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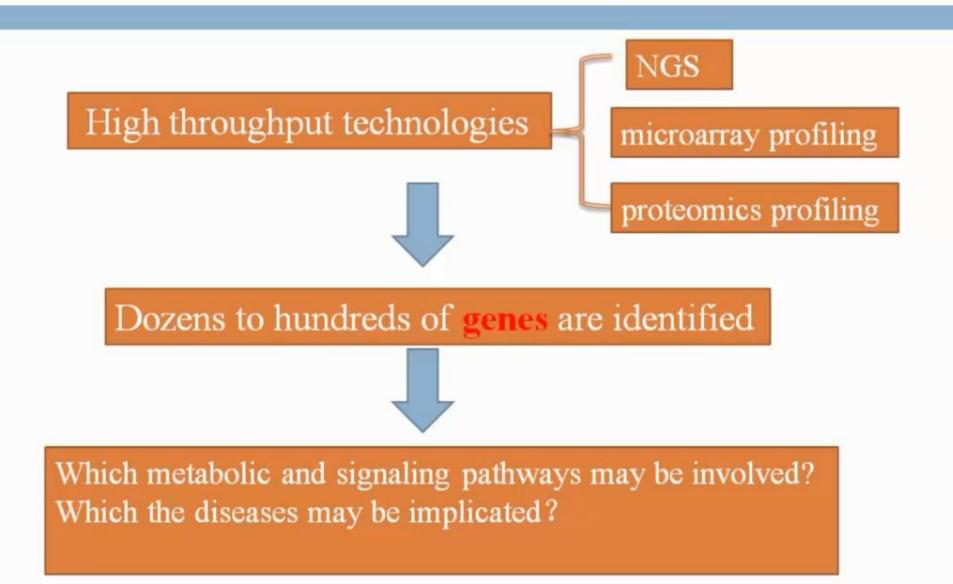
KOBAS 2.0: a web server for annotation and identification of enriched pathways and diseases

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KOBAS

(KEGG Orthology Based Annotation System)

What is the scientific question?



KOBAS 1.0

KOBAS server: a web-based platform for automated annotation and pathway identification

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- annotates an input set of genes or proteins by mapping to genes with known pathways in the KEGG PATHWAY database
- the first software to identify statistically significantly enriched pathways using a hypergeometric test.

KOBAS 2.0

Databases supported by KOBAS 2.0

Database name

Data content

KEGG PATHWAY
PID Curated Pathway
PID BioCarta Pathway
PID Reactome Pathway
BioCyc Pathway

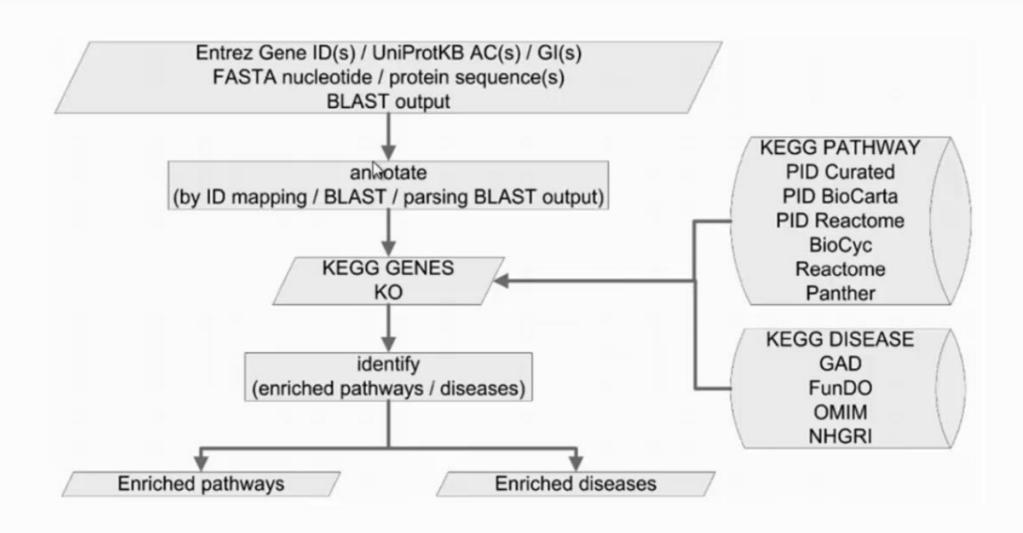
Reactome Pathway
Panther Pathway
OMIM Disease
KEGG DISEASE Disease
FunDO Disease
GAD Disease
NHGRI Disease



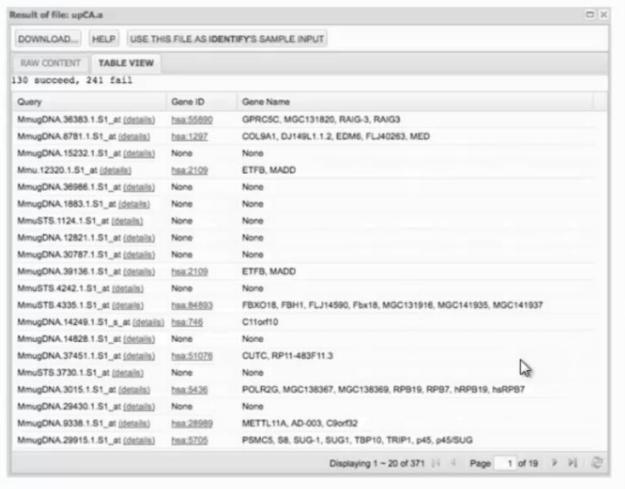
ID mapping

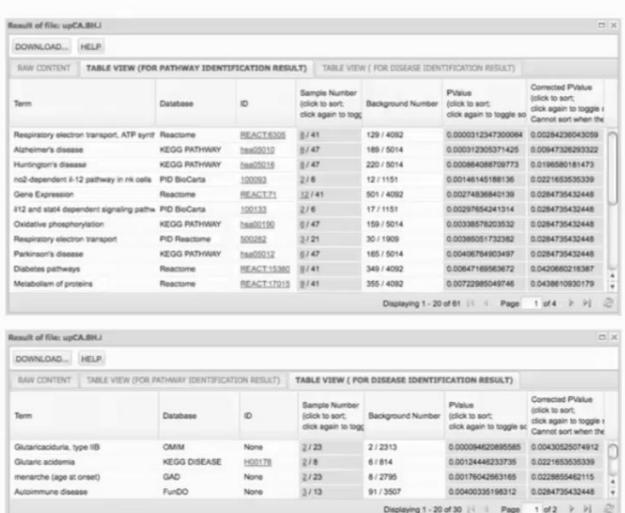
Sequence similarity mapping

The workflow of KOBAS 2.0



Application Example of KOBAS 2.0





KOBAS2.0 vs other tools

KOBAS 2.0 is more specific and informative than the lists of functional categories identified by the GO enrichment analysis tools, and offers more insights into the biological processes.

Reference

- Xie C, Mao X, Huang J, et al. KOBAS 2.0: a web server for annotation and identification of enriched pathways and diseases[J]. Nucleic acids research, 2011, 39(suppl 2): W316-W322.
- Wu J, Mao X, Cai T, et al. KOBAS server: a web-based platform for automated annotation and pathway identification[J]. Nucleic acids research, 2006, 34(suppl 2): W720-W724.
- □ http://kobas.cbi.pku.edu.cn/home.do

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