



icbi

THE INNOVATION CENTER FOR BIOMEDICAL INFORMATICS

G-DOC *Plus* demo

Translational research use case

using the Rembrandt dataset

Innovation Center for Biomedical Informatics
Georgetown University Medical Center

Case study


- Perform multi-omics analysis
- Example query:

*Compared patients with **Astrocytoma (low grade glioma)** with those with **Glioblastoma (GBM, high grade glioma)** in the NCI REMBRANDT study.*

Overview

- Register
- Login
- Navigation
- How to create patient groups
- Group comparison using gene expression data
- Group comparison using copy number data
- Clinical KM plot

G-DOC Plus front page



Welcome to GDOC Plus Beta!

The Georgetown Database of Cancer Plus other diseases (G-DOC Plus) is a precision medicine platform containing molecular and clinical data from thousands of patients and cell lines, along with tools for analysis and data visualization. The platform enables the integrative analysis of multiple data types to understand disease.

Precision Medicine

Translational research

Population genetics

Understanding Data in G-DOC Plus

It all begins with a study...

All data in G-DOC Plus derives from studies on topics such as breast cancer, wound healing, or even 1,000 Genomes. Each study may contain clinical and/or biospecimen data. Below is an overview of studies by topic.

* private studies, ones which are uploaded and marked private, are not counted here

dementia	pediatric cancers	breast cancer	colon cancer	lung cancer
studies: 1 patients: 30 biospecimen: 30	studies: 5 patients: 256 biospecimen: 256	studies: 28 patients: 3742 biospecimen: 4566	studies: 11 patients: 1064 biospecimen: 1727	studies: 1 patients: 478 biospecimen: 443
muscular dystrophy	liver cancer	cell_line_collectio	ovarian cancer	prostate cancer
studies: 1 patients: 36 biospecimen: 36	studies: 3 patients: 280 biospecimen: 468	studies: 1 patients: 0 biospecimen: 107	studies: 1 patients: 283 biospecimen: 564	studies: 1 patients: 218 biospecimen: 538
pancreatic cancer	brain cancer	stomach cancer	other	wound healing
studies: 1 patients: 52 biospecimen: 51	studies: 1 patients: 671 biospecimen: 804	studies: 1 patients: 197 biospecimen: 165	studies: 1 patients: 2816 biospecimen: 1092	studies: 2 patients: 87 biospecimen: 84
total				
studies: 59 patients: 10210 biospecimen: 10931				

News

GUMC News: Triple Negative Breast Cancer in African-American Women has Distinct Difference - 4/22/2015 [\[read\]](#)

Amarantus Options Blood-based Alzheimer's Biomarkers from Georgetown - 1/15/2015 [\[read\]](#)

iPAD Application Makes Boring Data Collection History - 12/3/2012 [\[read\]](#)

Biomedical Computational Review: Personalized Cancer Treatment - Seeking Cures Through Computation - 1/2/2012 [\[read\]](#)

OncoLive: Georgetown Lombardi Comprehensive Cancer Center: Innovation Steps Towards Individualized Treatment - 9/1/2011 [\[read\]](#)

Can get info on:

- Disease types
- Total number of studies for each disease type

First time user ? Register



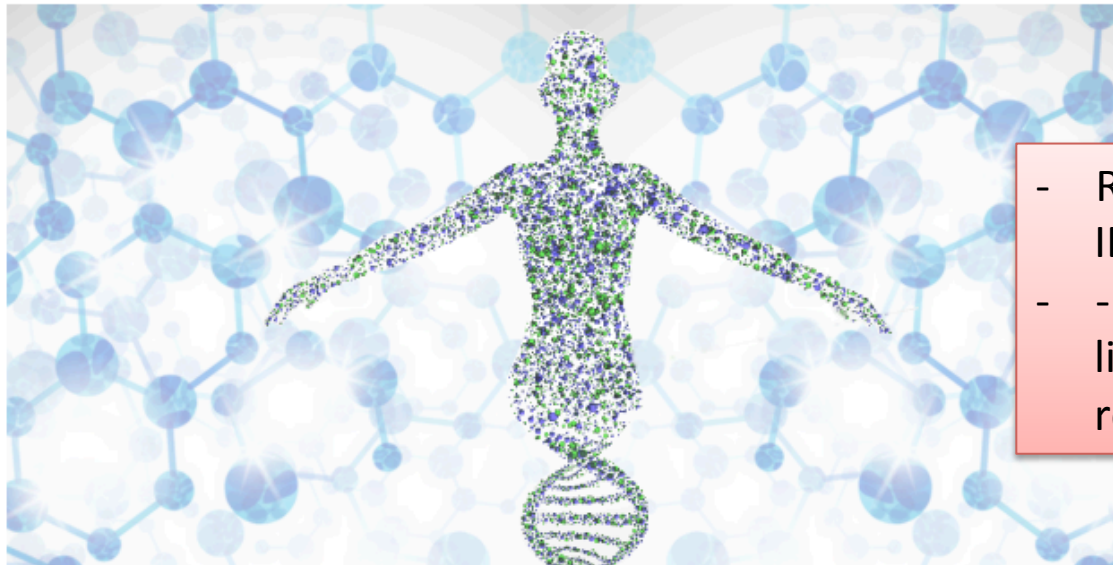
The Innovation Center for Biomedical Informatics (ICBI)
Lombardi Comprehensive Cancer Center

Thu Jan 22, 2015

email or net-id

Log In

[register now](#) | [forgot password](#)



Welcome to GDOC Plus Beta

Precision Medicine

- Register with Georgetown Net ID (or any other email).
- - You will get an email with a link. Click on link to confirm registration

Translational research

Population genetics

Understanding Data in G-DOC Plus

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News

October 02, 2014: ICBI Symposium 2014

[\[read\]](#)

May 02, 2014: Featured in Frontiers' Top 10
2013 Most viewed Genetics Research articles

[\[read\]](#)

March 12, 2014: AAAS Big Data Blog [\[read\]](#)

Login



The Innovation Center for Biomedical Informatics (ICBI)
Lombardi Comprehensive Cancer Center

Thu Jan 22, 2015

kb472

.....

