

Systems Biology Exercise

1. Log in to G-DOC (<https://gdoc.georgetown.edu>) and go to Studies.

Welcome back, your last login was Mon Jan 30, 2017. You can check if you have been granted access to new lists or analyses since your last login.

Welcome! The G-DOC Plus Launch Pad is your one-stop resource for learning more about G-DOC and getting started on the platform.

Studies, Lists, Analyses, Groups, Notifications, Help me pick a study

2. Select the study "CRC_Madhavan_2013_1."

Study ID	Sample Size	Description	Public Data Source	Disease	Investigator(s)	Public Data Source
CRC_BROSENG_2010_01	161	Candidate driver genes in focal chromosomal aberrations of stage II colon cancer	Public Data Source	COLON CANCER	PATIENT	Public Data Source
CRC_GALAMB_2010_01	165	Inflammation, adenoma and cancer: objective classification of colon biopsy specimens with gene expression signature	Public Data Source	COLON CANCER	PATIENT	Public Data Source
CRC_K_FORD_2007_01	200	Phase II exploratory pharmacogenomics study of cetuximab monotherapy in patients with advanced metastatic CRC	Public Data Source	COLON CANCER	PATIENT	Public Data Source
CRC_MADHAVAN_2013_01	280	Lombardi Induced Colorectal Cancer data	Louis Weiner, MD Stephen Byers, PhD John Marshall, MD	COLON CANCER	PATIENT	Michael Hains

3. Select the study by clicking on "Select Study."

Studies

CRC_MADHAVAN_2013_01 Details

Select Study

Study Name: CRC_MADHAVAN_2013_01 (id 280)
Study Abstract: Lombardi Induced Colorectal Cancer data
Principal Investigator(s): John Marshall, MD
Louis Weiner, MD
Stephen Byers, PhD
Disease: COLON CANCER
Point(s) of Contact: Michael Hains
Data Type Details: CLINIC | MICROARRAY | METABOLOMICS | COPY_NUMBER | MICRORNA

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SYSTEM REQUIREMENTS | CITATION POLICY | PUBLICATIONS USING G-DOC | DATA ACCESS POLICY | LICENSE INFO | CONTACT US | G-DOC 8 TEAM
Georgetown Lombardi Comprehensive Cancer Center
Georgetown University
Georgetown MEDICAL CENTER

4. From the Search menu, select "Explore clinical data and create groups."

Study Selected!

You have picked the study: CRC_MADHAVAN_2013_01*

Change my study | Help me pick another study

*Lambert Induced Colorectal Cancer data

Based upon the study you picked, here is a list of tools you can use:

Search <ul style="list-style-type: none"> • Genome Browser • Compound/Drug Targets • Findings • Explore Clinical Data and Create Groups • Gene Expression Data 	Analyze <ul style="list-style-type: none"> • Group Comparison • Chromosomal Instability Index • KM Clinical Plot • KM Gene Expression Plots • Classification • HeatMap Viewer
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Explore Clinical Data and Create Groups

Current Study: CRC_MADHAVAN_2013_01

Subject Search

Current Split Attribute: Recurrence/Relapse

Recurrence/Relapse	All Subjects
YES	20
NO	20
Total	40

Explore Clinical Data and Create Groups

Current Study: CRC_MADHAVAN_2013_01

Subject Search

Current Split Attribute: Recurrence/Relapse

Recurrence/Relapse	All Subjects
YES	<input type="checkbox"/> New Detailed Report <input checked="" type="checkbox"/> Save IDs as List
NO	<input type="checkbox"/> New Detailed Report <input checked="" type="checkbox"/> Save IDs as List
Total	<input type="checkbox"/> New Detailed Report <input checked="" type="checkbox"/> Save IDs as List

5. Select the Current Split Attribute "Recurrence/Relapse."

6. Click on the number in the table and select "Save IDs as a List" for 2 groups: "relapse yes" and "relapse no."

7. Save two lists of IDs with names:
CRC_rel_yes and CRC_rel_no.

8. Select "Compare Groups" from the main menu on the top of the page.

9. Select parameters for the Group Comparison T-test for two saved groups: CRC_rel_yes and CRC_rel_no. Choose gene expression as the data type and click "Submit Analysis."

