

Genetic Effects of a Foundation Tree on Networks of Leaf Modifying Arthropods

```
## Load datasets
pit <- read.csv('../data/acn/arth_cooc_PIT_Lau.csv')
pit[is.na(pit)] <- 0

## Should any genotypes be removed?
rm.1007 <- TRUE

## Restrict main analysis to live leaves only

### separating out "fungal" necrosis
### necrosis <- pit$fungal
pit <- pit[,colnames(pit) != 'fungal']

## Remove 1007
if (rm.1007){pit <- pit[pit[, "geno"] != "1007", ]}

## Remove mite
pit <- pit[, colnames(pit) != "mite"]

## combine pb
pb <- pit$pb.upper + pit$pb.lower + pit$pb.woody
pb.pred <- pit$pb.pred + pit$pb.woody.pred + pit$pb.hole
pb.abort <- pit$pb.abort
pit <- pit[,!(grepl('pb',colnames(pit)))]
pit <- data.frame(pit,pb.abort,pb.pred,pb)
pit <- data.frame(pit[,1:6],pit[,ncol(pit):7])
tree.info <- paste(pit[, "tree"], pit[, "geno"], pit[, "leaf.type"])
tree.arth <- pit[, 7:ncol(pit)]
tree.arth <- split(tree.arth, tree.info)
```