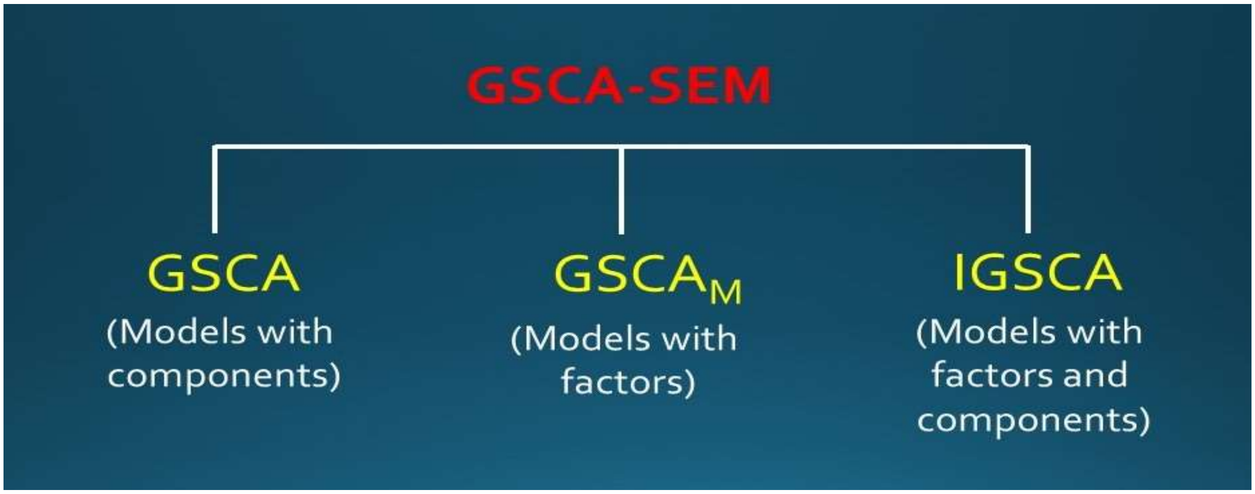

GSCA Pro for Windows User's Manual

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Website: www.gscapro.com
Facebook: https://www.facebook.com/GSCAPro
Twitter: https://twitter.com/GSCAPro
Google Discussion Group: https://groups.google.com/g/gsca-pro

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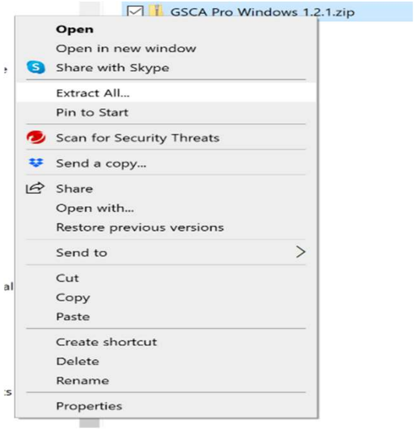
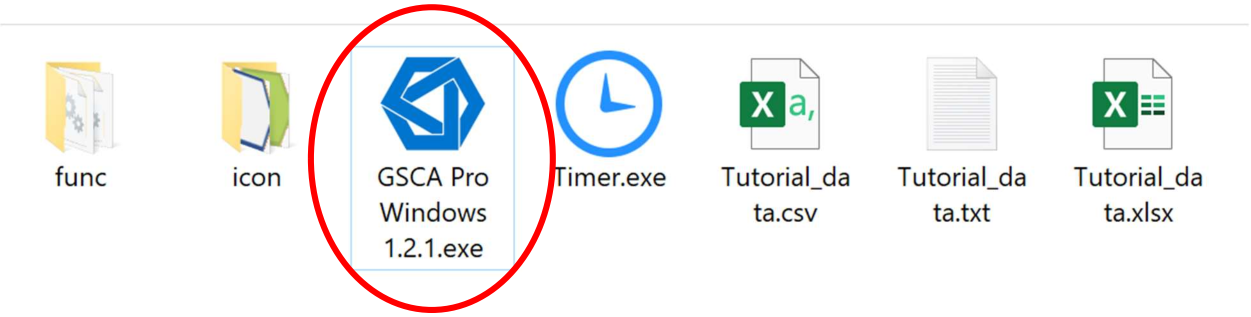
Downloading and Opening GSCA Pro

1. Users download **GSCA Pro 1.2.zip** from www.gscapro.com and **unzip** the file as follows:

   - Right-click the file, select Extract All, and then follow the instructions.

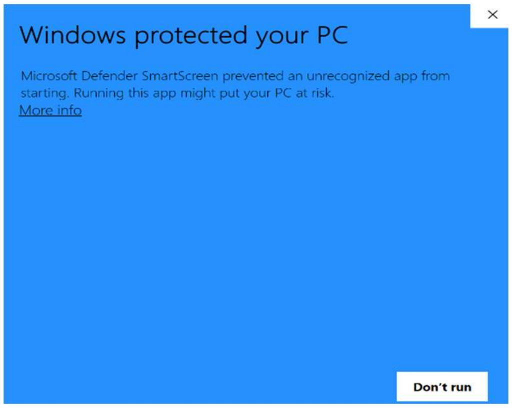


2. Then, double-click on **GSCA Pro Windows 1.2.exe** to open the software.



Important Notices

- When double-clicking on GSCA Pro 1.2.exe, **Windows 10** users will receive the "**Windows protected your PC**" warning message, as shown on the right. Here is what they need to do:
  - Don't click on the "Don't run" option
  - Click on the "More info" option
  - A new popup window will then appear
  - Click on "Run anyway"


Windows protected your PC

Microsoft Defender SmartScreen prevented an unrecognized app from starting. Running this app might put your PC at risk.
More info

- An antivirus program on users' PC can prevent GSCA Pro from running. Then, users need to temporarily disable their antivirus program, or add GSCA Pro to the antivirus program's Trusted Program List. Below is how to add a trusted program to several antivirus programs.

