

# UE Visualisation

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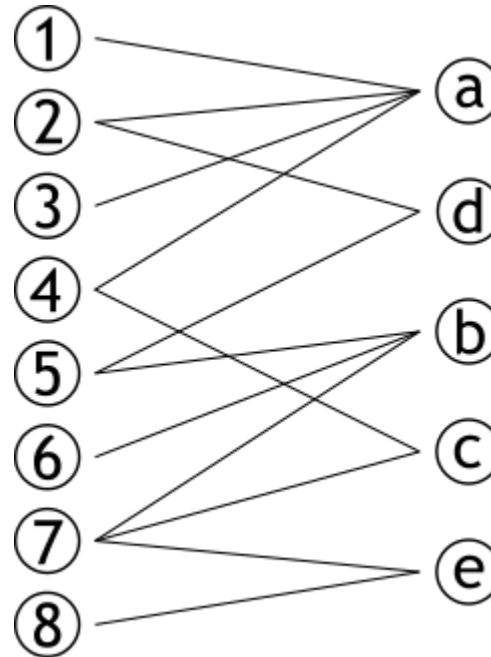
Hôpital Européen Georges Pompidou,  
Université de Paris

# Graphe bipartite

Graphe contenant deux  
sets de sommets

**complément  
déconnectés**

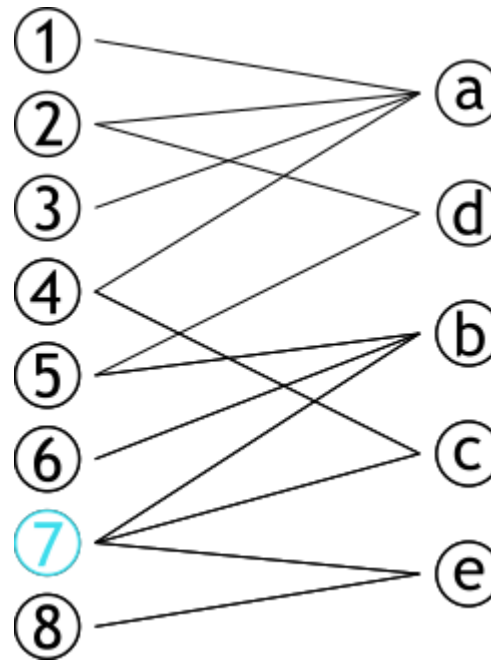
Dit aussi 2-coloriable



# Projection

Méthode permettant de créer **deux** graphes

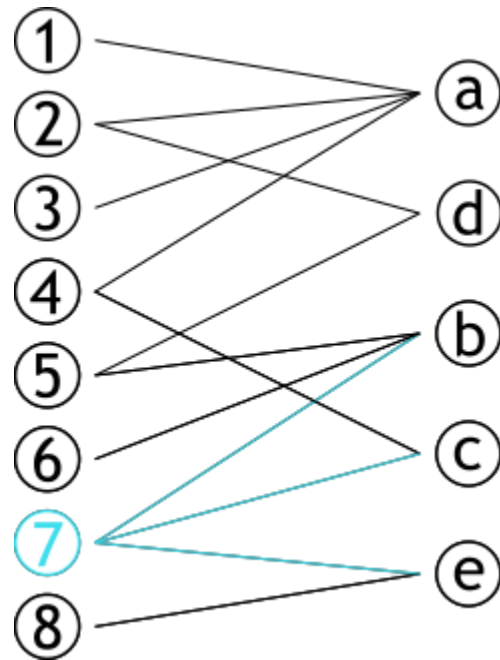
Les sommets d'une partie sont connectés s'ils partagent un sommet d'une autre partie



