

LAB 6 :

Visualization and analysis of functional gene networks using Cytoscape



Data used in the network

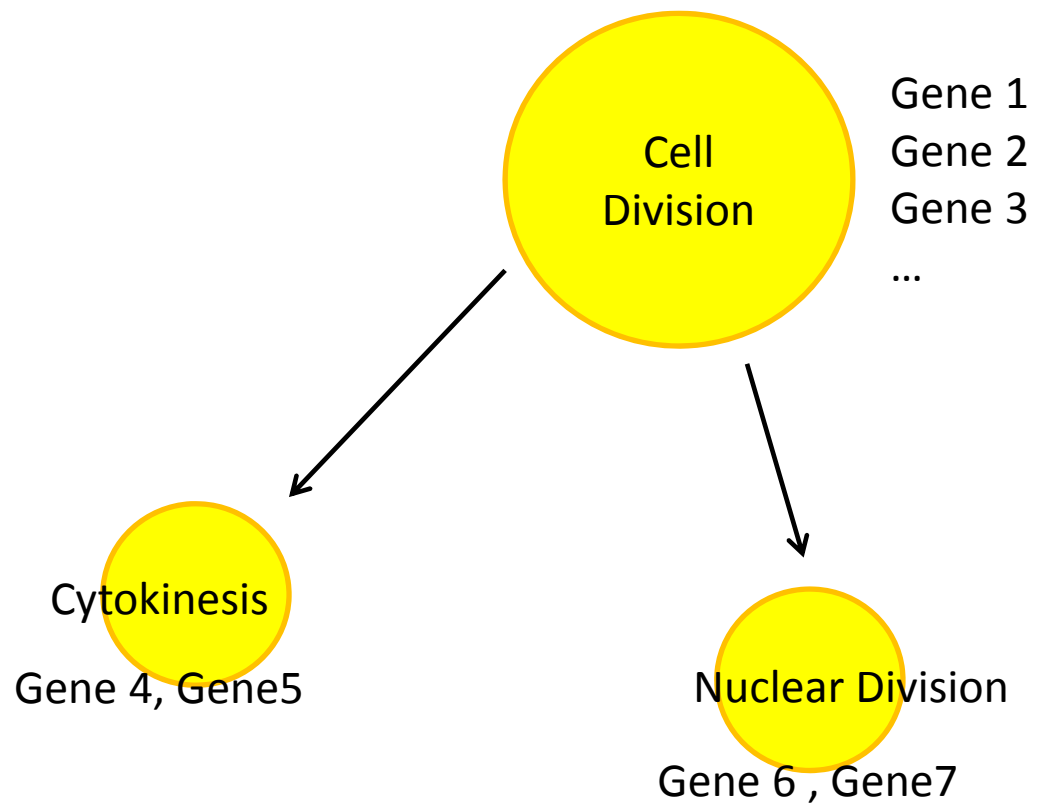
Samples are from 3 Breast cancer patients and 3 normal .

Breast cancer patients have specific type of cancer : Triple Negative Breast Cancer

Data downloaded from : Gene Expression Omnibus (GEO) → A whole collection of various expression data

Gene Ontology : Provides Hierarchy Structured annotation of genes. Described in 3 domains

- Molecular Function
- Cellular Component
- **Biological Process**



Report

Assignment : Draw given Network with Cytoscape on your own.

Things to include

1. Date of the experiment and the day (Tue, Wed, Thur, Fri)
2. Results with “figures of your own” (**1 network file with gradient color, 1 with BINGO output**)
3. Discussion
4. References

Discussion should include :

What the network visualization tells you.

- What information does the network give you? What can you tell from the expression data and function enrichment analysis using Bingo? → No correct answer for this. Just write what you think

Other type of visualization may give you additional points. If you have made modifications, describe what you have done in the report

Data to draw the network can be found in : www.netbiolab.org → teaching
Find Cytoscape at : www.cytoscape.org