Log In

[register now](#) | [forgot password](#)



Welcome to GDOC Plus Beta!

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Precision Medicine

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Understanding Data in G-DOC Plus

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2013 Most viewed Genetics Research articles

[\[read\]](#)

March 12, 2014: AAAS Big Data Blog [\[read\]](#)

G-DOC Plus Launch Pad!

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



Groups



Notifications **0**

It All Starts Here!



G-DOC has over seventy studies, We know this can be overwhelming! Let us guide you to choose the study that is relevant for your research.

[Let's Go! >](#)

What's your area of interest?

G-DOC Plus has three overlapping entry points for the user based on their interests. Choose your area of interest to launch the workflow.



Precision Medicine

Patients' molecular diagnostics and clinical data.



Translational Research

Analytic tools and workflows to enable discovery.



Population Genetics

Race-based, genomic reporting and comparison.



Select disease/data of interest

DEMENTIA

1
study

30
samples

30
biospecimen

PEDIATRIC CANCERS

5
studies

256
samples

256
biospecimen

BREAST CANCER

25
studies

3952
samples

4532
biospecimen

COLON CANCER

10
studies

1226
samples

1262
biospecimen

LUNG CANCER

1
study

478
samples

443
biospecimen

MUSCULAR DYSTROPHY

1
study

36
samples

36
biospecimen

LIVER CANCER

3
studies

298
samples

468
biospecimen

CELL_LINE_COLLECTIONS

1
study

60
samples

59
biospecimen

OVARIAN CANCER

1
study

1711
samples

564
biospecimen

PROSTATE CANCER

1
study

465
samples

538
biospecimen

PANCREATIC CANCER

1
study

52
samples

51
biospecimen

BRAIN CANCER

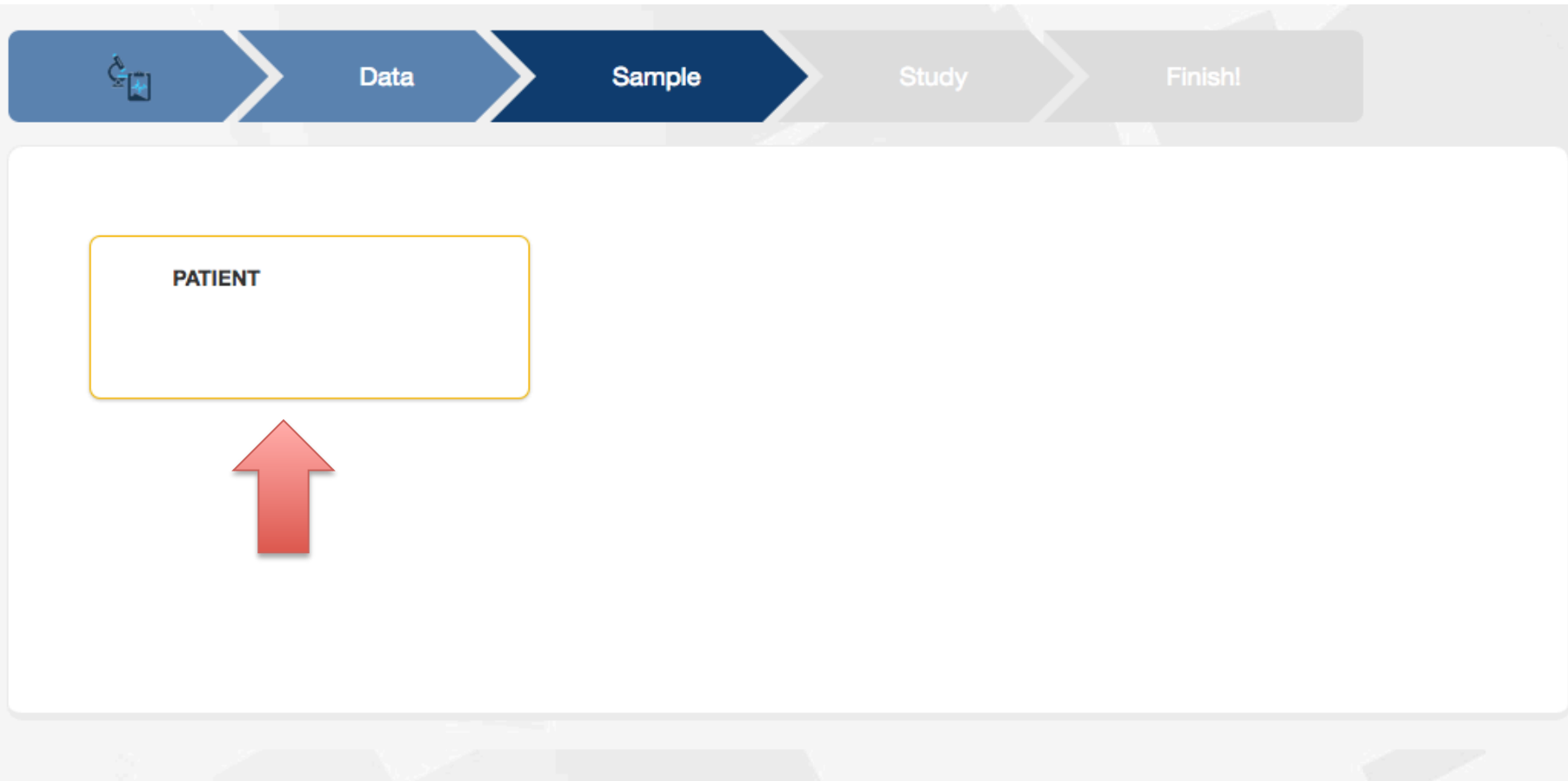
1
study

671
samples

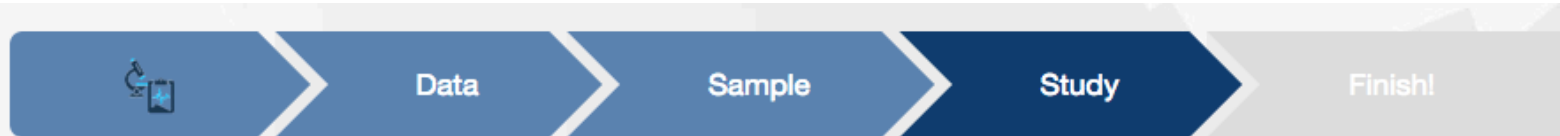
804
biospecimen



Choose between patient and cell line data



Select study



REMBRANDT

Title: NCI Rembrandt Study: Molecular Analysis of Brain Neoplasia

Data Type Details:
CLINIC,MICROARRAY,COPY_NUMBER

Abstract: This is the NCI Rembrandt Study: Molecular Analysis of Brain Neoplasia. Primary brain tumors are the fourth leading cause of cancer mortality in adults under the age of 54 years and the leading cause of cancer mortality in children in the United

671
samples

804
biospecimen

[More>>](#)

Note: If you click on “More”, you will see complete description of the dataset

Study selected. Let's now create some groups

[Data](#)[Sample](#)[Study](#)[Finish!](#)

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

Analyze

- [Classification](#)
- [KM Clinical Plot](#)
- [HeatMap Viewer](#)
- [KM Gene Expression Plots](#)
- [Group Comparison](#)
- [Chromosomal Instability Index](#)

Search

- [Gene Expression Data](#)
- [Explore Clinical Data and Create Groups](#)

Explore clinical data and create groups



Explore Clinical Data and Create Groups

Current Study: REMBRANDT

[change study?](#)

Filter [reset | tips | advanced search]

Demographics

- ☐ Age range
- ☐ Gender
- ☐ Race

Sample details

- ☐ Anti convulsant status
- ☐ Copy number data
- ☐ Gene expression data

[view all \(2 more ...\)](#)

Clinical evaluation

- ☐ Disease evaluation by MRI
- ☐ Neurologic exam score
- ☐ Performance Status Score: Karnofsky

