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> # ----- Libraries
> install.packages("igraph")
> library(igraph)
> library(ggplot2)
> # ----- Functions
> # Converts an edgelist to a graph
> edge2graph <- function(x,directed=FALSE){
+   if(dim(x)[2]<2) stop("Edgelist must have two columns")
+   el <- as.matrix(x)
+   el[,1] <- as.character(el[,1])
+   el[,2] <- as.character(el[,2])
+   return(graph.edgelist(el,directed=directed))
+ }
> # ----- Analysis
>
> data <- read.table("data/cytoscape-network.ssv", header = TRUE, stringsAsFactors = FALSE, sep = " ");
> tail(data) # DEBUG: make sure load whole file
> g$c <- edge2graph(data)
>   graph.edgelist(el, directed=FALSE)
> # Connected Components
> clusters(g$c)$no
> datasummary <- list(graph=c("Cytoscape","Gephi","igraph"),clusters=rep(0,3),graph=g_c)
> dfsummary <- data.frame()
> df$graph=datasummary$graph
> str(dfsummary)
> temp <- data.frame(degree=degree(g_c), betweenness=betweenness(g_c), closeness=closeness(g_c))
> qplot(closeness, degree, data=subset(temp,degree>1))
> qplot(degree, betweenness,data=subset(temp,degree>1), alpha=I(0.25))
> qplot(graph,clusters,data=datasummary)
> clusters(g_c)$no
> names(clusters(g_c))
>
```