Final Project (Pre-Normalization)

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```r
ch20 <- read.csv("~/Desktop/A 2020 Corn Harvest.csv", header = TRUE, quote = "\"")
cs20 <- read.csv("~/Desktop/A 2020 Corn Seeding.csv", header = TRUE, quote = "\"")
ch18 <- read.csv("~/Desktop/A 2018 Corn Harvest.csv", header = TRUE, quote = "\"")
cs18 <- read.csv("~/Desktop/A 2018 Corn Seeding.csv", header = TRUE, quote = "\"")
sh17 <- read.csv("~/Desktop/A 2017 Soybeans Harvest.csv", header = TRUE, quote = "\"")
sh19 <- read.csv("~/Desktop/A 2019 Soybeans Harvest.csv", header = TRUE, quote = "\"")
```

```r
ch20$row <- ceiling(ch20$Latitude/50)
ch20$column <- ceiling(ch20$Longitude/50)
ch20$cell <- ch20$row * 1000 + ch20$column
mch20<-aggregate(Yield~cell, data=ch20, mean)
lch20<-aggregate(Yield~cell, data=ch20, length)
merge1<-merge(mch20, lch20, by="cell")
names(merge1) <- c("cell", "YieldCH20", "CountCH20")
```

```r
cs20$row <- ceiling(cs20$Latitude/50)
cs20$column <- ceiling(cs20$Longitude/50)
cs20$cell <- cs20$row * 1000 + cs20$column
mcs20<-aggregate(AppliedRate~cell, data=cs20, mean)
lcs20<-aggregate(AppliedRate~cell, data=cs20, length)
merge2<-merge(mcs20, lcs20, by="cell")
names(merge2) <- c("cell", "AppliedRateCS20", "CountCS20")
```

```r
ch18$row <- ceiling(ch18$Latitude/50)
ch18$column <- ceiling(ch18$Longitude/50)
ch18$cell <- ch18$row * 1000 + ch18$column
mch18<-aggregate(Yield~cell, data=ch18, mean)
lch18<-aggregate(Yield~cell, data=ch18, length)
merge3<-merge(mch18, lch18, by="cell")
names(merge3) <- c("cell", "YieldCH18", "CountCH18")
```

```r
sh17$row <- ceiling(sh17$Latitude/50)
sh17$column <- ceiling(sh17$Longitude/50)
sh17$cell <- sh17$row * 1000 + sh17$column
msh17<-aggregate(Yield~cell, data=sh17, mean)
lsh17<-aggregate(Yield~cell, data=sh17, length)
merge4<-merge(msh17, lsh17, by="cell")
names(merge4) <- c("cell", "YieldSH17", "CountSH17")
```

```r
cs18$row <- ceiling(cs18$Latitude/50)
cs18$column <- ceiling(cs18$Longitude/50)
cs18$cell <- cs18$row * 1000 + cs18$column
mcs18<-aggregate(AppliedRate~cell, data=cs18, mean)
lcs18<-aggregate(AppliedRate~cell, data=cs18, length)
merge5<-merge(mcs18, lcs18, by="cell")
names(merge5) <- c("cell", "AppliedRateCS18", "CountCS18")


sh19$row <- ceiling(sh19$Latitude/50)
sh19$column <- ceiling(sh19$Longitude/50)
sh19$cell <- sh19$row * 1000 + sh19$column
msh19<-aggregate(Yield~cell, data=sh19, mean)
lsh19<-aggregate(Yield~cell, data=sh19, length)
merge6<-merge(msh19, lsh19, by="cell")
names(merge6) <- c("cell", "YieldSH19", "CountSH19")


m1 <- merge(merge1, merge2, by="cell")


m2 <- merge(merge3, merge4, by="cell")


m3 <- merge(merge5, merge6, by="cell")


mfinal <- merge(m1, m2, by="cell")


mydata <- merge(mfinal, m3, by="cell")


finaldata <- mydata[mydata$CountCH20 > 30 & mydata$CountCS20 > 30 & mydata$CountCH18 > 30 & mydata$Coun


