**Small tutorial of KGG for Gene-, Pathway and Protein-protein interaction-based association analysis**

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**Input data:**

1. Meta-analysis test statistics of Crohn's disease (http://www.broadinstitute.org/~jcbarret/ibd-meta/)

CrohnMetaPValueSetChr1.txt

1. Known risk gene list of Crohn's disease

CrohnCandidateGeneSet.txt

**Operations:**

1. Copy the **KGGSample** folder of the miaoxin/IBG2013/KGG/ into your folder.
2. Create a KGG project : **Project->Create Project**



1. Import original association file (load statistics or p values): **Data->Import Original Association File**



1. Load candidate genes (Susceptibility genes almost established for a disease): **Data->Define Candidate Genes**



1. Build an analysis Genome by RSID (~2min): **Data->Build Analysis Genome by RSID**



1. Gene-based association analysis by GATES (~10sec.) **Gene->Association Scan**



1. Gene-based association analysis by HYST(~10sec.) **Gene->Association Scan**



1. Export gene-based association p-values and their SNPs: **Gene->Annotation & Export**



1. View LD structure of SNPs within a gene:  **Gene->LD Plot Annotation**



1. Pathway gene set-based association analysis by HYST (~1 min.) **Module->** **Pathway gene set-based Association**





1. Protein-protein interaction-based association analysis by HYST (~1 min.) **Module->Protein interaction-based Association**