# Projection

Méthode permettant de créer **deux** graphes

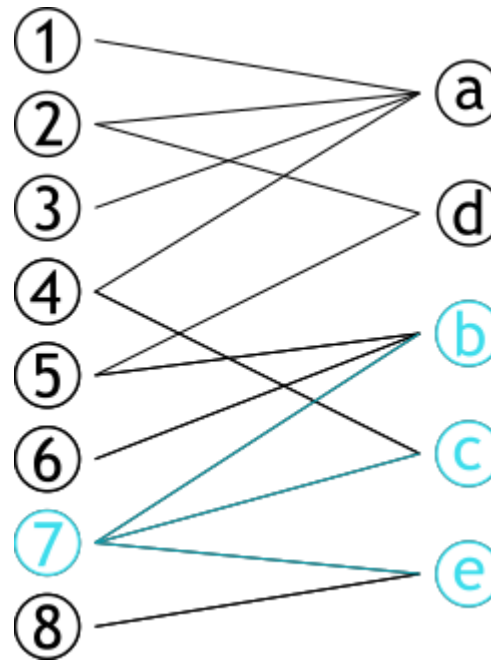
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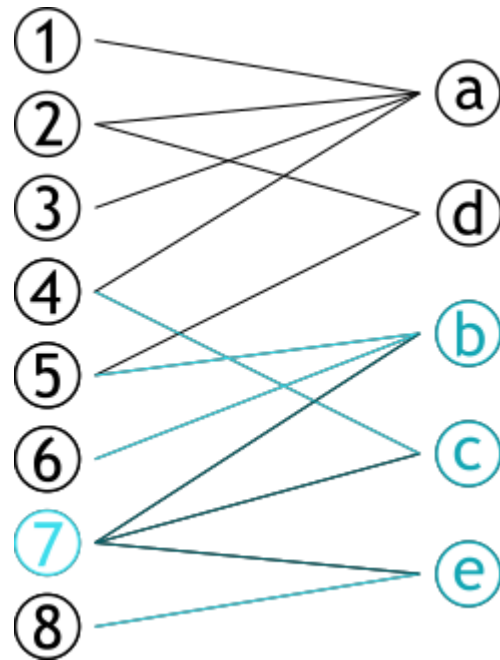
Les sommets d'une partie sont connectés s'ils partagent un sommet d'une autre partie



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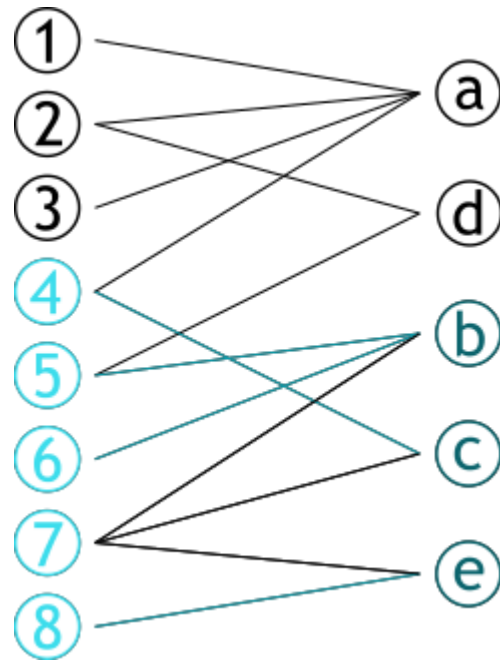
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# Projection

Méthode permettant de créer **deux** graphes

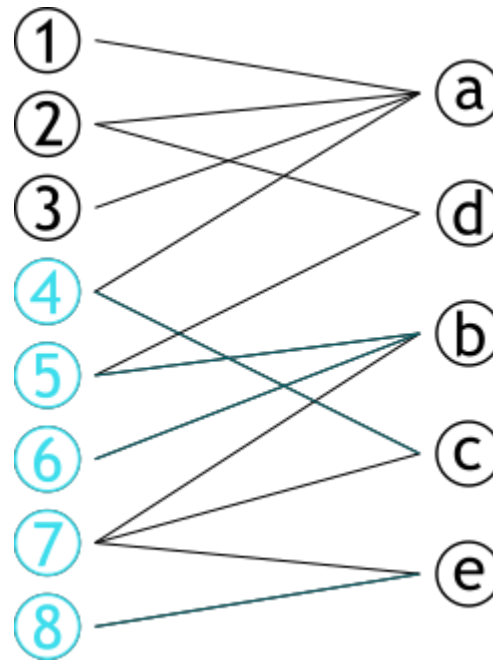
Les sommets d'une partie sont connectés s'ils partagent un sommet d'une autre partie