Outcome

- ☐ Event indicator for overall survival
- ☒ Overall survival in months

Subject Search

Current Split Attribute

Type of disease

Type of disease	All Subjects
OLIGODENDROGLIOMA	86
ASTROCYTOMA	170
UNKNOWN	68
UNCLASSIFIED	1
NON TUMOR	31
GBM	261
MIXED	13
Total	630

This page allows you to explore the clinical data. This is an online shopping type of experience. Feel free to check and uncheck the boxes on the left – this will update the patient numbers in the table.

e.g. In this example you can see that among there are 86 Oligodendroglioma patients, 170 Astro and 261 GBM patients

Let's save the Astro and GBM patients

Explore Clinical Data and Create Groups

Current Study: REMBRANDT

[change study?](#)

Filter [reset | tips | advanced search]

Demographics

- ☐ Age range
- ☐ Gender
- ☐ Race

Sample details

- ☐ Anti convulsant status
- ☐ Copy number data
- ☐ Gene expression data

[view all \(2 more ...\)](#)

Subject Search

Current Split Attribute

Type of disease

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GBM	261

View Detailed Report

Save ids as list

To save a list of patients, click on the **hyperlinked number**, and select “**Save ids as list**”. Repeat this procedure to create as many number of patient groups as needed.

E.g.: Click on “170” to save Astro patient list. Click on “261” to save GBM patient list

Note: “View detailed report” shows a detailed clinical report of those selected patients.

Enter a name for the list, and click “Save”

Study: REMBRANDT [change study?](#)

Subject Search

[reset](#) | [tips](#) | [advanced search](#)

[phenotypes](#)
[change](#) ⓘ
ⓘ
ⓘ



[details](#)
convulsant status ⓘ
number data ⓘ
expression data ⓘ
(more ...)

[evaluation](#)
evaluation by MRI ⓘ
logic exam score ⓘ

Save your list

List Type:	clinical, patient
List Name:	<input type="text" value="astro"/>
<div><button>Cancel</button><button>Save</button>close</div>	

GBM	261
MIXED	13
Total	630



Now we want to compare the Astrocytoma patients with GBM patients

Go to Study Options -> Group comparison

The screenshot shows the G-DOC Plus web application interface. The top navigation bar includes links for Home, Studies, Lists, Analyses, Groups, Notifications, Study Options (highlighted with a red box), and Help. The main header reads 'Explore Clinical Data and'. Below this, it states 'Current Study: REMBRANDT' with a 'change study?' link. On the left, there are filter sections for 'Demographics' (Age range, Gender, Race) and 'Sample details' (Anti convulsant status, Copy number data, Gene expression data). The 'Subject Search' section shows a 'Current Split Attribute' dropdown set to 'Type of disease'. Below this is a table with the following data:

Type of disease	All S
OLIGODENDROGLIOMA	86
ASTROCYTOMA	170
UNKNOWN	68
UNCLASSIFIED	1
NON TUMOR	31
GBM	261
MIXED	13

The 'Study Options' dropdown menu is open, showing categories 'Study Selected' (REMBRANDT), 'SEARCH' (Genome Browser, Compound/Drug Targets, Findings, Explore Clinical Data and Create Groups, Gene Expression Data), and 'ANALYZE'. The 'ANALYZE' section includes 'Group Comparison' (highlighted with a blue bar and a red arrow), 'Chromosomal Instability Index', 'KM Clinical Plot', 'KM Gene Expression Plots', 'Classification', and 'HeatMap Viewer'.

