**Pathway activity level pipeline and Pathway significance pipeline**

1. Run Kegg-kaas experiment on sample
2. Use Mozilla Firefox add-ons  “Link Gopher 1.3.3”

* open kegg result page “pathway map”
* use this filter “<http://www.kegg.jp/kegg-bin/show_pathway?@>” with link gopher to copy all green nodes per pathway. These are part of the pathway urls. Save the output in a file called All\_KGML\_URL.txt.

1. java code: extract all green node (KoNames.java)

- Read “green\_pathway” containing url of ko pathway for green nodes (green nodes are organisms specific genes)

* input file: All\_KGML\_URL.txt
* output files: koNames.txt and setKonames

- eg:

input: http://www.kegg.jp/kegg-bin/show\_pathway?@ko00073/reference%3dwhite/default%3d%23bfffbf/K13356/K13357

Output: 2 text files containing: ko00073: #green and the other, ko00073: K13356, K13357 enumerate all green nodes (Count and save all K# after green color - #bfffbf) -

Result. ko00073: 2 and ko00073: K13356, K13357

These names are used as input to the next step. eg  ko00073 becomes ko00073.xml

1. Downloaded KGML file (eg. ko00073.xml) from Kegg using wget. This is a one time operation since ko xml file do not change.

wget "http://www.kegg.jp/kegg-bin/download?entry=ko00073&format=kgml" -O ko00073.xml

**NB: Some pathway do not have an associated KGML files. eg:** [**http://www.kegg.jp/kegg-bin/download?entry=ko01210&format=kgml**](http://www.kegg.jp/kegg-bin/download?entry=ko01210&format=kgml)

**to see what the pathway looks like, browse this url** [**http://rest.kegg.jp/get/ko01212/kgml**](http://rest.kegg.jp/get/hsa01212/kgml)

1. Run KGMLPathway2Graph tool to convert pathway (KGML file) into graph of node and vertices. The ouput is a directory “Group” containing all graph

eg. The downloaded file ko00073.xml will be an input to KGMLPathway2Graph tool to download all vertices and edges in the graph.

1. Step 4 and 5 are computed through a script - /data1/blanche/Bugula/Ko/koDownload.sh - and the output (graph) is saved in a directory.

* Input is a text file containing url of all pathway: koNames.txt from step 3
* output: All downloaded kgml files in a directory (koXML) and their corresponding graph files in another directory (Group or KoGrp)

1. Significance of pathway: This is computed through python script which takes as input the directory group from step 5 and a set of green nodes - setKonames - per pathway from step 3 and output a p\_value describing the significance of the pathway.