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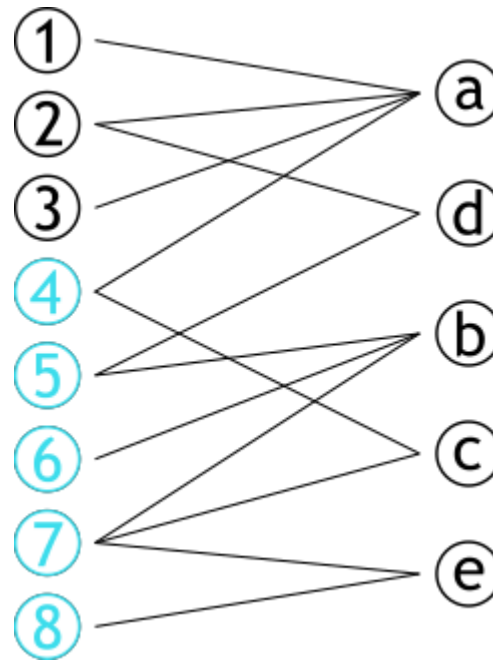




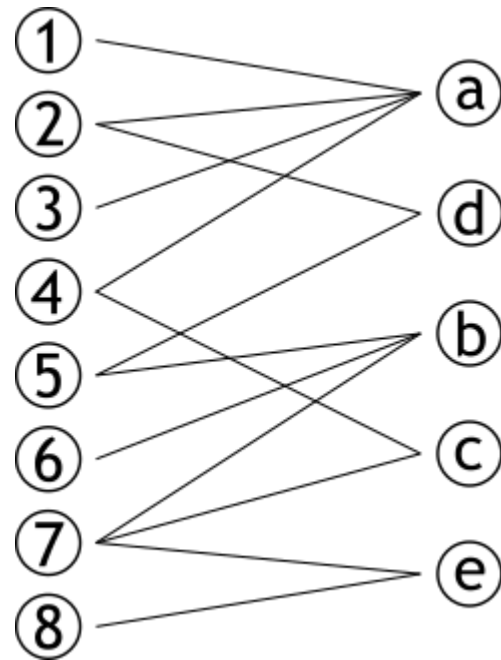
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Méthode permettant de créer **deux** graphes

