

GANreproduce Quick Start Guide

Oct. 13, 2018

Program MATLAB (2016a for demonstration)

Type *Package (GANreproduce.m)*

Title *A package for reproducing the results reported in the manuscript entitled:*

*A trio of genes in germinal center B cells mediates the pathogenesis of
blood cancers*

Version *1.4*

Date *2018/10/11*

Authors *Wei-Quan Fang and Ming-Jing Hwang*

Maintainer *Wei-Quan Fang <deleapoli@gmail.com>*

Description *In this work, we analyzed lymphoma-related gene expression and
clinical data and identified a regulatory motif of germinal center
B cell genes.*

Repository *GITHUB*

Publication *Submitted*

Launch the Package

Three steps are needed to launch the *GANreproduce* Package.

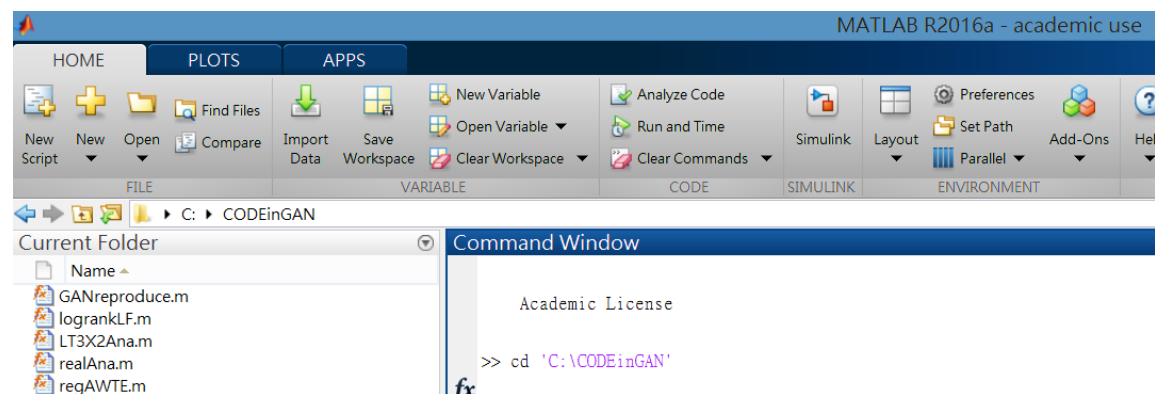
Step1: Download the two files, **DATAinGAN** and **CODEinGAN**, from the web-site <https://github.com/IBMSn121/GAN-paper1>.

GitHub, Inc. [US] https://github.com/IBMSn121/GAN-paper1		
IBMSn121 Update README.md Latest commit 6f143b5 5 hours ago		
CODEinGAN	Create filenameCode.txt	6 hours ago
DATAinGAN	Create filenameData.txt	6 hours ago
LICENSE	Initial commit	3 months ago
README.md	Update README.md	5 hours ago

and put them in C:\

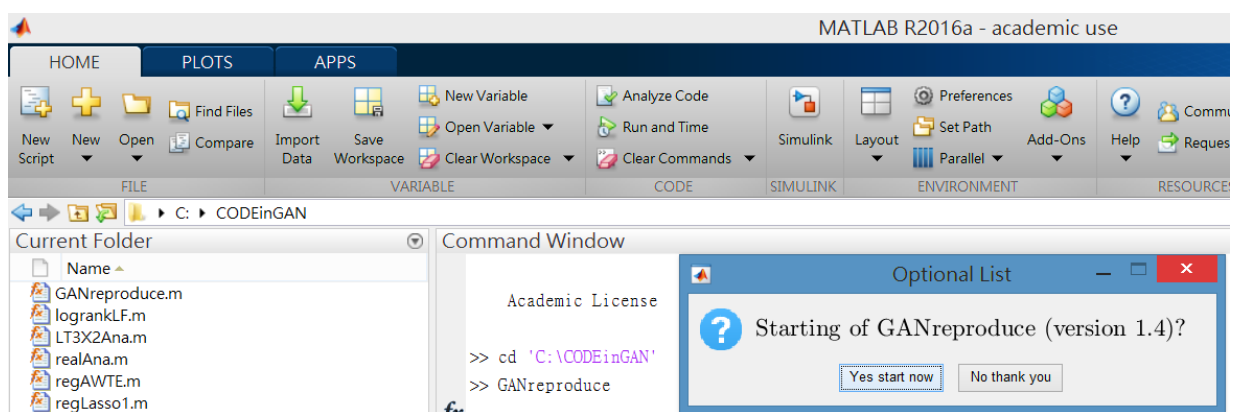
CODEinGAN	2018/10/1'
DATAinGAN	2018/10/9
Program Files	2017/5/18
Program Files (x86)	2018/5/17

Step2: Open MATLAB program window and type **cd 'C:\CODEinGAN'** in it, then press **ENTER**.



