**Course Syllabus**

**Hands on: Pathway Analysis**

**Time:** Monday, Apr 4th, 11:45 am -1:15 pm

**Place:** Virtual

**Course Teaching Faculty:**

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**Course Description:**

The course consists of a about 20-30 mins lecture, discussions, and follow up computer exercises. Topics to be covered will include 3 major tools used for the pathway analysis (GSEA, DAVID, and IPA) with the gene expression data generated from NGS platform.

**Student Learning Objectives/Outcomes:**

Students are expected to understand the basic knowledge of each tool, including data input, parameter settings, expected output and output annotations, as well as the statistical methods that each tool applied. After the course, students need to know the pros and cons of each tool and select the right tool for their specific research purposes.

**Prerequisite for the hands-on training:**

1): Gene Set Enrichment Analysis (GSEA)

Register for GSEA with a email address: <http://www.gsea-msigdb.org/gsea/login.jsp>

After registering, download and install corresponding GSEA based on the platform used: <http://www.gsea-msigdb.org/gsea/downloads.jsp>

Read the original publication of GSEA: <https://www.pnas.org/doi/10.1073/pnas.0506580102>

Optional: read the user guide of GSEA:

<https://www.gsea-msigdb.org/gsea/doc/GSEAUserGuideFrame.html>

2): GenePattern for data preprocess

Create a free account: https://cloud.genepattern.org/gp/pages/login.jsf

3): The Database for Annotation, Visualization and Integrated Discovery (DAVID)

Optional: read the tutorial: <https://david.ncifcrf.gov/helps/tutorial.pdf>

4): QIAGEN Ingenuity Pathway Analysis (QIAGEN IPA)

Optional: request a 2-week trail account

<https://qiagen.pathfactory.com/trial_request/?cmpid=CM_QDI_DISC_IPA-InTRIAL-Resource_0721_website_QDI_IPA&utm_source=IPAWebPage>

The trail only last for 2 weeks, so make sure only request and download the trail version of IPA after 3/21/2022.

Recommended content:

<https://qiagen.pathfactory.com/l/ipa-in-trial-nurture-2/?cmpid=CM_QDI_DISC_IPA-InTRIAL-Resource_0321_website_QDI_IPA>

5): Source data used for hands on training

The data are from the The Cancer Genome Atlas (TCGA) project and comprise the RNA-seq counts from 5 breast cancer patients and 5 healthy individuals.

https://raw.githubusercontent.com/sheffield-bioinformatics-core/rna-seq-in-galaxy/gh-pages/tcga\_raw\_counts.csv

All course related documents, including source data and processed data and results, can be downloaded from https://github.com/yliuphys/Pathway-analysis-hands-on-training-2022-spring