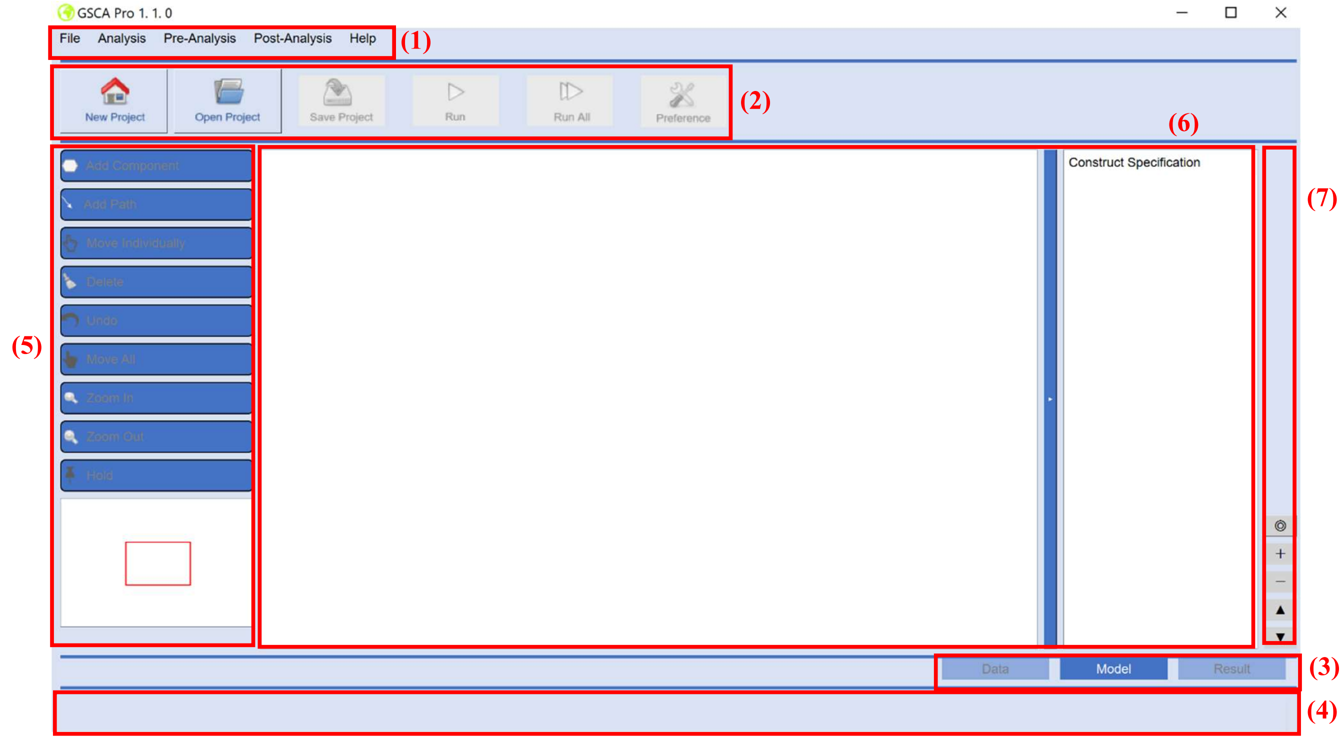
  - Trend Micro: https://docs.trendmicro.com/all/ent/officescan/v11.1/en-us/osce_11.1_sp1_agent_olh/Trusted-Program-List.html
  - McAfee: https://community.mcafee.com/t5/SecurityCenter/How-to-add-programs-to-the-Trusted-List/td-p/72462
  - Norton: https://www.providesupport.com/help/troubleshooting/norton-internet-security

- **Windows 7** users may receive the "**Windows cannot access the specified device, path, or file**" warning message. Then, please refer to the following link: https://support.microsoft.com/en-us/topic/-windows-cannot-access-the-specified-device-path-or-file-error-when-you-try-to-install-update-or-start-a-program-or-file-46361133-47ed-6967-c13e-e75d3cc29657

- We do not recommend creating GSCA Pro's folder within an existing folder whose contents are synchronized by a cloud storage service (e.g., Dropbox's folder). This may interrupt the execution of the software or turn it off suddenly.

GSCA Pro's Graphical Interface

Upon opening *GSCA Pro*, the following graphical interface will appear.



(1) **Menu Bar** contains top-level menus, including [File], [Analysis], [Pre-Analysis], [Post-Analysis], and [Help].
  - In [File], users can create a new project, open an old project, save a current project, save a project as a different file, or exit the program.
  - In [Analysis], users can select various analytic features of GSCA.
  - In [Pre-Analysis], users can calculate descriptive statistics.
  - In [Post-Analysis], users can conduct a supplementary analysis after fitting models, including model comparison, mediation analysis, or conditional process analysis.
  - In [Help], users can find information on the program, developers, or citation.

(2) **Shortcuts**
  - [New Project] is used to create a new project.
  - [Open Project] is used to open an existing project.
  - [Save Project] is used to save a current project.
  - [Run] is used to fit a specified model to data.
  - [Run All] is used to fit all specified models to the same data at once.

- [Preference] is used for users to choose various estimation options (e.g., the maximum number of iterations, number of bootstrap samples, missing data options, etc.)

(3) **View Tap**
  - [Data] displays the data that users uploaded into GSCA Pro.
  - [Model] is used to create or revise a model.
  - [Result] displays results after estimating a model.

(4) **Status Bar** displays the names of the project and the analysis type that users currently select and conduct.

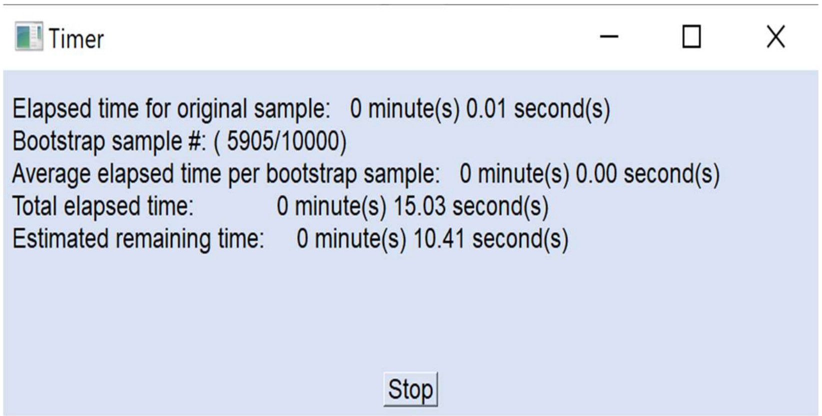
(5) **Tool Panel** contains all tools that users can use for specifying a model or conducting an analysis.