(*Please check* that GANreproduce Package **GANreproduce.m** can be seen in the MATLAB panel of **Current Folder** after this step)

Step3: Type **GANreproduce** and press **ENTER** to launch the GANreproduce Package and start *dialog boxes* for reproducing the results.

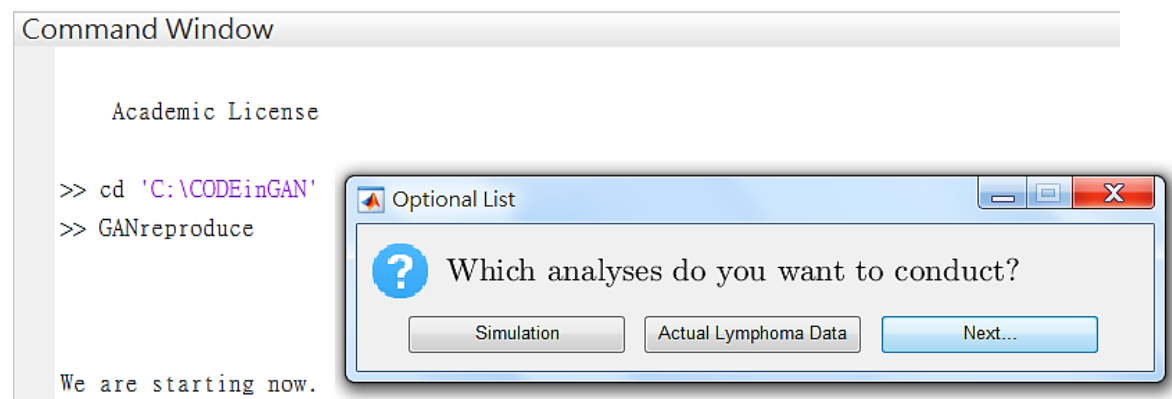


Examples

Three examples, concerning **Actual Lymphoma Data Analysis**, **Linear Trend Analysis** and **Clinical Controversy Analysis**, were provided for reproducing the results via GANreproduce Package with selections of *user friendly dialog boxes*.

Example 1 (Actual Lymphoma Data Analysis)

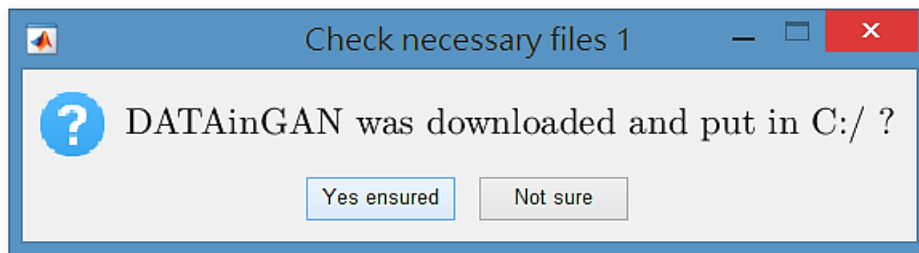
Click **Yes start now** after the launch of the Package, then click **Actual Lymphoma Data**.