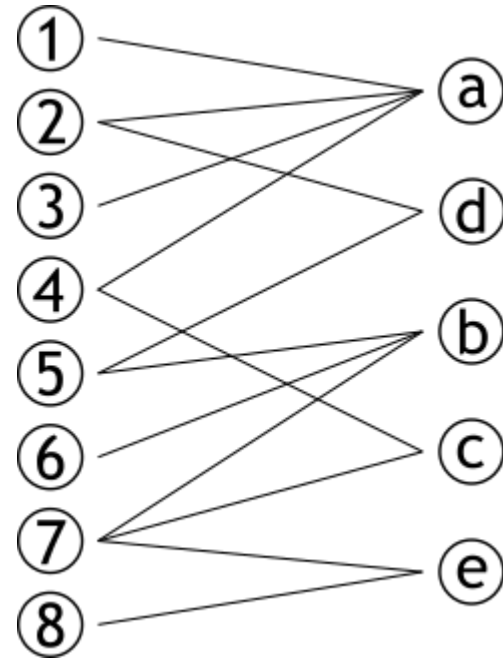
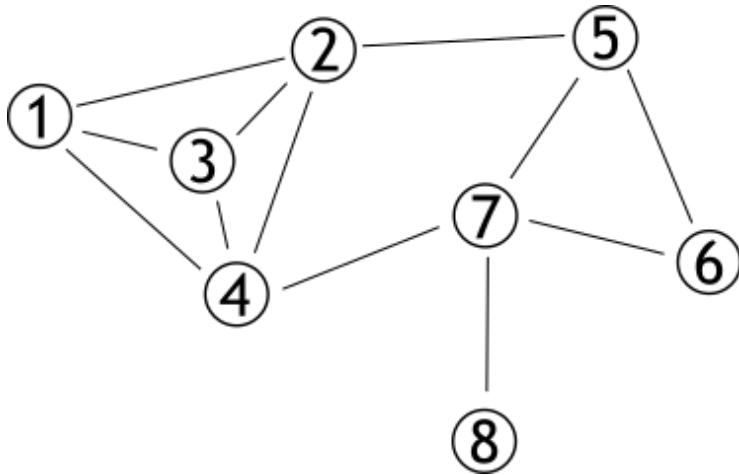
Les sommets d'une partie sont connectés s'ils partagent un sommet d'une autre partie



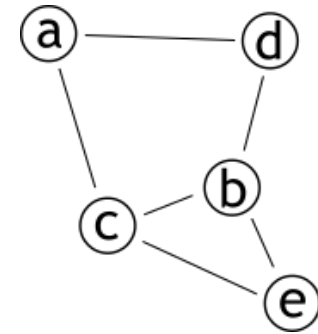
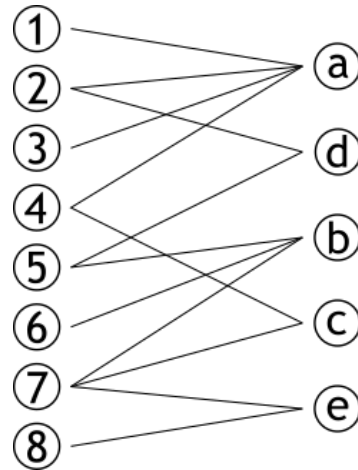
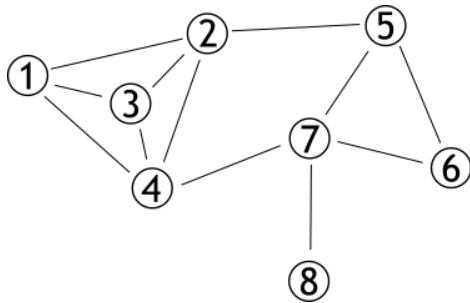
# Projection