Combined.dat <- finaldata[,c(1,2,4,6,8,10,12)]


pairs(Combined.dat)
```
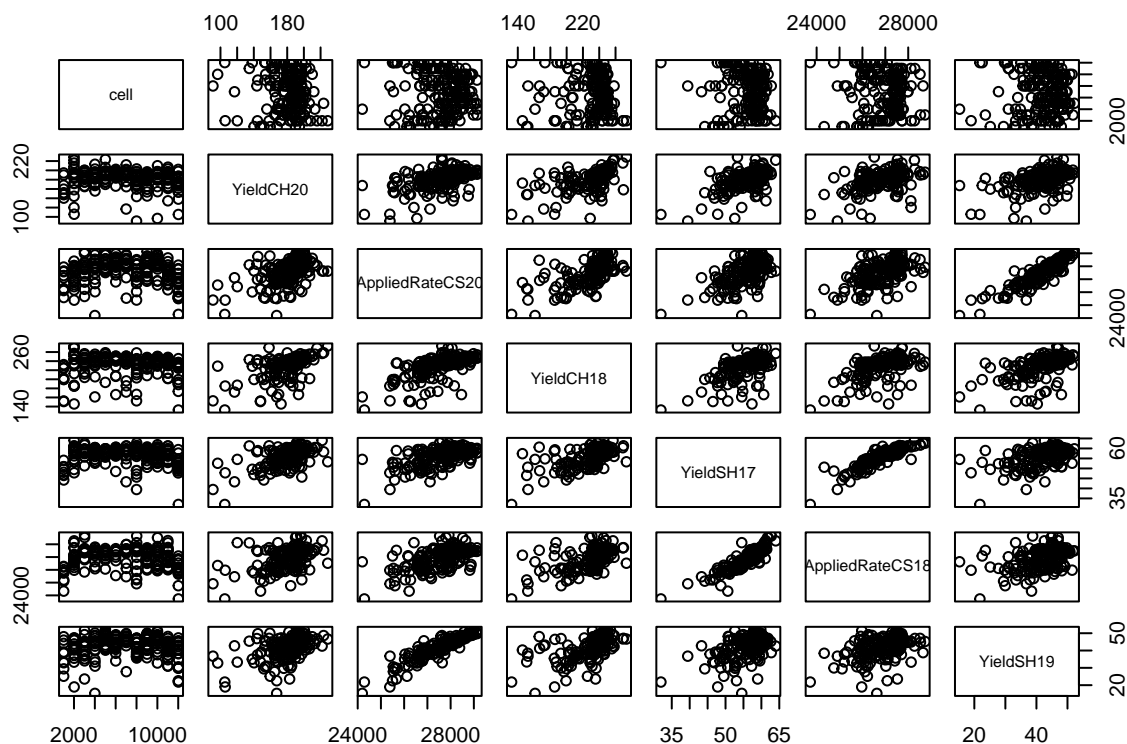
```r
if (!require("BiocManager", quietly = TRUE))
    install.packages("BiocManager")
BiocManager::install(version="3.15")
```

```
## Bioconductor version 3.15 (BiocManager 1.30.18), R 4.2.0 (2022-04-22)
```

```r
BiocManager::install("Rgraphviz")
```

```
## Bioconductor version 3.15 (BiocManager 1.30.18), R 4.2.0 (2022-04-22)
```

```
## Warning: package(s) not installed when version(s) same as current; use 'force = TRUE' to
##   re-install: 'Rgraphviz'
```

```r
library(bnlearn)
names(Combined.dat) <- c("cell", "Y20", "AR20", "Y18", "Y17", "AR18", "Y19")
modela.dag <- model2network("[Y17][AR18|Y17][Y18|AR18:Y17]")
fit1 = bn.fit(modela.dag, Combined.dat[,c('Y17','AR18','Y18')])
#fit1
strengtha <- arc.strength(modela.dag, Combined.dat[,c('Y17','AR18','Y18')])
strength.plot(modela.dag, strengtha)
```