Select the two groups

Select a baseline group and a comparison group(s) 

Select baseline group: astro

Select comparison group: gbm

p-value:

0.0001

Fold Change:

2

Statistical Method:

T-Test: Two Sample Test

Multiple Comparison Adjustment:

False Discovery Rate(FDR): Ben

Data-Type:

GENE EXPRESSION

Dataset:

mas5 normalization

Select baseline group (less screwed up group), comparison group, and settings for the comparison analysis.

Click “Submit analysis”

STEP 1

Compare two groups using gene expression data

Notifications

Below are your latest running analyses. Once completed, click on the Analysis name to see detailed results.

GROUP_COMPARISON (2:05 1/22/2015)

Complete



Once you click “submit analysis”, you will be re-directed to the “Notifications” page. Once the status is “Complete”, click on “Group comparison”

Results of group comparison

Analysis Results	
Statistical Method	TTest
Adjustment	FDR
Fold Change	2
Pvalue	0.0001
Study	REMBRANDT
Data File	REMBRANDT.Rda
Baseline Group	astro
Groups	gbm

List Name:

Save Selected ↓

View HeatMap for selected reporters

These are the results of the group comparison – shows list of 1015 Differentially expressed genes (DEGs)

You can sort this table based on any of the columns.

In this example, they are sorted based on fold change

Analysis Results									
<input type="checkbox"/>	Reporter ID	Gene Symbol	p-value	Fold Change	Mean Baseline (lo	Mean Group (log	Std Baseline	Std Group	Target Data
<input type="checkbox"/>	1562264_at	LOC339685	2.448×10^{-13}	-5.752	8.047	5.523	3.003	2.886	
<input type="checkbox"/>	213375_s_at	N48P2L1	0.000×10^0	-5.434	11.476	9.034	1.790	1.882	
<input type="checkbox"/>	221252_s_at	GSG1	0.000×10^0	-5.374	9.526	7.101	2.335	2.644	
<input type="checkbox"/>	219045_at	RHOF	0.000×10^0	-5.169	6.937	4.568	2.263	1.941	
<input type="checkbox"/>	237015_at		0.000×10^0	-5.067	7.301	4.960	2.002	1.778	
<input type="checkbox"/>	1561123_at		8.654×10^{-12}	-5.035	8.759	6.427	2.609	3.103	
<input type="checkbox"/>	208806_at	CHD3	0.000×10^0	-4.969	10.344	8.031	2.097	1.860	
<input type="checkbox"/>	236316_at	FAM3C	0.000×10^0	-4.571	5.137	2.944	2.361	1.802	
<input type="checkbox"/>	221365_at	MLNR	1.383×10^{-13}	-4.386	10.003	7.870	2.430	2.467	
<input type="checkbox"/>	1560758_at		0.000×10^0	-4.197	7.502	5.432	2.125	1.657	
<input type="checkbox"/>	228079_at	C3orf58	1.533×10^{-14}	-4.168	7.455	5.396	2.638	1.982	
<input type="checkbox"/>	233049_s_at	MYH7R	0.000×10^0	-4.080	6.954	4.926	2.457	1.890	

Discussion

- One of the most down-regulated gene RHOF
 - 5 fold under-expressed in the GBM group compared to the Astrocytoma group.
 - From literature: RHOF is down regulated in GBM patients through the over expression of their activators
- MLNR : also 4 fold under expressed in GBM
 - Literature: Similar changes in expression in MLNR were found in low-grade gliomas of Chinese patients

Save gene and reporter list

Analysis Results	
Statistical Method	TTest
Adjustment	FDR
Fold Change	2
Pvalue	0.0001
Study	REMBRANDT
Data File	REMBRANDT.Rda
Baseline Group	astro
Groups	gbm

List Name:

AstroVsGBM.Rep

Save Selected ↓

View HeatMap for selected reporters

2. Save
a) gene list
b) reporter list

1. Select all
results

Analysis Results									
<input checked="" type="checkbox"/>	Reporter ID	Gene Symbol	p-value	Fold Change	Mean Baseline (lo	Mean Group (log	Std Baseline	Std Group	
<input checked="" type="checkbox"/>	1562264_at	LOC339685	2.448×10^{-13}	-5.752	8.047	5.523	3.003	2.886	
<input checked="" type="checkbox"/>	213375_s_at	N4BP2L1	0.000×10^0	-5.434	11.476	9.034	1.790	1.882	
<input checked="" type="checkbox"/>	221252_s_at	GSG1	0.000×10^0	-5.374	9.526	7.101	2.335	2.644	
<input checked="" type="checkbox"/>	219045_at	RHOF	0.000×10^0	-5.169	6.937	4.568	2.263	1.941	
<input checked="" type="checkbox"/>	237015_at		0.000×10^0	-5.067	7.301	4.960	2.002	1.778	
<input checked="" type="checkbox"/>	1561123_at		8.654×10^{-12}	-5.035	8.759	6.427	2.609	3.103	
<input checked="" type="checkbox"/>	208806_at	CHD3	0.000×10^0	-4.969	10.344	8.031	2.097	1.860	
<input checked="" type="checkbox"/>	236316_at	FAM3C	0.000×10^0	-4.571	5.137	2.944	2.361	1.802	
<input checked="" type="checkbox"/>	221365_at	MLNR	1.383×10^{-13}	-4.386	10.003	7.870	2.430	2.467	
<input checked="" type="checkbox"/>	1560758_at		0.000×10^0	-4.197	7.502	5.432	2.125	1.657	
<input checked="" type="checkbox"/>	228079_at	C3orf58	1.533×10^{-14}	-4.168	7.455	5.396	2.638	1.982	
<input checked="" type="checkbox"/>	233949_s_at	MYH7B	0.000×10^0	-4.080	6.954	4.926	2.457	1.890	