# Projection



# Projection



# OMIM

*Online Mendelian Inheritance in Men*

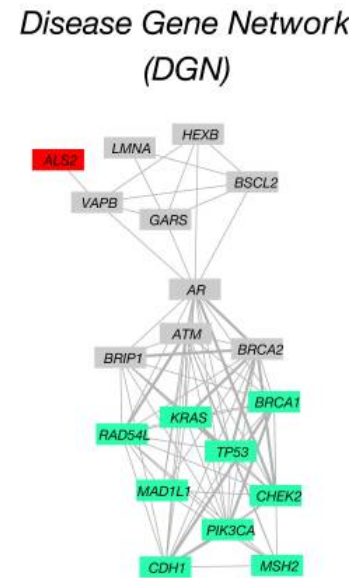
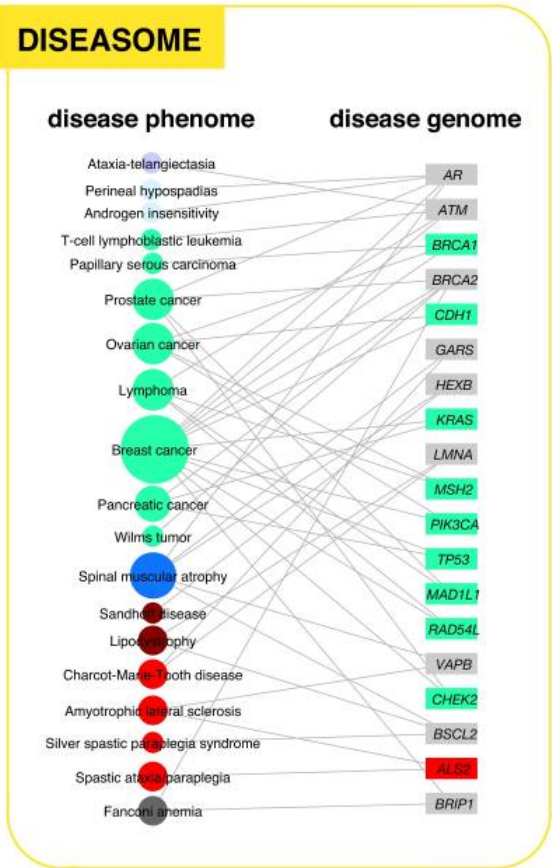
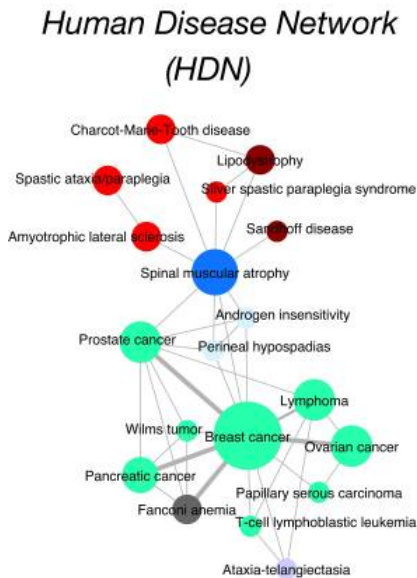
Base de données d'associations connues gène ↔ phénotype

