 3



```
# MCF7 breast cancer - 8 time-points
```

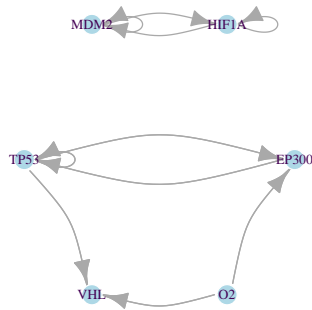
```
par(mfrow = c(1,3))
```

```
plot(breast_MCF7.p, vertex.label.color="#440154ff", vertex.color="lightblue", vertex.frame.color="white",  
     main="MCF7 breast\n 8 steps")
```

```
# all samples breast cancer merged
```

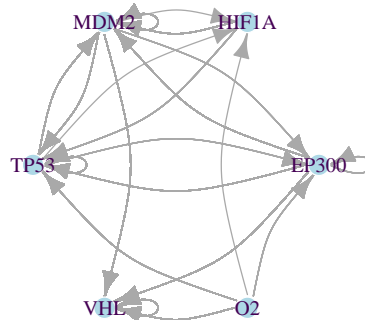
```
par(mfrow = c(1,1))
```

**MCF7 breast  
8 steps**



```
plot(all.p, vertex.label.color="#440154ff", vertex.color="lightblue", vertex.frame.color="white", layout=
      main="All breast cell-lines")
```

**All breast cell-lines**



```
HIFaxis.net <- loadNetwork("boolean_network_HIFaxis.bn")
HIFaxis.p <- plotNetworkWiring(HIFaxis.net, plotIt=F)
HIFaxis.net
```

```
## Boolean network with 6 genes
##
## Involved genes:
## EP300 HIF1A MDM2 TP53 VHL O2
##
## Transition functions:
## EP300 = (!VHL & TP53) | (VHL & !TP53)
## HIF1A = !VHL & ((!O2 & EP300 & !TP53) | (!O2 & !MDM2))
## MDM2 = TP53 & !VHL
```

```
## TP53 = !MDM2 | (!O2 & EP300 & VHL)
## VHL = HIF1A & !TP53
## O2 = 0
##
## Knocked-out and over-expressed genes:
## O2 = 0
```

```
plot(HIFaxis.p, vertex.label.color="#440154ff", vertex.color="lightblue", vertex.frame.color="white",
     main="HIF axis Network\n Theoretical")
```