(6) **Main Window** displays users' data, models, or analysis results.

(7) **Model Bar** shows a list of models that users specified. Users can add (+), delete (-), move up (▲), or move down (▼) a model.

Timer

When an analysis runs longer than 5 seconds, the below timer will appear, displaying how many bootstrap samples have been run and how much time the analysis will take to complete.



```
Elapsed time for original sample:   0 minute(s) 0.01 second(s)
Bootstrap sample #: ( 5905/10000)
Average elapsed time per bootstrap sample:   0 minute(s) 0.00 second(s)
Total elapsed time:           0 minute(s) 15.03 second(s)
Estimated remaining time:     0 minute(s) 10.41 second(s)
```

General Information

1. How to Prepare Data for *GSCA Pro*

GSCA Pro is run on individual-level raw data. The raw data file can be prepared in various formats (.txt, .csv, or .xlsx). The specific data format for *GSCA Pro* is as follows:

- The first row can contain the names of indicators. The name of each indicator should be separated by a space, tab, comma, semicolon, or column (.xlsx). Refer to the example data files (*tutorial_data.txt*, *tutorial_data.csv*, and *tutorial_data.xls*).
- If the first row does not contain the names of indicators, by default, the indicators will be named V1, V2, …, and V*J* (*J* is the number of indicators).
- The data input begins on the second row. Data from an observation, or responses by an individual on each indicator, should be separated by a space (.txt), a comma (.csv), or a column (.xlsx).
- Data for each observation appear on a single row.
- Data must not include non-numeric characters or blank cells.
- Data may include missing values. Any numeric value can be used to indicate missing values (the default value is -9999) and should be used consistently in the data.

Exemplary Data and Model

Part of Bergami and Bagozzi's (2000) organizational identification data is used for illustrative purposes. The number of observations is 305. Figure 1 displays the model specified for the data. This model includes 4 components (**hexagons**) and 21 indicators (**boxes**): Organizational Prestige (OP) is associated with 8 indicators (cei1 – cei8), Organizational Identification (OI) with 6 indicators (ma1 – ma6), Affective Commitment-Joy (AC_{Joy}) with 4 indicators (orgcmt1, 2, 3 and 7), and Affective Commitment – Love (AC_{Love}) with 3 indicators (orgcmt5, 6, and 8).

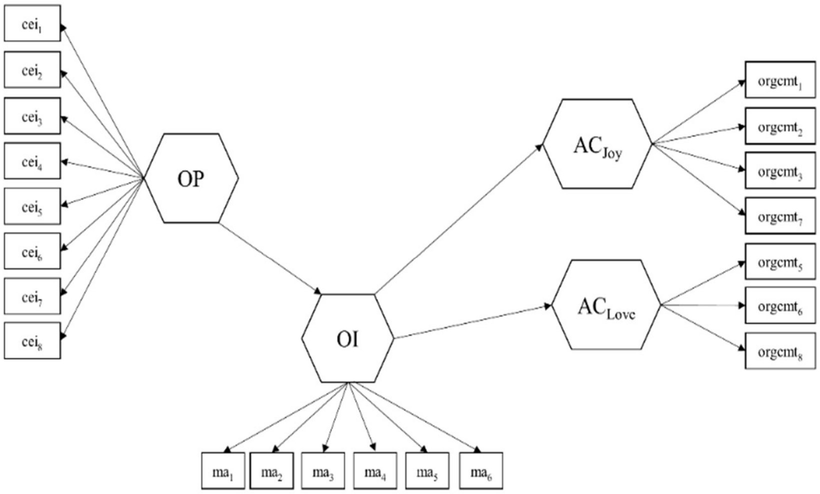
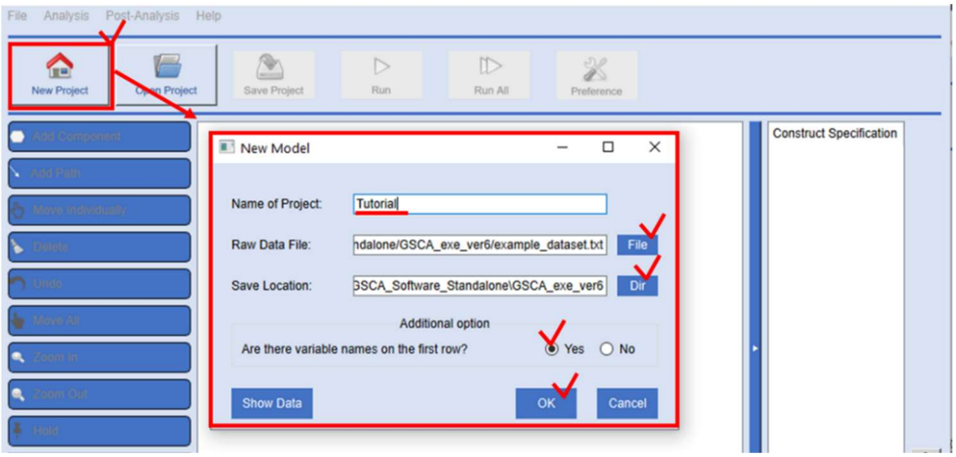


Figure 1. The specified model for the example data.

2. How to Start New Project or Open Old Project

- To start a new project, click on the **[New Project]** shortcut. Users name a new project, upload a data file, set a directory for saving the project, and indicate whether the names of indicators appear in the first row of the data file (default). Then, click on [OK].