<https://omim.org>

<https://maximewack.com/files/OMIM.csv>

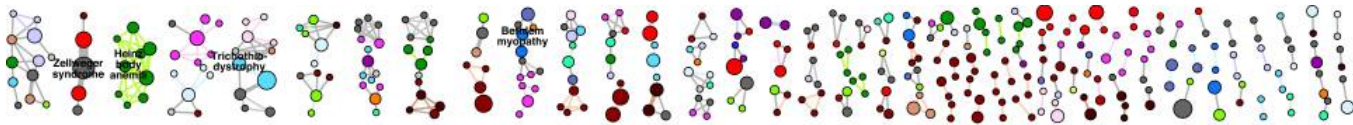
# The Human Disease Network

<https://www.ncbi.nlm.nih.gov/pubmed/17502601>

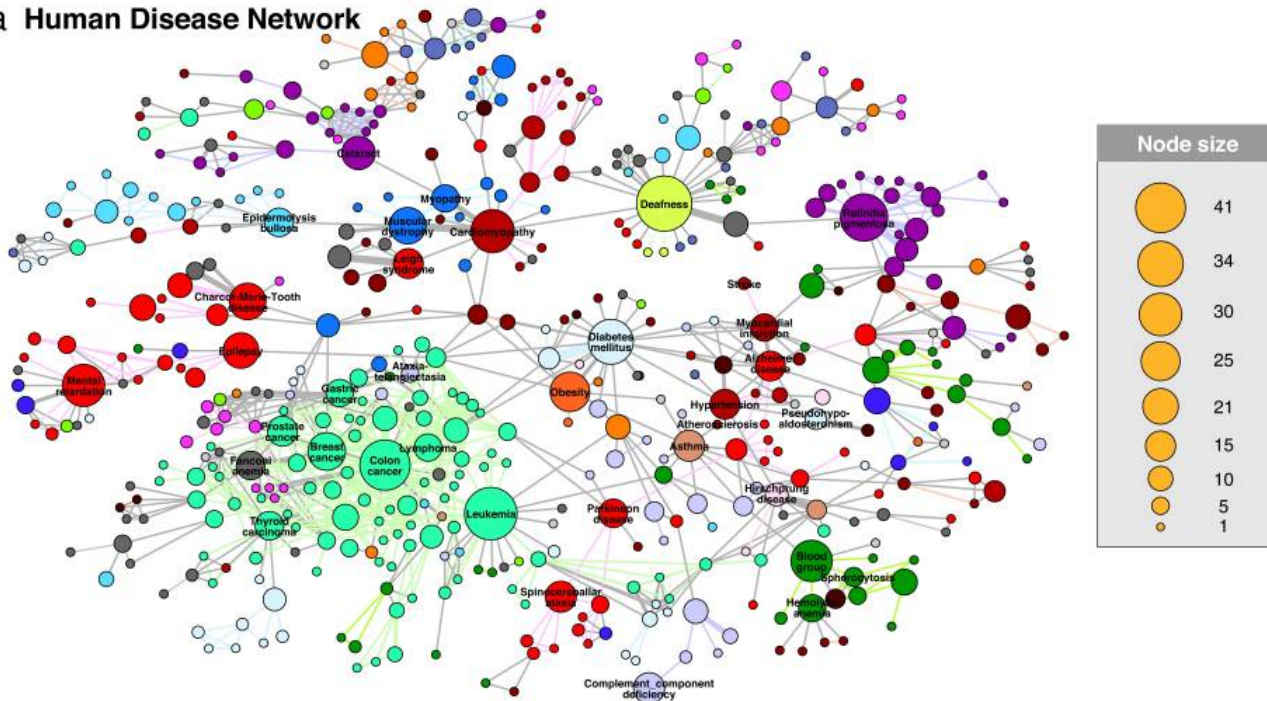


# The Human Disease Network

<https://www.ncbi.nlm.nih.gov/pubmed/17502601>



**a Human Disease Network**



# Librairies

```
library(igraph)  
library(ggraph)  
library(tidyverse)
```



igraph

# Créer des graphes

```
# Graphe sans arête
graph.empty(n = 10, directed = T)

# Graphe complètement connecté
graph.full(n = 10, directed = F, loops = F)

# Graphe en étoile
graph.star(n = 10, mode = "out")
```

# Chargement du graphe

```
read_csv("lab06_data/OMIM.csv") -> OMIM
```

Search:

| Disease  | Gene     |
|--|----------|
| ACYL-CoA DEHYDROGENASE, SHORT-CHAIN, DEFICIENCY OF | ACADS    |
| ADAMS-OLIVER SYNDROME 1                            | ARHGAP31 |
| ADAMS-OLIVER SYNDROME 2                            | DOCK6    |
| ADAMS-OLIVER SYNDROME 3                            | RBPJ     |
| ADENINE PHOSPHORIBOSYLTRANSFERASE DEFICIENCY       | APRT     |
| LUNG CANCER  | CYP2A6   |
| LUNG CANCER  | EGFR     |
| LUNG CANCER  | TNFSF6   |
| LUNG CANCER  | IRF1     |

# Chargement du graphe

```
graph.data.frame(OMIM, directed = F) -> graphe
```

```
## IGRAPH d3876e8 UN-- 6288 4234 --  
## + attr: name (v/c)  
## + edges from d3876e8 (vertex names):  
## [1] ADRENAL HYPERPLASIA, CONGENITAL, DUE TO 17-ALPHA-HYDROXYLASE DEFICIENCY  
## [2] 17-BETA-HYDROXYSTEROID DEHYDROGENASE X DEFICIENCY  
## [3] 2-METHYLBUTYRYL-CoA DEHYDROGENASE DEFICIENCY  
## [4] THREE M SYNDROME 1  
## [5] THREE M SYNDROME 2  
## [6] 3-METHYLCROTONYL-CoA CARBOXYLASE 1 DEFICIENCY  
## [7] 3-METHYLCROTONYL-CoA CARBOXYLASE 2 DEFICIENCY  
## + ... omitted several edges
```