Study options -> Classification

Current Study: REMBRANDT

Analysis Results

Statistical Method	TTest
Adjustment	FDR
Fold Change	2
Pvalue	0.0001
Study	REMBRANDT
Data File	REMBRANDT.Rda
Baseline Group	astro
Groups	gbm

List Name:

Save Selected ↓

Reporters
Gene Symbols

View HeatMap for selected reporters

Study Selected

REMBRANDT

SEARCH

Genome Browser

Compound/Drug Targets

Findings

Explore Clinical Data and Create Groups

Gene Expression Data

ANALYZE

Group Comparison

Chromosomal Instability Index

KM Clinical Plot

KM Gene Expression Plots

Classification

HeatMap Viewer

Analysis Results

<input type="checkbox"/>	Reporter ID	Gene Symbol	p-value	Fold Change	Mean Baseline (lo	Mean Group (log	Std Baseline	Std Group	Target Data
<input type="checkbox"/>	1554491_a_at	SERPINC1	0.000 x 10 ⁰	11.664	6.373	9.917	3.599	3.634	
<input type="checkbox"/>	1555409_a_at	BAGE2	0.000 x 10 ⁰	11.033	9.236	12.700	2.535	1.862	
<input type="checkbox"/>	1568931_at		0.000 x 10 ⁰	9.091	10.129	13.314	2.520	1.877	
<input type="checkbox"/>	1568930_at	EFCAB1	0.000 x 10 ⁰	8.427	10.350	13.425	2.416	1.820	
<input type="checkbox"/>	1563637_at	LOC729652	0.000 x 10 ⁰	8.276	6.496	9.545	2.064	2.250	
<input type="checkbox"/>	1558869_at		0.000 x 10 ⁰	8.176	6.467	9.498	2.441	2.280	
<input type="checkbox"/>	226635_at	LOC401504	0.000 x 10 ⁰	8.039	5.550	8.557	2.411	2.393	

Perform PCA

Select a subject list, optional reporter list, classification method, and datatype/dataset ⓘ

Subject Criteria

☐ All Subjects

☒ Select Groups:

gbm_all
R_oligo
R_astro
R_gbm
R_gbm+oligo+ast
R_nonTumor
R_mixed
Rem_Oligo
Rem_Astro
Astro_C_G

