Connecting PathVisio to the World

PathVisioRPC is an XMLRPC interface of PathVisio allowing access to PathVisio functions from within different programming languages.

Example: Data Visualization & Pathway statistics with PathVisioRPC

### Input
- Table with gene, protein, metabolite data; pathways; databases;

### Code
```r
# Load library
library(XMLRPC)

# Set working directory
setwd(WORK.DIR)

# Set server address
host <- paste("http://localhost:", port, sep="")

# Make pgex
xml.rpc(host,"MakePgexHandler.createPgex", inputFile, dbFile, species)
gexFile <- paste(inputFile,".pgex",sep="")

# Create Visualization
xml.rpc(host,"VisXmlHandler.createVisualization", gexFile, Gradient, Gcolors, Gvalues, Rule, Rcolors, Rexpression)

# Get results
```

### Results
- Information used to calculate the Z score for each pathway displayed.
- The pathways are ordered by Z score, beginning with highest score.
- The legend shows the colors used for the visualization.

### Use PathVisioRPC in your chosen language to:
- Create pathways with a set of significant genes, proteins, metabolites, interactions, ...
- Get a list of participating genes from a pathway
- Visualize gene, protein, metabolite, flux, ... data on pathways
- Perform pathway statistics
- Export analysis results in pdf, png, svg, html formats
- Easily incorporate PathVisio into workflows