Name of Project: Tutorial

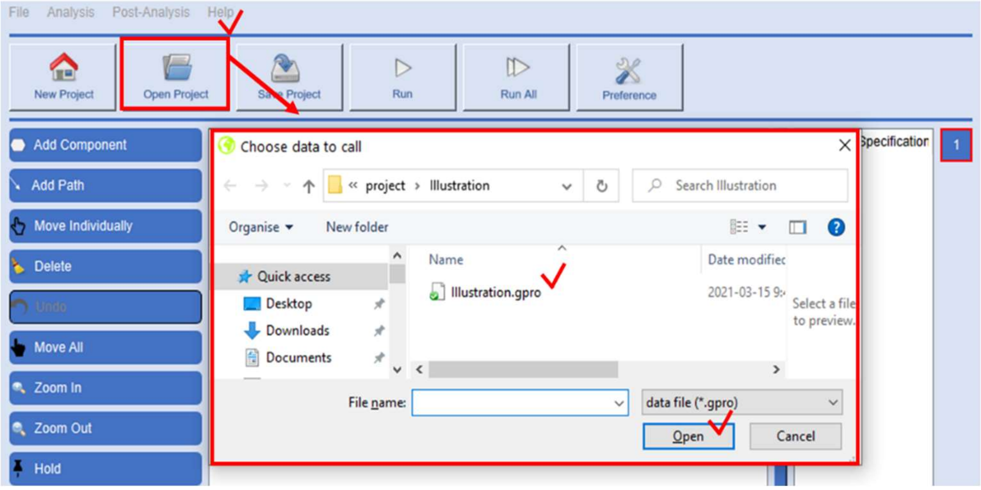
Raw Data File: hdalone/GSCA_exe_ver6/example_dataset.txt

Save Location: 3SCA_Software_Standalone\GSCA_exe_ver6

Additional option

Are there variable names on the first row? ● Yes ○ No

- To open an old project, click on the **[Open Project]** shortcut, search the directory that contains a project file of interest, click on the file, and click on [Open].



« project › Illustration

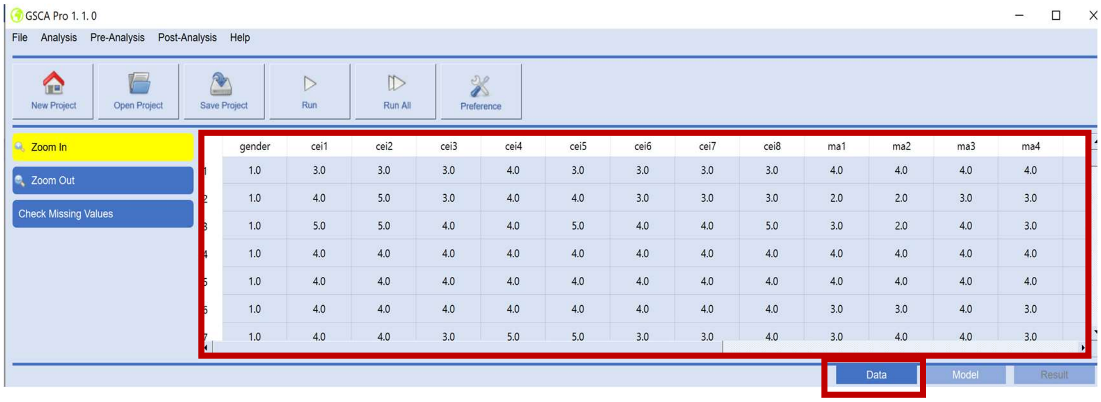
Illustration.gpro 2021-03-15 9:

File name:

data file (*.gpro)

3. How to Check Uploaded Data

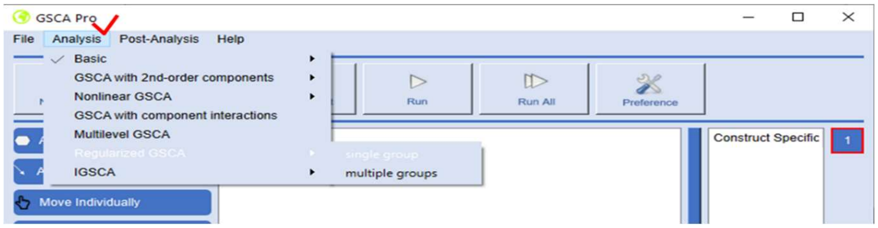
- To review uploaded data, click on the **[Data]** tap.
- Users can increase or decrease cell size by clicking on [Zoom in] or [Zoom Out] on the left-hand window.
- Users can check the number of missing values per observation or variable by clicking on [Check Missing Values] on the left-hand window.



	gender	cei1	cei2	cei3	cei4	cei5	cei6	cei7	cei8	ma1	ma2	ma3	ma4
1	1.0	3.0	3.0	3.0	4.0	3.0	3.0	3.0	3.0	4.0	4.0	4.0	4.0
2	1.0	4.0	5.0	3.0	4.0	4.0	3.0	3.0	3.0	2.0	2.0	3.0	3.0
3	1.0	5.0	5.0	4.0	4.0	5.0	4.0	4.0	5.0	3.0	2.0	4.0	3.0
4	1.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0
5	1.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0
6	1.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	3.0	3.0	4.0	3.0
7	1.0	4.0	4.0	3.0	5.0	5.0	3.0	3.0	4.0	3.0	4.0	4.0	3.0

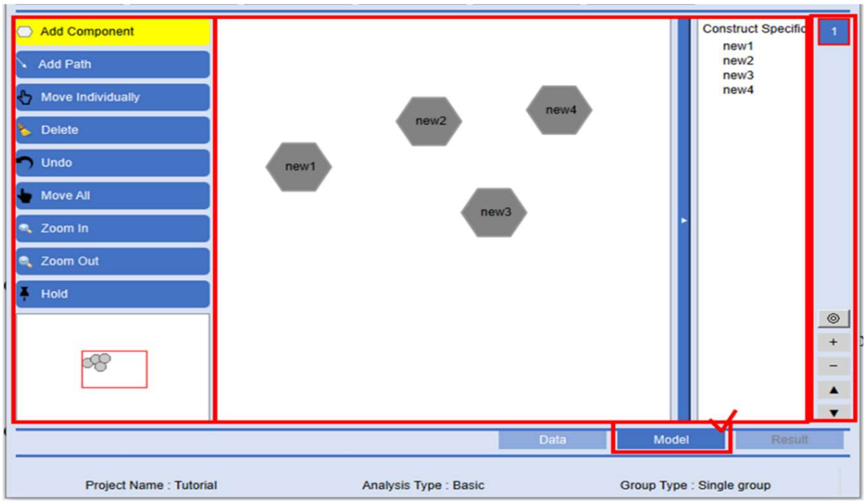
4. How to Choose Analysis Type

- Users can choose an analysis type in [**Analysis**] on the Menu Bar.