Due date : 2014 . 04 . 30

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Installing JAVA














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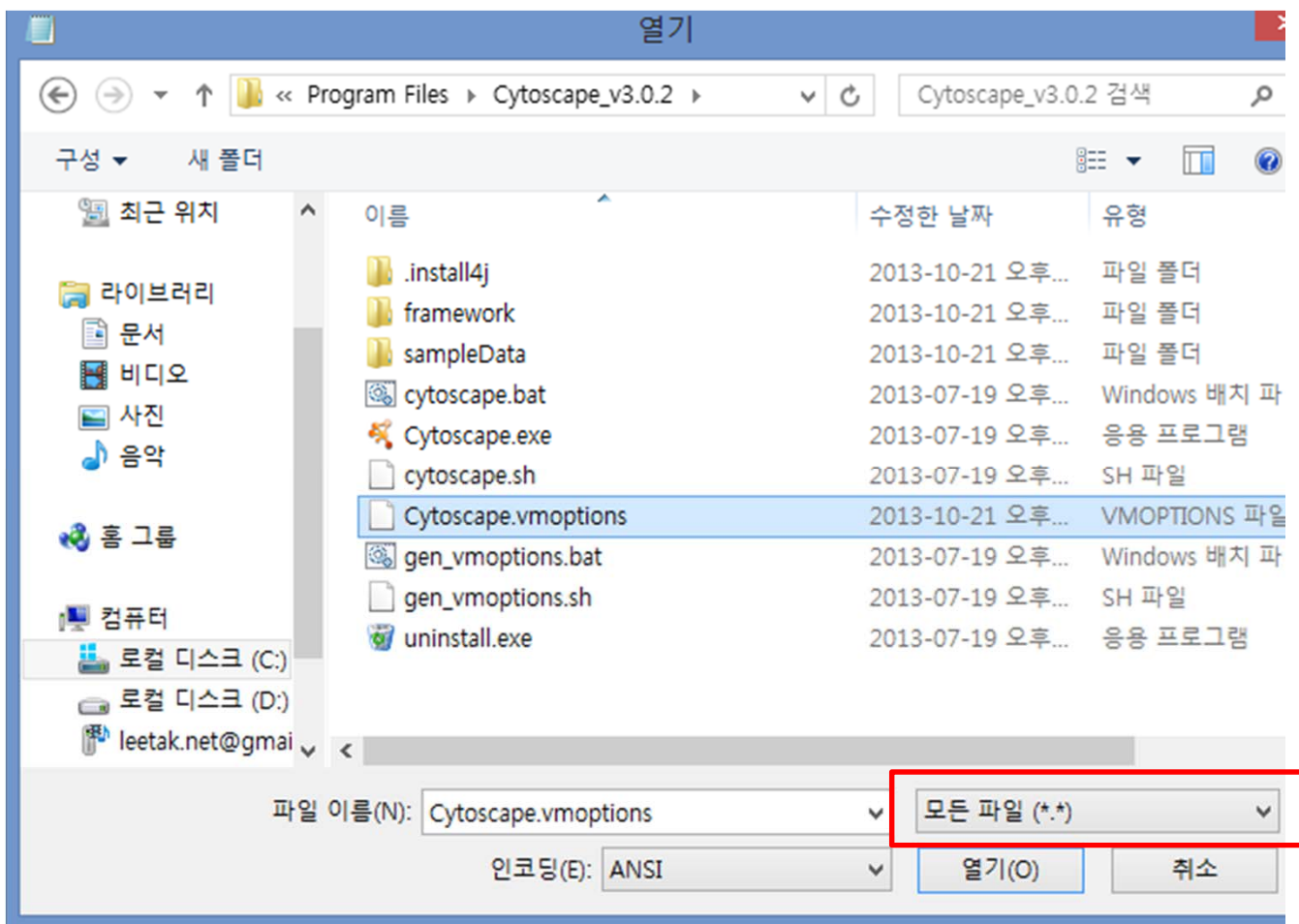
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자바 충돌 문제 해결

메모장을 “관리자 권한”으로 실행

파일 → 열기 → cytoscape 파일 → Cytoscape_vmoptions 파일을 열기



모든 파일 선택

자바 충돌 문제 해결

메모장을 “관리자 권한”으로 실행

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-Xmx1250m 을 -Xmx512m으로 수정하여 저장

내용 보강

Using BiNGO

Using the file to install BINGO and running it.

1. Apps → App manager → install from file (lower left) → Select “BiNGO jar”

2. Running BiNGO

Apps → BiNGO

Select ontology file : → custom : “ file : gene_ontology_ext.obo”

Select namespace → ---

Select organism/annotation → custom “ file : GOBP.BiNGO.txt”

Then start BiNGO, Be sure to select genes for analysis