Add
Remove

astro
gbm

Select the two groups of interest group

Use Reporter List:
AstroVsGBM.Rep ⓘ

Select the reporter list saved in the previous step

Classification Method:
PCA: Principal Component Ar ▾

Data-Type:
GENE EXPRESSION ▾

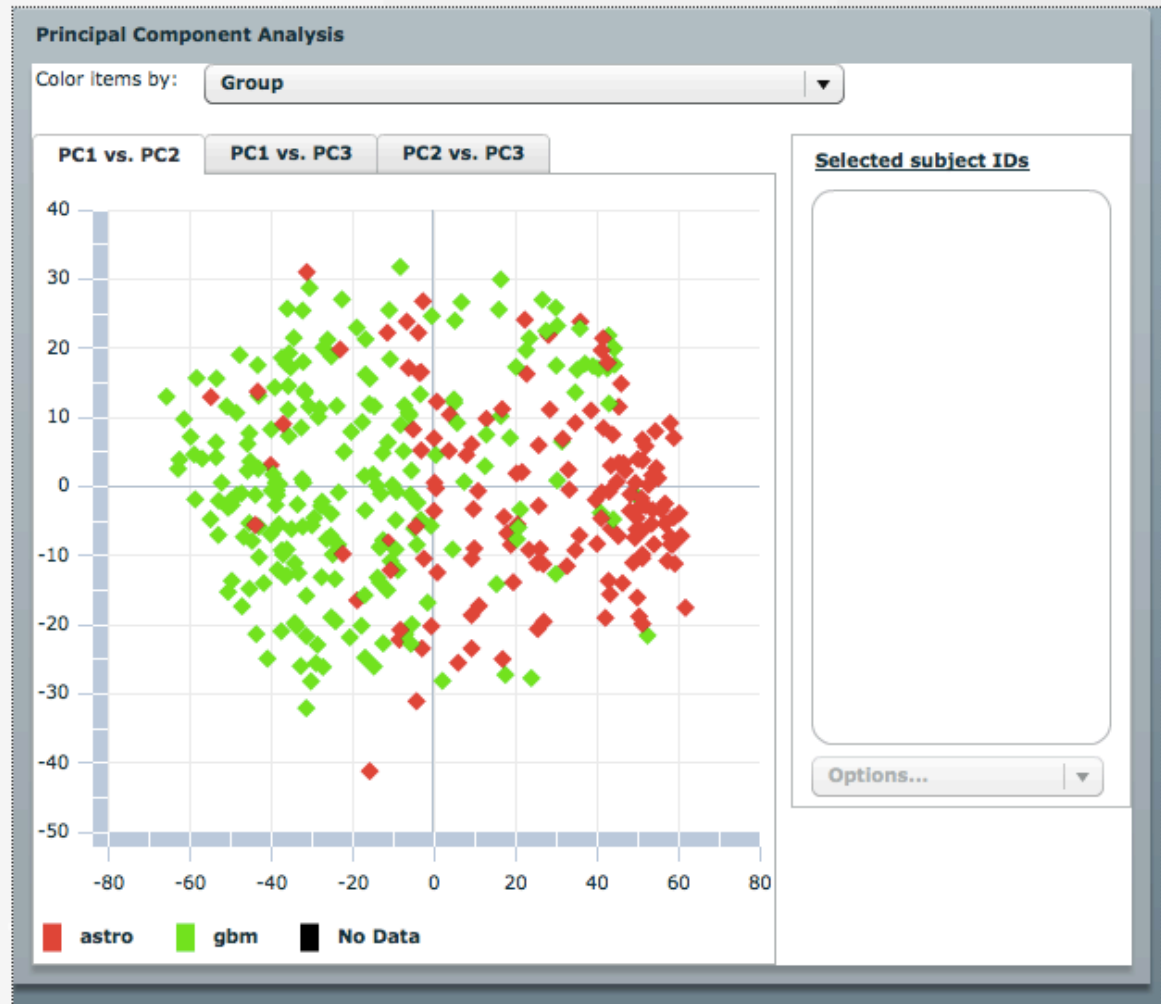
Dataset:
mas5 normalization ▾

Submit Analysis

PCA results

PCA Results

Current Study: REMBRANDT



Classification analysis showing decent separation (but some overlap present)

STEP 2

**Compare two groups using copy
number data**

Group comparison on copy number data

Select baseline group (less screwed up group), comparison group, and settings for the comparison analysis.

Click “Submit analysis”

Perform Group Comparison Analysis

Current Study: REMBRANDT [change study?](#)

Select a baseline group and a comparison group(s) [i](#)

Select baseline group: astro

Select comparison group: gbm

p-value:
.05

Fold Change:
1

Statistical Method:
T-Test: Two Sample Test

Multiple Comparison Adjustment:
None

Data-Type:
COPY_NUMBER

Dataset:
Cytobands-level Chromosom

Results of group comparison

Analysis Results	
Statistical Method	TTest
Adjustment	NONE
Fold Change	1
Pvalue	.05
Study	REMBRANDT
Data File	REMBRANDT_CIN_CYTOBANDS_XBA.Rda
Baseline Group	astro
Groups	gbm

List Name:

Save Selected ↓

View HeatMap for selected reporters


Showing differentially changed cytobands. Top results

- 8q arm
- 7p
- 10q

Analysis Results								
<input type="checkbox"/>	Reporter ID	Cytoband	p-value	Fold Change	Mean Baseline (lo	Mean Group (log	Std Baseline	Std Group
<input type="checkbox"/>	8q24.13	8q24.13	5.372×10^{-5}	-1.612	1.147	0.458	1.337	0.697
<input type="checkbox"/>	8q24.22	8q24.22	5.946×10^{-5}	-1.606	0.906	0.222	1.390	0.661
<input type="checkbox"/>	8q23.3	8q23.3	6.877×10^{-4}	-1.580	1.193	0.533	1.513	0.813
<input type="checkbox"/>	8q24.21	8q24.21	1.320×10^{-4}	-1.542	1.005	0.380	1.255	0.686
<input type="checkbox"/>	8q24.12	8q24.12	1.141×10^{-4}	-1.507	0.839	0.247	1.287	0.574
<input type="checkbox"/>	8q23.1	8q23.1	6.497×10^{-3}	-1.405	1.208	0.717	1.258	0.841
<input type="checkbox"/>	8q22.3	8q22.3	1.649×10^{-3}	-1.371	0.805	0.350	1.118	0.612
<input type="checkbox"/>	8q22.1	8q22.1	9.246×10^{-3}	-1.361	0.928	0.484	1.180	0.801
<input type="checkbox"/>	8q24.23	8q24.23	9.751×10^{-4}	-1.343	0.580	0.155	1.028	0.527
<input type="checkbox"/>	8q23.2	8q23.2	7.976×10^{-3}	-1.307	0.938	0.552	1.024	0.674
<input type="checkbox"/>	8q24.11	8q24.11	3.261×10^{-4}	-1.294	0.471	0.099	0.862	0.396

Chromosome instability index (CIN)

Study options -> Chromosome instability index



HomeStudiesListsAnalysesGroupsNotificationsStudy Options▼Help

Analysis Results

Current Study: REMBRANDT

Analysis Results

Statistical Method	TTest
Adjustment	NONE
Fold Change	1
Pvalue	.05
Study	REMBRANDT
Data File	REMBRANDT_CIN_CYTOBANDS_XBA.Rda
Baseline Group	astro
Groups	gbm

List Name:

Save Selected ↓

View HeatMap for selected reporters

Study Selected

REMBRANDT

SEARCH

Genome Browser

Compound/Drug Targets

Findings

Explore Clinical Data and Create Groups

Gene Expression Data

ANALYZE

Group Comparison

Chromosomal Instability Index

KM Clinical Plot

KM Gene Expression Plots

Classification

HeatMap Viewer

Perform CIN analysis

Chromosomal Instability Index

Current Study: REMBRANDT [change study?](#)

Select a baseline group and a comparison group(s)

Select baseline group: astro

Select comparison group: gbm

Submit Analysis

Notifications

Below are your latest running analyses. Once completed, click on the Analysis name to see detailed results.