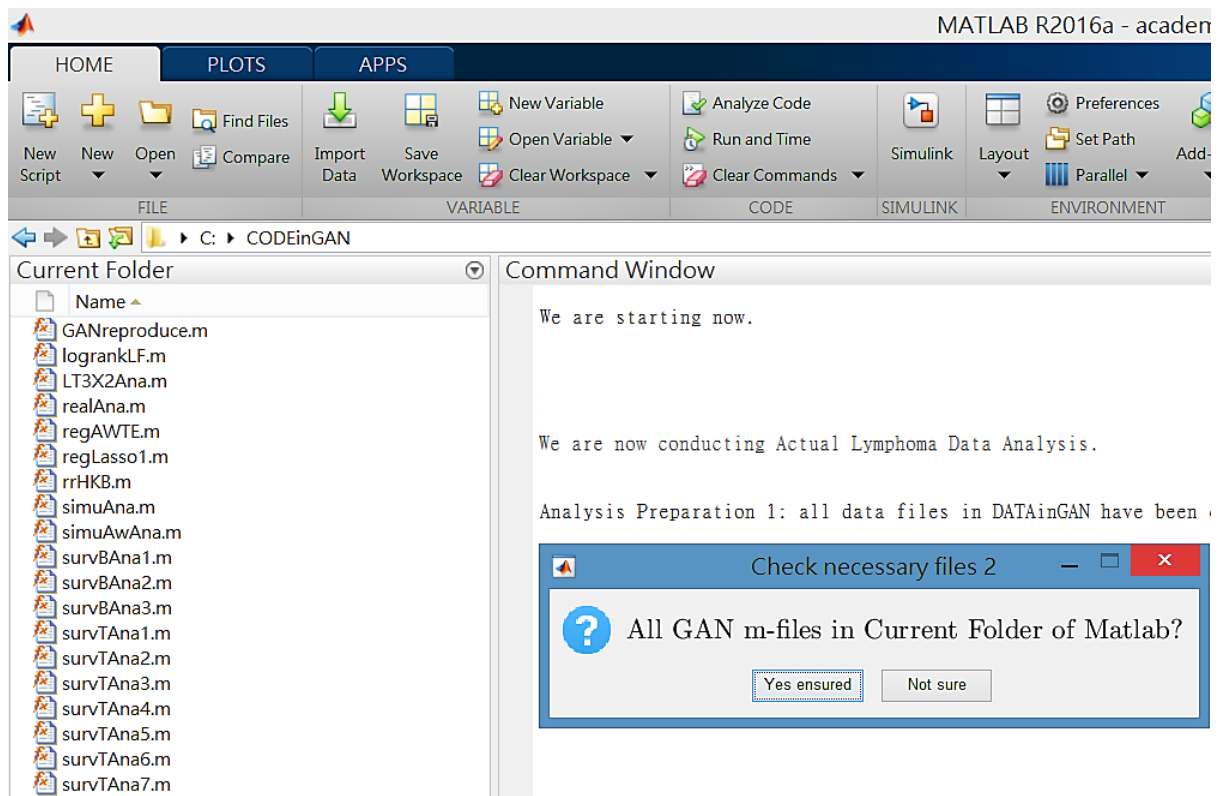
Ensure all the data in DATAinGAN were set up right and click **Yes ensured**.

Command Window

We are now conducting Actual Lymphoma Data Analysis.

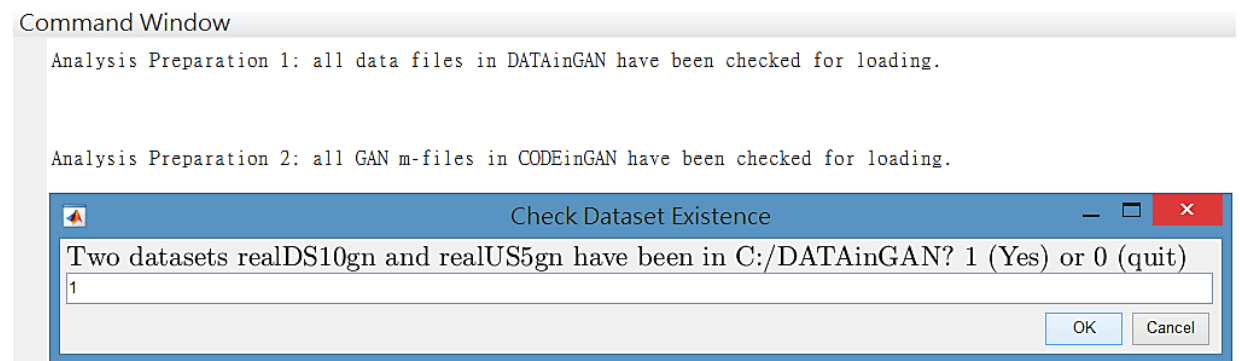


Ensure all the codes in CODEinGAN were set up right and click **Yes ensured**.