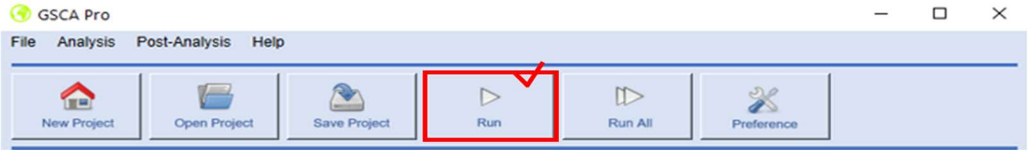
5. How to Specify Model

- Users can specify a model on the Main Window. When they have viewed their data or analysis results, they can click on the **[Model]** tap to specify or view a model.
- Users can specify a model with tools in the Tool Panel. A detailed description of model specification is provided in the following chapters.



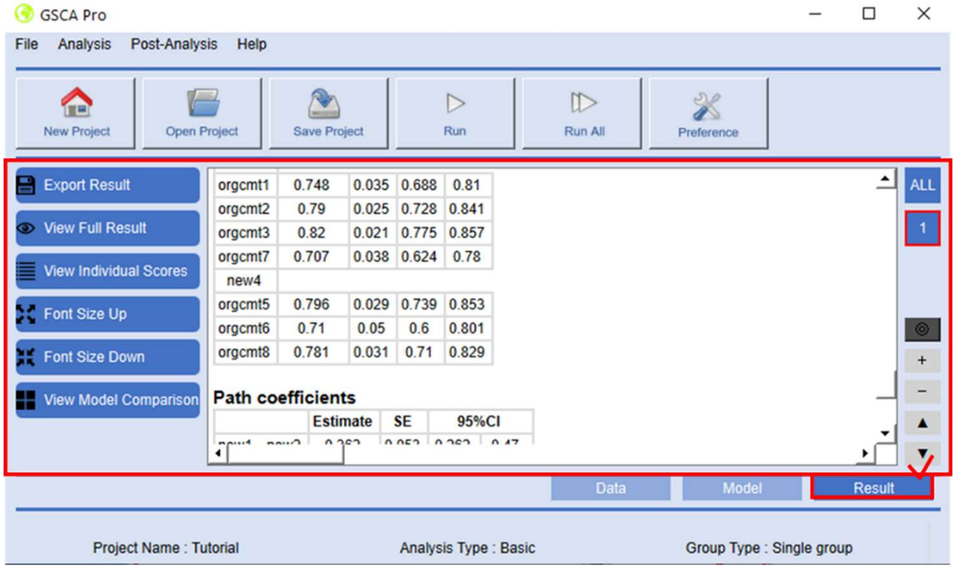
6. How to Fit Model

- Click on the **[Run]** shortcut to fit a specified model to the uploaded data.



7. How to View Analysis Result

- *GSCA Pro* automatically displays analysis results after fitting a model. Users can also click on the **[Result]** tab to view the results.



orgcmt1	0.748	0.035	0.688	0.81
orgcmt2	0.79	0.025	0.728	0.841
orgcmt3	0.82	0.021	0.775	0.857
orgcmt7	0.707	0.038	0.624	0.78
new4				
orgcmt5	0.796	0.029	0.739	0.853
orgcmt6	0.71	0.05	0.6	0.801
orgcmt8	0.781	0.031	0.71	0.829