CIN (4:14 12/11/2015)

PCA (3:21 12/11/2015)

Complete

Complete



CIN heat map

Click on CHROMOSOME number to see CYTOBAND heat map



- Click on Chromosome 8
- Shows this CYTOBAND heatmap
- The two groups (relapse, no relapse) are separated by green line
- Black color = no instability (normal)
- Red color indicates instability
- Darker the red, higher the instability

Discussion

- Conclusion from group comparison results and CIN heatmaps
 - high level of chromosomal instability chromosome 8q arm
 - Aberrations in the 8q arm in Astrocytoma patients are known in literature
 - Also lists 7p and 10q regions
 - 7p and 10q regions are known to be highly amplified in GBM patients

STEP 3

Compare two groups using clinical data (Survival analysis)

How to do a clinical KM plot

From either the home page, or the current page you are in, go to Study options - > KM Clinical plot

The screenshot shows the G-DOC Plus Launch Pad interface. The top navigation bar includes links for Home, Studies, Lists, Analyses, Groups, Notifications, Study Options, and Help. The 'Study Options' dropdown menu is open, showing a list of options: Study Selected, REMBRANDT, SEARCH, Genome Browser, Compound/Drug Targets, Findings, Explore Clinical Data and Create Groups, Gene Expression Data, ANALYZE, Group Comparison, Chromosomal Instability Index, **KM Clinical Plot** (highlighted with a red arrow), KM Gene Expression Plots, Classification, and HeatMap Viewer. The main content area features a grid of icons for Studies, Lists, Groups, Notifications (with a badge of 1), and Help me pick a study. The background text reads: 'G-DOC Plus Launch Pad' and 'Welcome! The G-DOC Plus Launch Pad is your one-stop re started on the platform.'

G-DOC Plus Launch Pad

Welcome! The G-DOC Plus Launch Pad is your one-stop re started on the platform.

Home Studies Lists Analyses Groups Notifications Study Options Help

kb472

Study Selected

REMBRANDT

SEARCH

Genome Browser

Compound/Drug Targets

Findings

Explore Clinical Data and Create Groups

Gene Expression Data

ANALYZE

Group Comparison

Chromosomal Instability Index

KM Clinical Plot

KM Gene Expression Plots

Classification

HeatMap Viewer

Studies

Lists

Groups

Notifications 1

Help me pick a study

Create Clinical KM Plot

Current Study: REMBRANDT [change study?](#)

Select Patient Groups:

Rem_GBM
Rem_Oligo
Rem_Astro
Rem_NonTumor

Add
Remove

astro
Gbm

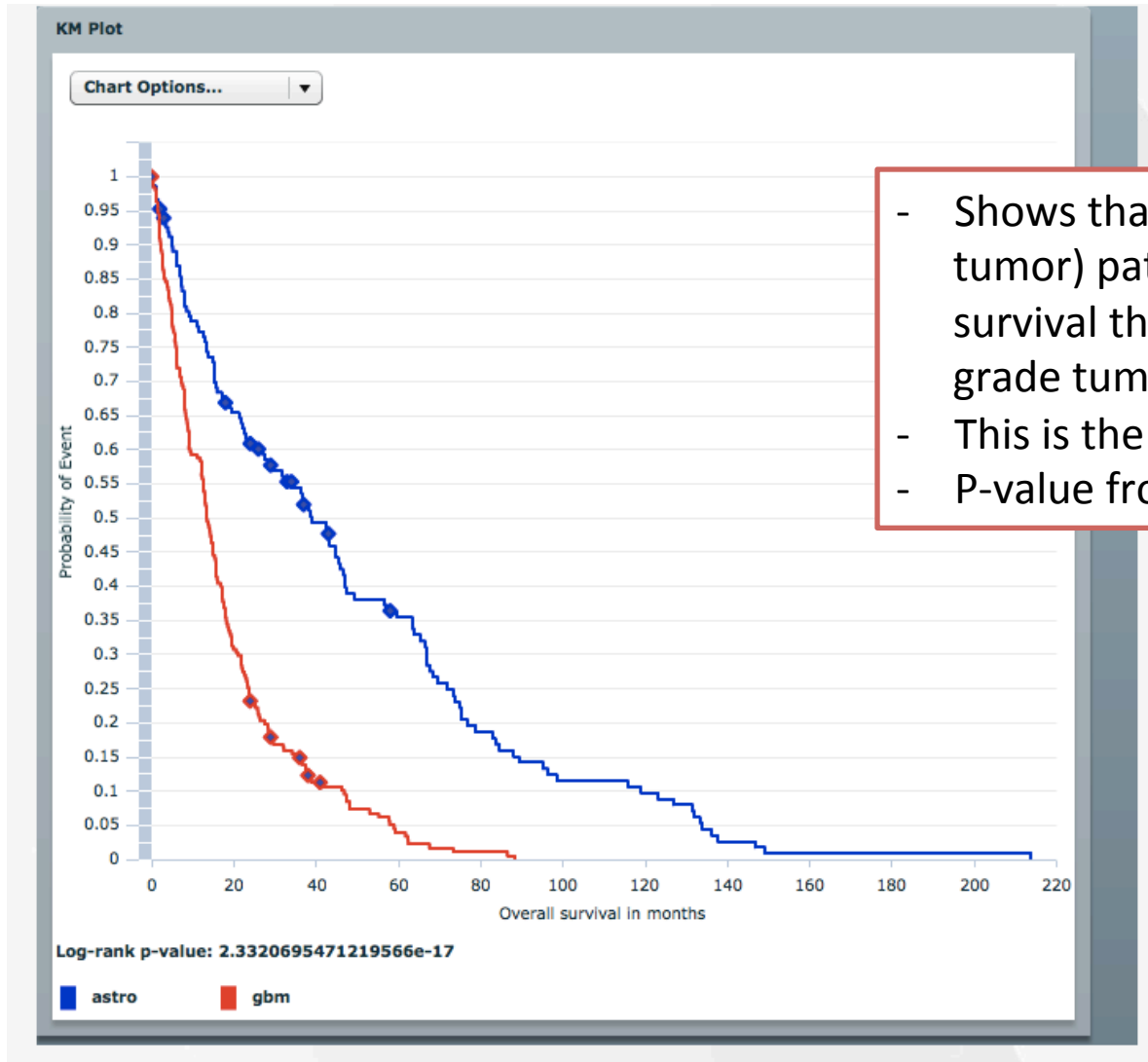
Select Endpoint:

Overall survival in months ▾

Plot

- Select patient group(s) of interest using the “add” button
- Select endpoint
- Click “plot”