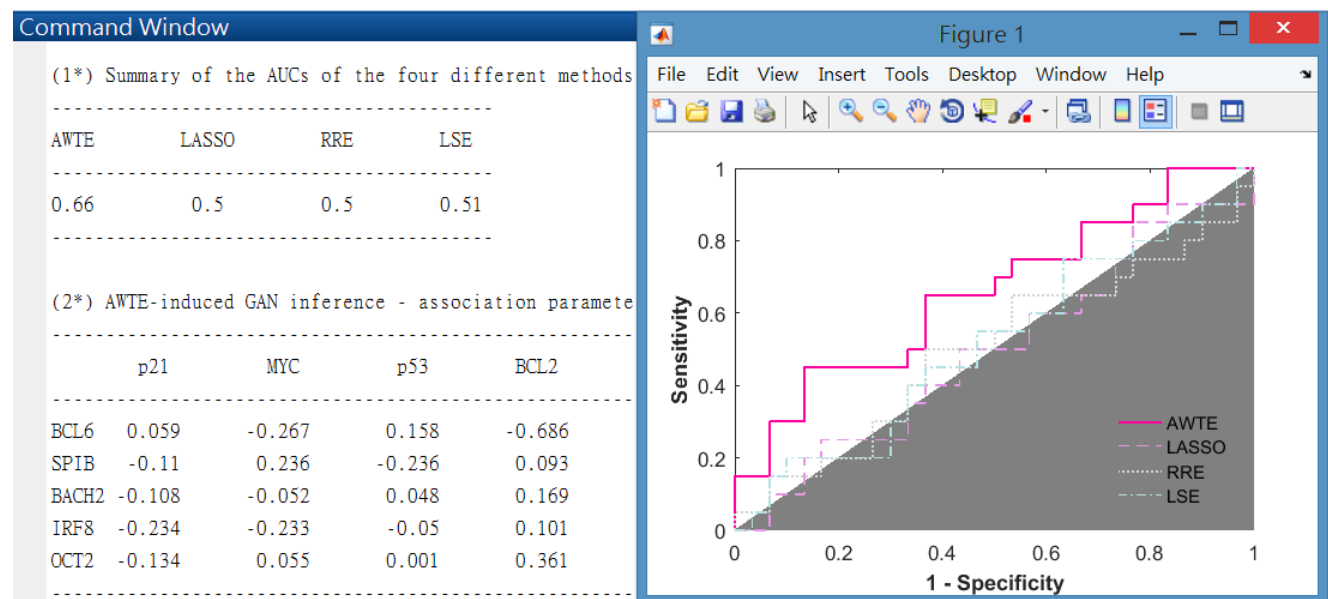


Check the two datasets realDS10gn and realUS5gn used in the analysis of the actual lymphoma data were set up right, then input **1** and click **Ok** to confirm

the setting.



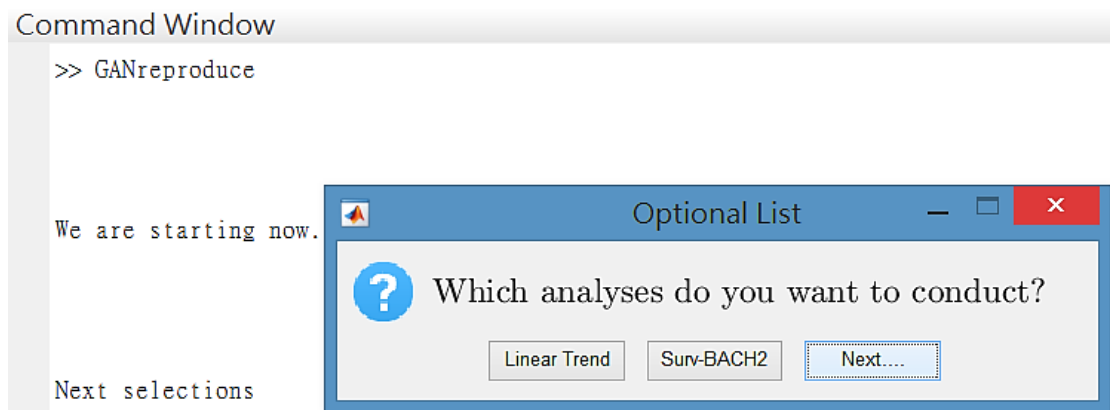
Results for Actual Lymphoma Data Analysis were reproduced on the **Figure** and **MATLAB Command Window**.