```
## Loading required namespace: Rgraphviz
```
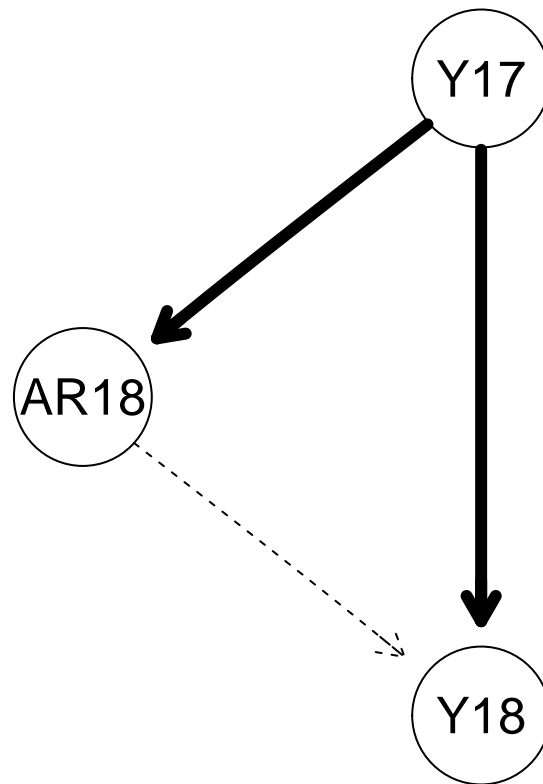
```
modelb.dag <- model2network("[Y19][AR20|Y19][Y20|AR20:Y19]")
fit2 = bn.fit(modelb.dag, Combined.dat[,c('Y19','AR20','Y20')])
#fit2
strengthb <- arc.strength(modelb.dag, Combined.dat[,c('Y19','AR20','Y20')])
strength.plot(modelb.dag, strengthb)
```
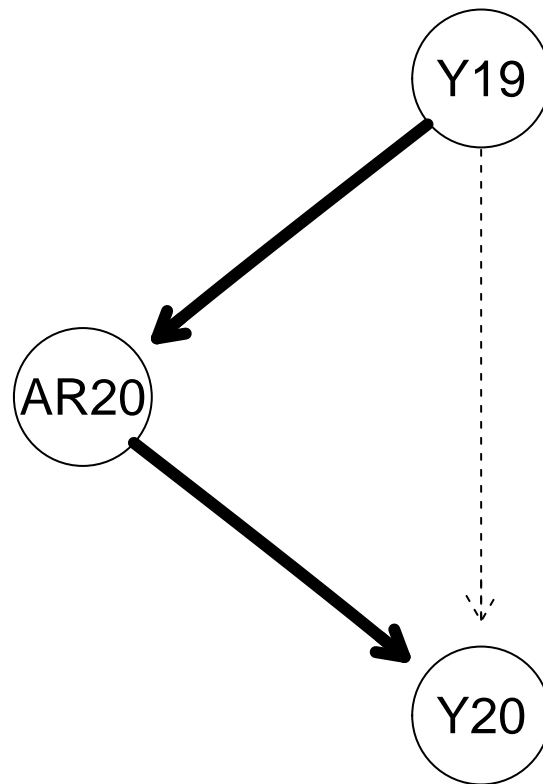
```
library(bnlearn)
model1.dag <- model2network("[Y17][AR18|Y17][Y18|AR18:Y17][Y19|Y17:AR18:Y18][AR20|Y19][Y20|AR20:Y19]")
strength1 <- arc.strength(model1.dag, Combined.dat[,c('Y17','AR18','Y18','Y19','AR20','Y20')])
strength.plot(model1.dag, strength1)
```