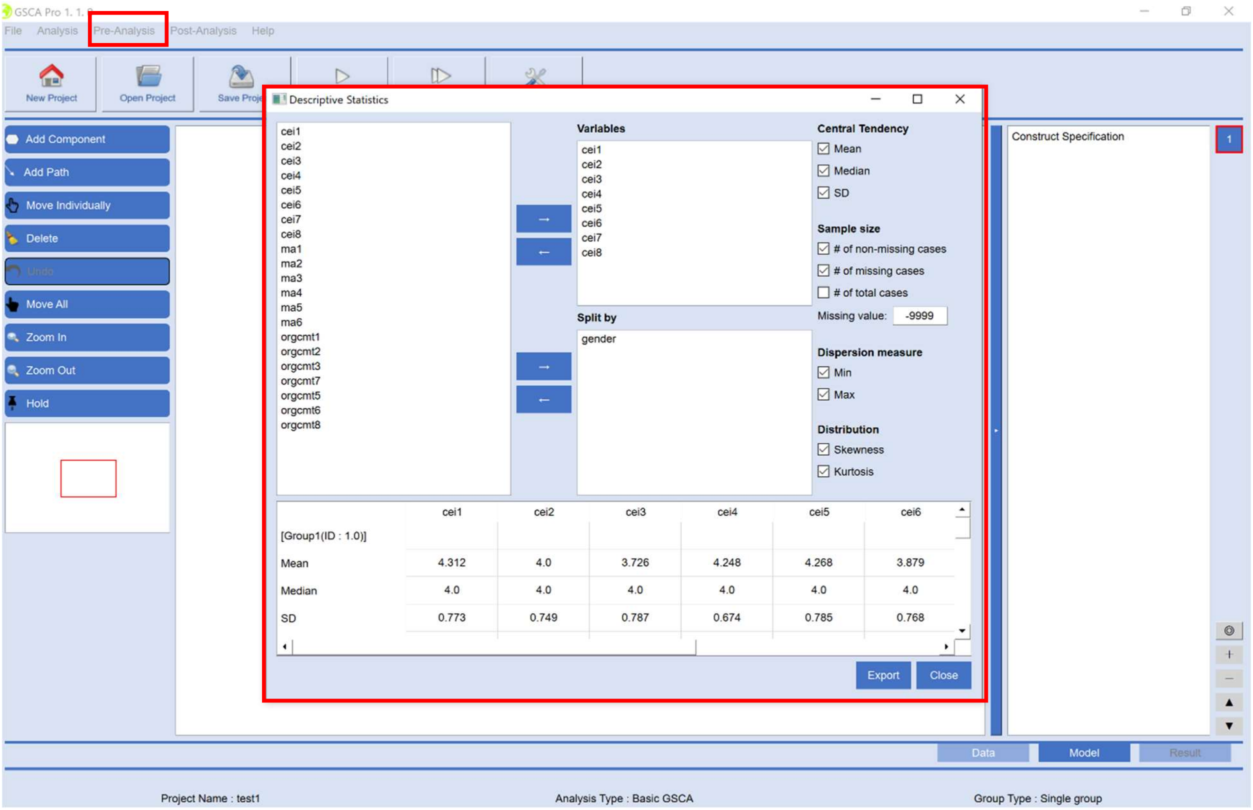
Path coefficients

	Estimate	SE	95%CI

Project Name : Tutorial
Analysis Type : Basic
Group Type : Single group

Pre-Analysis – Descriptive Statistics

- To calculate descriptive statistics for the data, select "**Pre-Analysis → Descriptive Statistics**"
    - Select variables on the left-hand window and move them to the upper right-hand window labelled "**Variables**."
    - Choose which descriptive statistics are calculated for the selected variables.
    - Users can calculate descriptive statistics for the variables in different groups by moving a grouping variable (e.g., gender) to the lower right-hand window labelled "**Split by**."
    - Users can export the calculated descriptive statistics in CSV format by clicking on the icon **[Export]** at the bottom.



Variables
cei1
cei2
cei3
cei4
cei5
cei6
cei7
cei8

Split by
gender

Central Tendency
☑ Mean
☑ Median
☑ SD

Sample size
☑ # of non-missing cases
☑ # of missing cases
☐ # of total cases
Missing value: -9999

Dispersion measure
☑ Min
☑ Max

Distribution
☑ Skewness
☑ Kurtosis

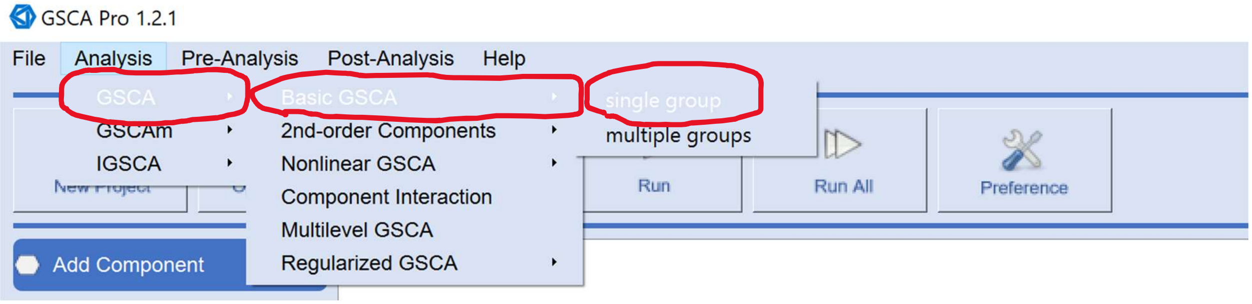
	cei1	cei2	cei3	cei4	cei5	cei6
[Group1(ID : 1.0)]						
Mean	4.312	4.0	3.726	4.248	4.268	3.879
Median	4.0	4.0	4.0	4.0	4.0	4.0
SD	0.773	0.749	0.787	0.674	0.785	0.768

Project Name : test1
Analysis Type : Basic GSCA
Group Type : Single group

GSCA (generalized structured component analysis) can be used for specifying and estimating models with components (or weighted composites) of indicators only. GSCA Pro uses a hexagon to signify a component in a path diagram. It currently implements various features of GSCA as shown below.

Analysis – Basic GSCA: Single Group Analysis

- To begin, select "**Analysis → GSCA → Basic GSCA → single group**" under the [**Analysis**] menu.



1. Specify a structural equation model

Users can specify their structural equation model with the following steps.

Step 1: Draw components

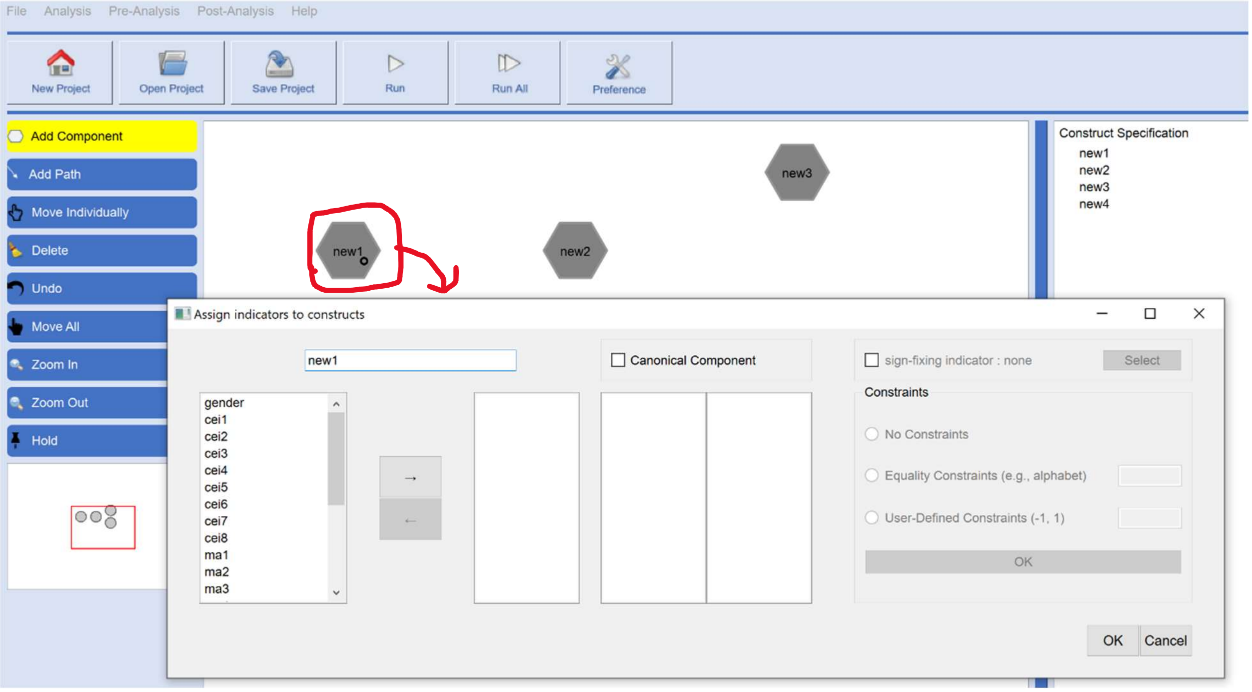
Users are to draw components before assigning variables to them as follows:

- Click once on **[Add Component]** in the Tool Panel.
- Click the left mouse button with the cursor placed in the Main Window as many times as the number of components. In the present example, four clicks resulted in the creation of four components. By default, the four components were initially named *new1* to *new4*.

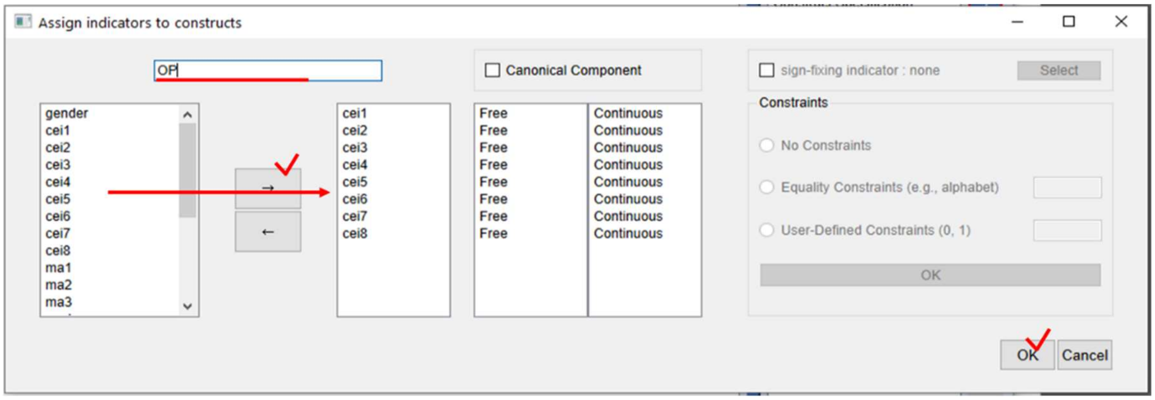
Step 2: Assign indicators to components (measurement model)

After drawing components, users are to specify their measurement model as follows:

- Double-click on an individual component (a hexagon). Then, the "**Assign Indicators to Constructs**" window will appear.



- In the "**Assign Indicators to Constructs**" window,
  - Users can rename the component by typing a new name.
  - Users select the appropriate indicators in the list, which appears on the left-hand dialog window, and move them to the right-hand dialog window ("**Free**" means a free loading to be estimated).
  - Optionally,
    - Users can choose whether the component is specified as a canonical component, often known as a formative component, which does not involve loadings.
    - If users want to align the sign of each indicator's weight with the correlation of a certain indicator (a sign-fixing indicator) with the component, they can indicate which indicator is used as the sign-fixing indicator.
    - Users can constrain certain loadings to be equal (Equality Constraints) or constant (User-Defined Constraints). Refer to page 18.
  - Click on OK.

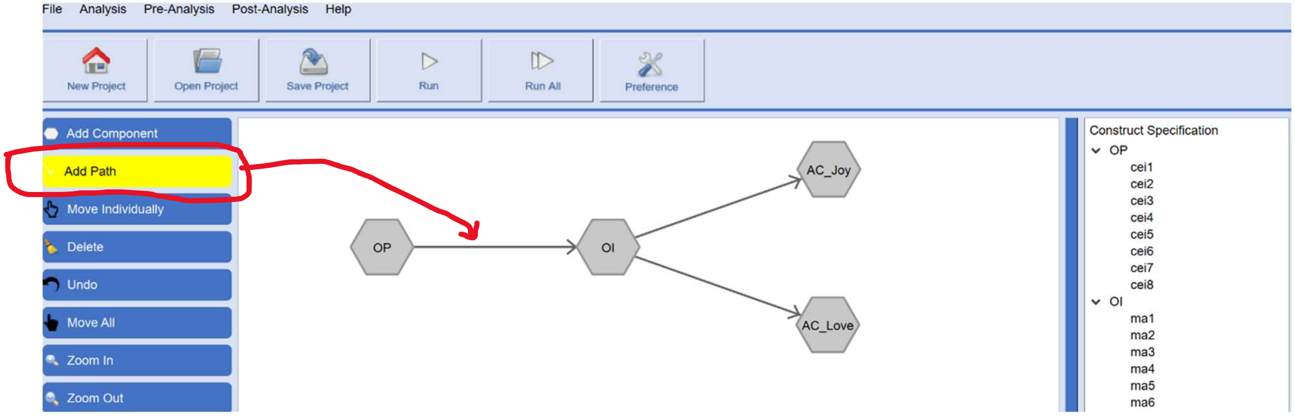


- Repeat the above steps for the remaining components.

<u>Step 3: Draw path coefficients (structural model)</u>

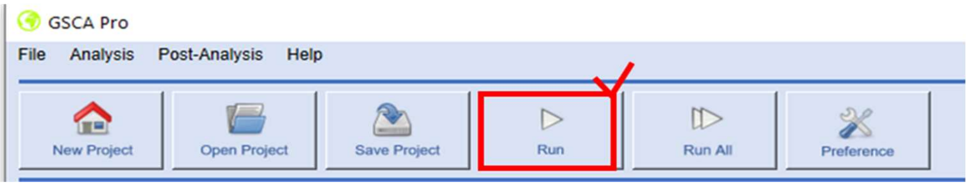
Path coefficients are to be drawn as follows:

- Click once on **[Add Path]** in the Tool Panel.
- Drag a path from an independent component to the corresponding dependent component. Repeat the above steps until all paths are drawn.