Example 2 (Linear Trend Analysis)

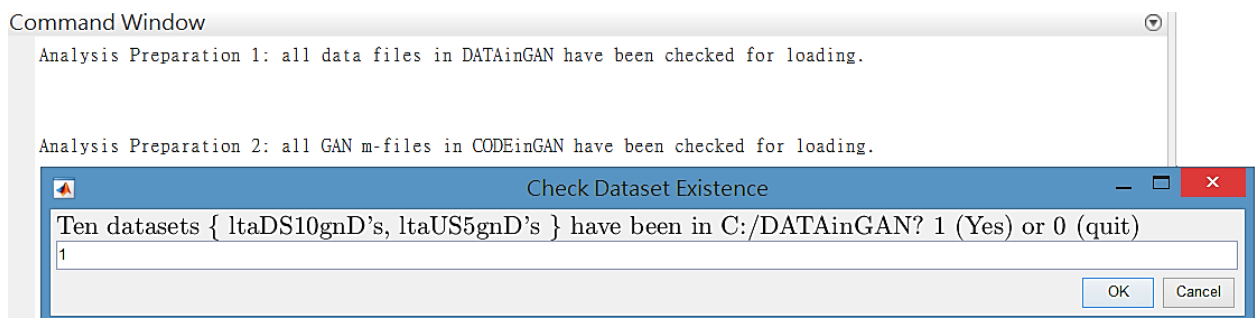
Click **Yes start now** after the launch of the Package, then click **Next...** and

Linear Trend.



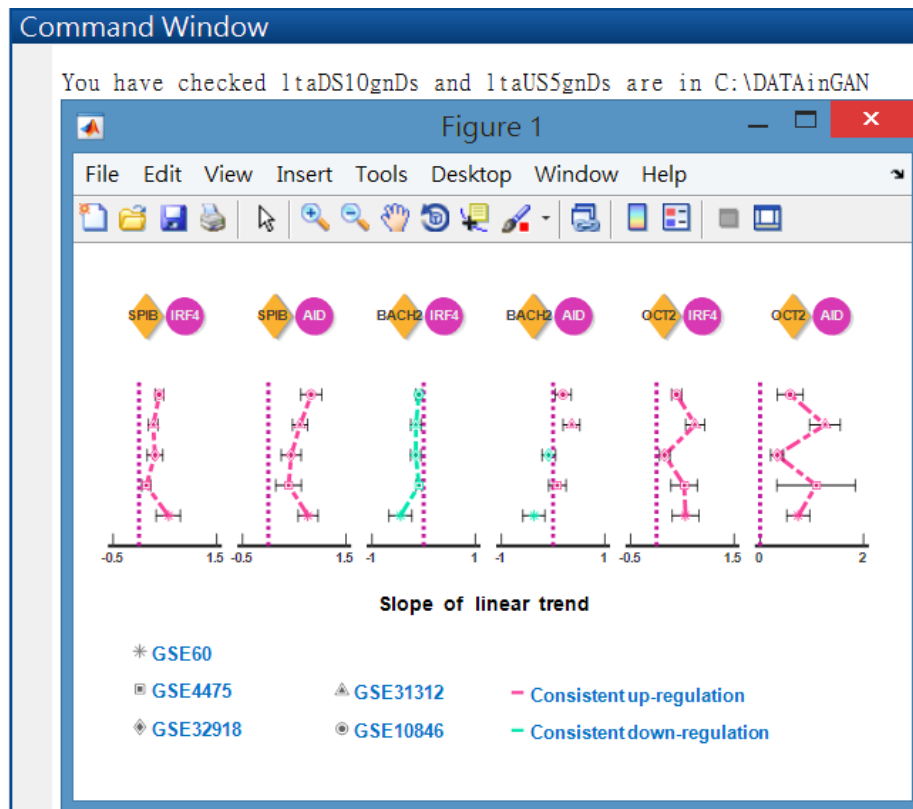
↓

Click **Yes ensured** twice and check the necessary files, datasets and codes, as in Example 1, then input **1** and click **Ok** to confirm the setting.



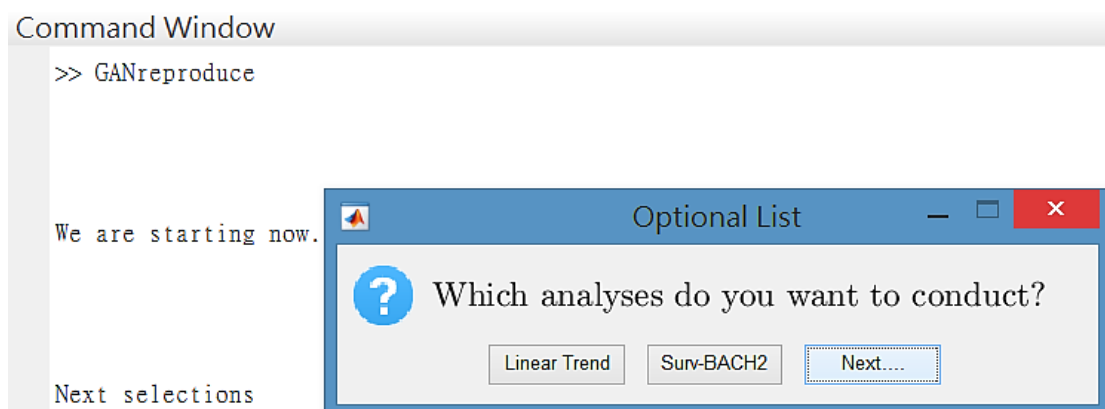
↓

Results for Linear Trend Analysis were reproduced on the **Figure**.