Clinical KM plot results



- Shows that GBM (high grade tumor) patients have worse survival than Astrocytoma (lower grade tumor)
- This is the expected result
- P-value from log rank test < 0.05

Conclusion

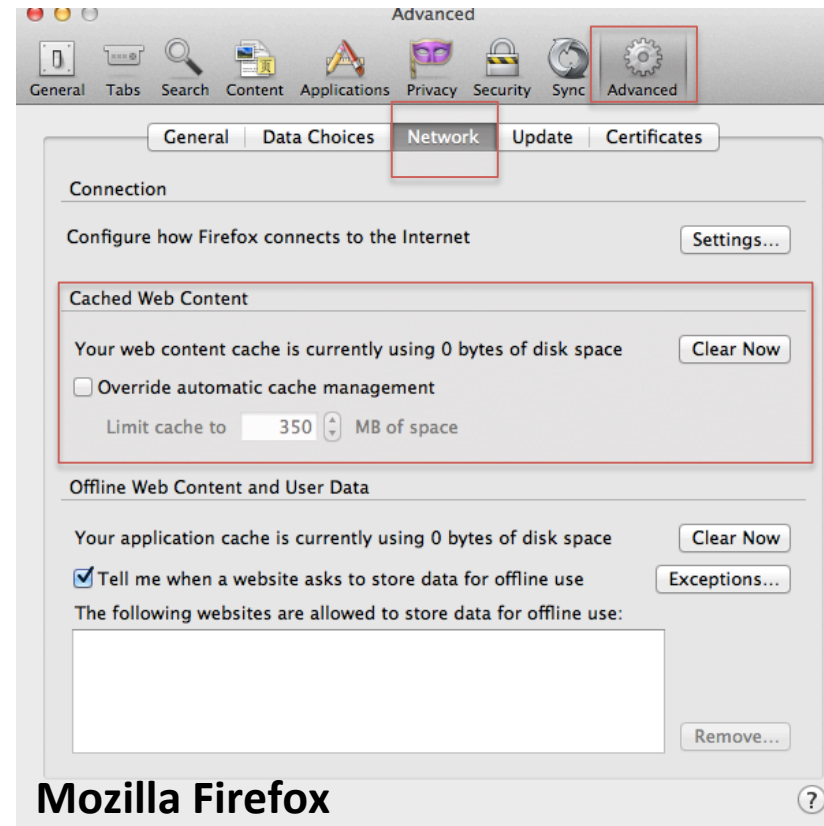
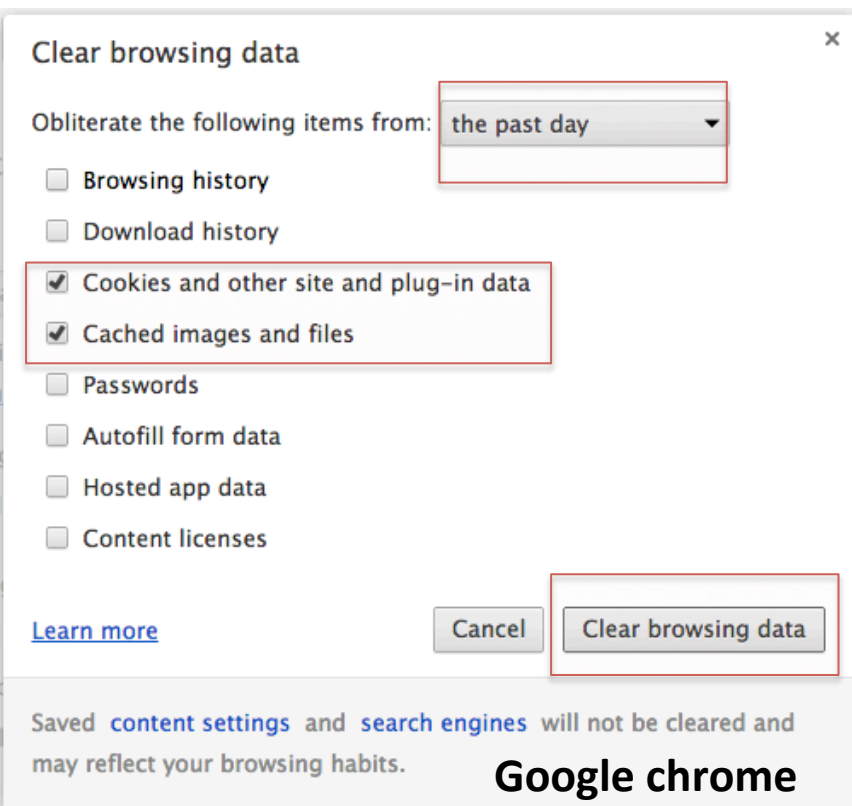
- G-DOC *Plus* enables users to
 - generate new hypotheses from existing data
 - perform such in silico meta-analysis of disparate studies.
- There is added value in obtaining new insights into the etiology, diagnosis, treatment, and prevention of diseases from re-analyzing published datasets

General tips

- G-DOC *Plus* works best if you don't use the **back** button in the web browser repeatedly.
- Once you select a study, most tools will be easily available from the the top menu bar inside G-DOC *Plus*.

Clearing cache

- If the G-DOC web page does not respond after several seconds, try:
 - refreshing the page.
 - Log out and log back in, and try again
 - If the above two do not work, its possible that your web browser cache may need to be cleared
 - For Google chrome, go to **Settings** -> **Show Advanced Settings** -> Under “Privacy”, select **Clear Browsing data**
 - For Mozilla Firefox, go to **Preferences** -> **Advanced** -> **Network** -> Under “Cached Web Content” -> **Clear now**



- We are working hard to improve G-DOC *Plus*. Please feel free to email your questions and comments (no homework questions please) to us at :gdoc-help@georgetown.edu