10. When the analysis is complete, click on "Group Comparison" to view results.

11. Save complete Gene List from table by selecting all the rows and typing in a name for the list.

12. Open the Gene Ontology website in a new window (<http://geneontology.org/page/go-enrichment-analysis>). Then copy and paste the gene names from the list exported from G-DOC to the text entry window on the left of the page.

13. Find saved gene list under Lists option in the main menu. Export it, and download it to your local computer as a .txt file. Then open it.

14. Save the gene list and then open this .txt file on your local computer.

15. Open the Gene List on your local computer and copy the gene names on the clipboard.

16. Paste your gene list from your clipboard to the Gene Ontology webpage, and click on "submit" to run GO Enrichment Analysis.

17. Wait until the analysis is complete and results are displayed (in PANTHER). Explore the results of GO enrichment analysis in PANTHER. Locate the table on the bottom of the webpage with a list of enriched biological processes. Sort the table by the column number (number of overlapping genes from your list). Click one on label number to sort in descending order.

PANTHER
Classification System

Now includes comprehensive GO annotations directly imported from the GO database

Analysis Summary: Please report in publication [\(?\)](#)

Analysis Type: PANTHER Overrepresentation Test (release 20160715)	
Annotation Version and Release Date: GO Ontology database Released 2017-01-26	
Analyzed List:	upload_1 (Homo sapiens) Change
Reference List:	Homo sapiens (all genes in database) Change
Annotation Data Set: GO biological process complete ▾	
<input checked="" type="checkbox"/> Use the Bonferroni correction for multiple testing (?)	

Results [\(?\)](#)

Mapped IDs:	Reference list 20972 out of 20972	upload_1 57 out of 59
Unmapped IDs:	0	5
Multiple mapping information:	0	2

Bonferroni count: 8204

[Export results](#)

Displaying only results with P<0.05; [click here to display all results](#)

GO biological process complete	Homo sapiens (REF) #	upload_1 (▼ Hierarchy) NEW! (?) # expected Fold Enrichment +/- P-value
positive regulation of cAMP-mediated signaling	12	3 .03 88.86 + 4.88E-02
cytokine-mediated signaling pathway	466	10 1.31 7.63 + 5.59E-03
↳ response to cytokine	727	11 2.05 5.38 + 4.27E-02
positive regulation of immune system process	954	13 2.68 4.84 + 1.65E-02
↳ regulation of immune system process	1392	15 3.92 3.83 + 4.22E-02
Unclassified	3763	6 10.59 .57 - 0.00E00

Analyzed List: upload_1 (Homo sapiens) [Change](#)

Reference List: Homo sapiens (all genes in database) [Change](#)

Annotation Data Set: [GO biological process complete](#) ▾

Use the Bonferroni correction for multiple testing [\(?\)](#)

Results [\(?\)](#)

Mapped IDs:	Reference list 20972 out of 20972	upload_1 57 out of 59
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Multiple mapping information:	0	2

Bonferroni count: 8204

[Export results](#)

Displaying only results with P<0.05; [click here to display all results](#)

GO biological process complete	Homo sapiens (REF) #	upload_1 (Hierarchy) NEW! (?) ▼ # expected Fold Enrichment +/- P-value
regulation of immune system process	1392	15 3.92 3.83 + 4.22E-02
positive regulation of immune system process	954	13 2.68 4.84 + 1.65E-02
response to cytokine	727	11 2.05 5.38 + 4.27E-02
cytokine-mediated signaling pathway	466	10 1.31 7.63 + 5.59E-03
Unclassified	3763	6 10.59 .57 - 0.00E00
positive regulation of cAMP-mediated signaling	12	3 .03 88.86 + 4.88E-02

[amigo.geneontology.org/amigo/term/GO:0002682](#)

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Quick search

Search

19. Click on the names of the biological processes to learn more about them.