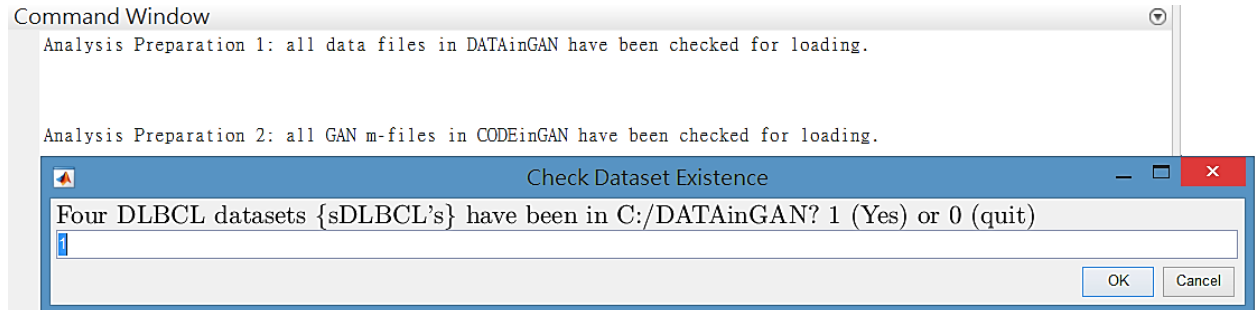
Example 3 (Clinical Controversy Analysis)

Click **Yes start now** after the launch of the Package, then click **Next...** and **Surv-BACH2**.



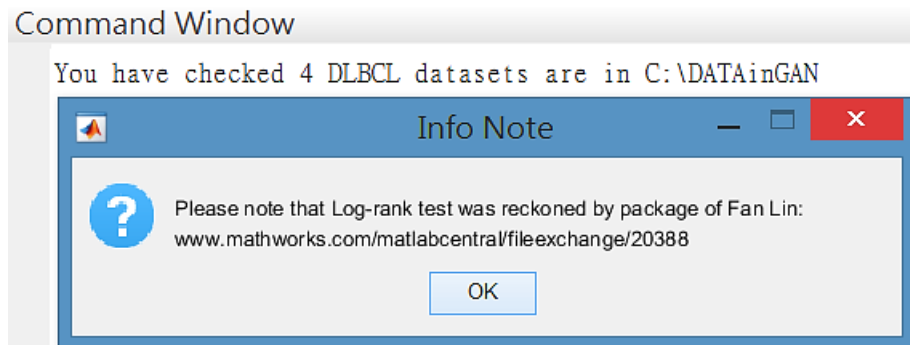
↓

Click **Yes ensured** twice and check the necessary files, datasets and codes, as in Example 1, then input **1** and click **Ok** to confirm the setting.



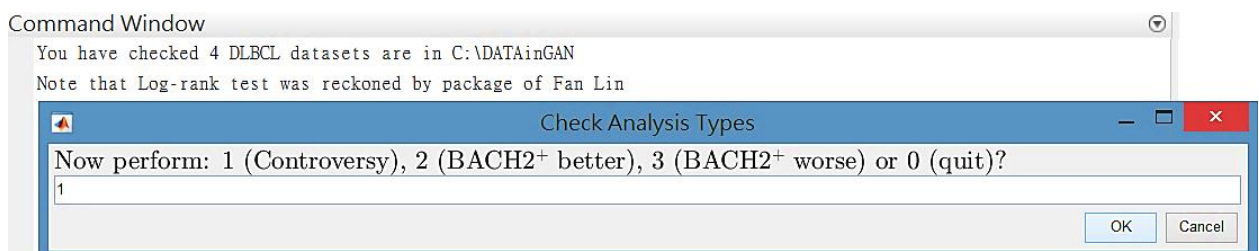
↓

Receive the information on the package used for log-rank statistical testing and click **Ok**.



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Select analytical type (e.g., Controversy), input **1** and click **Ok**.



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Results for Clinical Controversy Analysis were reproduced as shown below.

