

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.

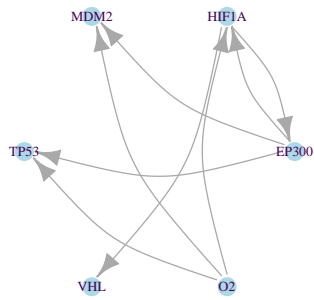
<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE41491>

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.

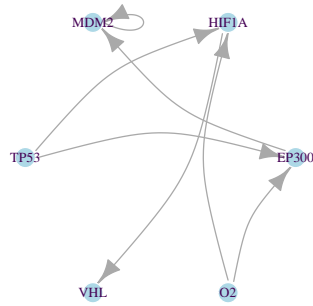
Network inference:

```
# 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")
```

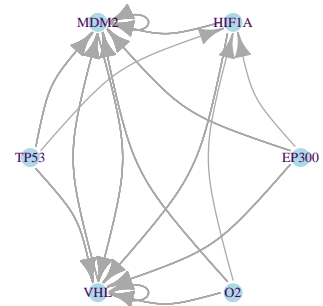
MDA-MB231 breast
4 steps, replicate 1



MDA-MB231 breast
4 steps, replicate 2



MDA-MB231 breast
4 steps, replicate 3



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

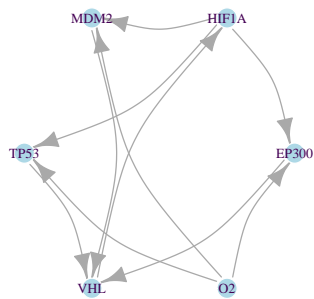
```
par(mfrow = c(1,3))
```

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

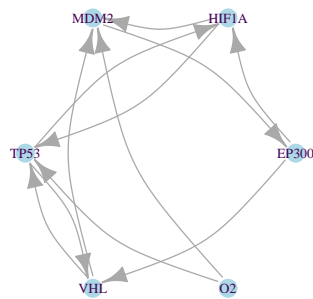
```
plot(breast_MCF7.2.p, vertex.label.color="#440154ff", vertex.color="lightblue", vertex.frame.color="white",  
     main="MCF7 breast\n 4 steps, replicate 2")
```

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

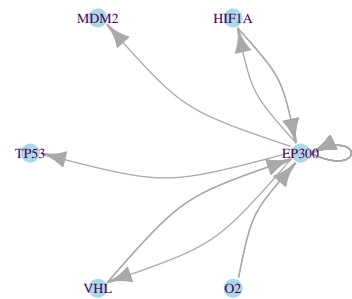
MCF7 breast
4 steps, replicate 1



MCF7 breast
4 steps, replicate 2



MCF7 breast
4 steps, replicate 3



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

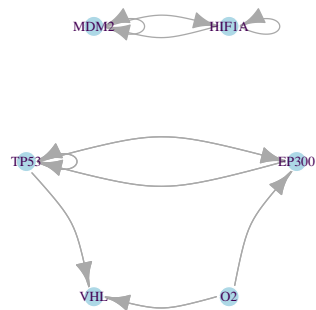
```
par(mfrow = c(1,3))
```

```
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

