Naming issues in CoExp

## What we have

We have a set of networks, ni, each network ni has a list of genes, g(ni). The original labelling of such genes, i.e. g(ni), is arbitrary including

* Ensemble genes
* Gene symbols
* Cluster id for microarray HuEx array v2.0 definition

And we have a function, fromAnyToEnsembl we can use with any g(ni) and this will return a list of ids. For each element in g(ni), it returns either the element unchanged or a possible Ensembl ID. If the element is unchanged is because it was already an Ensembl id or because that id is unknown.

## What we need

We need an API that allows, for a given set of gene symbols or Ensembl IDs, and a list of networks, {ni}.

* Find what symbols/Ensembl ids are found in each networks
* For those that are not found there: suggest other IDs that might correspond to what you need and where are they

# What can we use

We already have fromAnyToEnsembl. Capable of translating from any to Ensembl. We can start from there.

## What the GUI would be

We will design a GUI in two phases. In the initial window, the user inputs the networks he wants and the genes to be used at the analysis. When he clicks OK, it calls a new methods that reports on naming, returning a matrix of genes columns, networks in columns. TRUE/FALSE in cells.

reportOnGeneIDs = function(tissues, categories, genes)

We then display this data frame as an excel sheet we can download. We highlight those genes and networks with any false values. In this same view, we include buttons for “Proceed” and “Go Back” to proceed with the analysis anyway and to go back to edit the list of genes and try again, respectively.

As a future work, for any ID not found in a desired network, we may try to suggest alternative IDs which are equivalent to the source ID, which are in the network. This would be an alternative View, to work on a single network, and a list of problematic IDs.