# Informations sur le graphe

## Sommets

```
vcount (graphe)
```

```
## [1] 6288
```

## Arêtes

```
ecount (graphe)
```

```
## [1] 4234
```

# Informations sur le graphe

Dirigé ?

```
is.directed(graphe)
```

```
## [1] FALSE
```

Voisins d'un sommet

```
neighbors(graphe, V(graphe)[2019])
```

```
## + 1/6288 vertex, named, from d3876e8:
```

```
## [1] SLC25A3
```

# Projection

```
# Établir les types (gène, phénotype)
V(graphe)$type <- bipartite.mapping(graphe)$type

# Créer les projections
projs <- bipartite.projection(graphe)

# Séparer les projections en deux graphes
HDN <- projs$proj1
HGN <- projs$proj2
```

# HDN

HDN

```
## IGRAPH 58fb0bd UNW- 3512 2839 --
## + attr: name (v/c), weight (e/n)
## + edges from 58fb0bd (vertex names):
## [1] 17-BETA-HYDROXYSTEROID DEHYDROGENASE X DEFICIENCY--MENTAL RETARDATION,
## [2] 17-BETA-HYDROXYSTEROID DEHYDROGENASE X DEFICIENCY--MENTAL RETARDATION,
## [3] 3-HYDROXYACYL-CoA DEHYDROGENASE DEFICIENCY --HYPERINSULINEMIC HY
## [4] 3-METHYLGLUTACONIC ACIDURIA, TYPE III --OPTIC ATROPHY 3, AU
## [5] 46,XX SEX REVERSAL 1 --46,XY SEX REVERSAL
## + ... omitted several edges
```



# HGN

HGN

```
## IGRAPH f5f35d8 UNW- 2776 2810 --
## + attr: name (v/c), weight (e/n)
## + edges from f5f35d8 (vertex names):
## [1] AKR1C2--AKR1C4    LMNA  --MYBPC3    LMNA  --ZMPSTE24  GNAS  --SSTR5
## [5] GNAS  --AIP        GNAS  --STX16    GNAS  --GNASAS1  COL2A1--COL11A2
## [9] FGFR3 --KRAS        FGFR3 --HRAS      FGFR3 --RB1      FGFR3 --PIK3CA
## [13] FGFR3 --AKT1       FGFR3 --APC       FGFR3 --TP53     FGFR3 --NRAS
## [17] FGFR3 --FLCN      FGFR3 --MLH3     FGFR3 --ODC1     FGFR3 --CCND1
## [21] FGFR3 --PLA2G2A   FGFR3 --PTPRJ    FGFR3 --EP300    FGFR3 --BUB1B
## [25] FGFR3 --TLR2      FGFR3 --TLR4     FGFR3 --AURKA    FGFR3 --BCL10
## [29] FGFR3 --AXIN2    FGFR3 --PDGFRL   FGFR3 --KIT      FGFR3 --STK11
## + ... omitted several edges
```

# Décomposition en sous-graphes

```
HDN %>%  
  decompose -> diseases
```

# ggraph

```
graph_one <- function(graph)
{
  ggraph(graph) +
    geom_edge_diagonal() +
    geom_node_label(aes(label = name))
}
```

# Filtrer sous-graphes < 10 sommets

```
diseases %>%  
  keep(map_dbl(diseases, vcount) >= 10) %>%  
  map(graph_one) -> plots
```

# Malformations cardiaques

```
plots[[5]]
```

# Surdités

```
plots[[9]]
```

# Ostéogénèses imparfaites

```
plots[[12]]
```

# Export

```
write.graph(HDN, file = "diseases.graphml", format = "graphml")  
write.graph(HGN, file = "genes.graphml", format = "graphml")
```