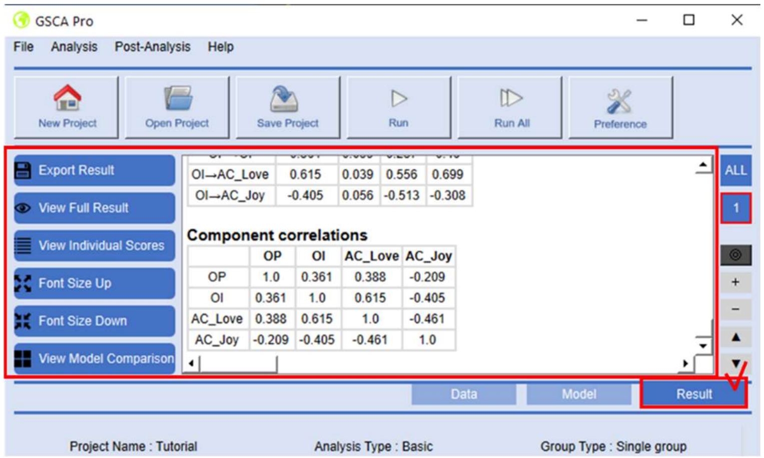
2. Run *GSCA Pro*

- Once the above steps are complete, users can run *GSCA Pro* for fitting the specified model to the data. This is done by clicking on the **[Run]** shortcut.



3. View and Interpret Basic Results

- When the program is finished running, basic analysis results are displayed in the "**Result**" tab.



OI→AC_Love	0.615	0.039	0.556	0.699
OI→AC_Joy	-0.405	0.056	-0.513	-0.308

Component correlations

	OP	OI	AC_Love	AC_Joy
OP	1.0	0.361	0.388	-0.209
OI	0.361	1.0	0.615	-0.405
AC_Love	0.388	0.615	1.0	-0.461
AC_Joy	-0.209	-0.405	-0.461	1.0

Project Name : Tutorial
Analysis Type : Basic
Group Type : Single group

- The basic analysis results of our example are below.

```
=================================================================
Model Number : 1

Analysis Type : Basic / Single group
Execution Date : Wed Feb 24 14:13:05 2021
Number of bootstrap samples : 100

The ALS algorithm converged in 4 iterations (convergence criterion = 0.0001)

Elapsed time for original sample: 0 minute(s) 0.01 second(s)
Average elapsed time per bootstrap sample: 0 minute(s) 0.00 second(s)
Total elapsed time: 0 minute(s) 0.20 second(s)
=================================================================
```

Model fit measures

FIT	AFIT	FITs	FITm	GFI	SRMR	OPE	OPEs	OPEm
0.535	0.532	0.168	0.606	0.985	0.048	0.466	0.845	0.394

The above table provides various model fit measures in GSCA.

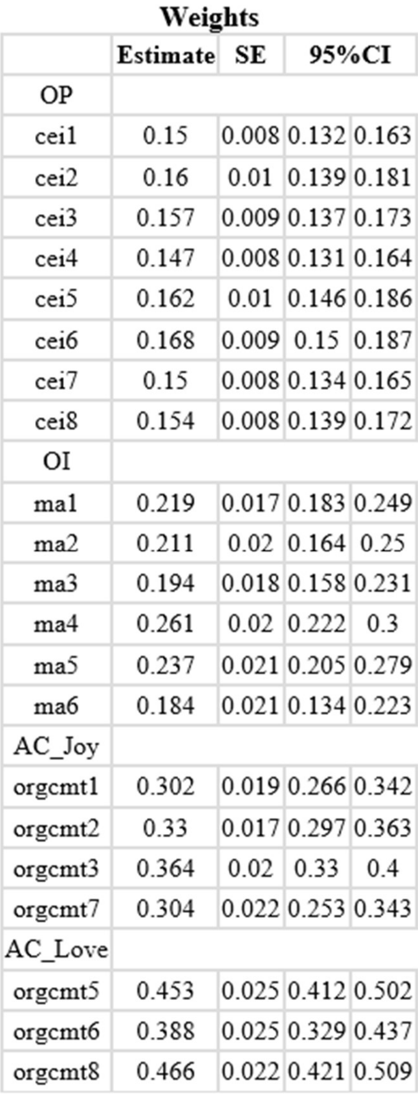
- **FIT** indicates the total variance of all variables (indicators and components) explained by a particular model specification. Like R squared in linear regression, the values of FIT range from 0 to 1. The larger this value, the more variance in the variables is accounted for by the specified model. For example, FIT = .50 indicates that 50% of the total variance of all variables is explained by the model. There is no rule of thumb cutoff for FIT, which is indicative of an acceptable fit.

- **AFIT** (Adjusted FIT) is similar to FIT but takes model complexity into account. Like Adjusted R-squared in linear regression, AFIT cannot be interpreted in the same way as FIT (i.e., the proportion of the total variance explained). Instead, it can be used only for comparing competing models. The model with the largest AFIT value may be chosen among competing models.
- **FIT_S** indicates the total variance of all components explained by a particular structural model specification. The values of FIT_S range from 0 to 1. The larger this value, the more variance in the components is accounted for by the specified structural model.
- **FIT_M** indicates the total variance of all indicators explained by a particular measurement model specification. The values of FIT_M range from 0 to 1. The larger this value, the more variance in the indicators is accounted for by the specified measurement model.
- **GFI** (goodness-of-fit index) and **SRMR** (standardized root mean squared residual). Both are proportional to the difference between the sample covariances and the covariances reproduced by the parameter estimates of GSCA. A recent study suggested the following rules-of-thumb cutoff criteria for GFI and SRMR in GSCA (Cho, Hwang, Sarstedt, & Ringle, 2020)

    - When sample size = 100, a GFI ≥ .89 and an SRMR ≤ .09 indicate an acceptable fit. Although both indexes can be used to assess model fit, using the SRMR with the above cutoff value may be better than using the GFI with the suggested cutoff value. Also, if SRMR ≤ .09, then a GFI cutoff value of ≥ .85 may still be indicative of an acceptable fit.

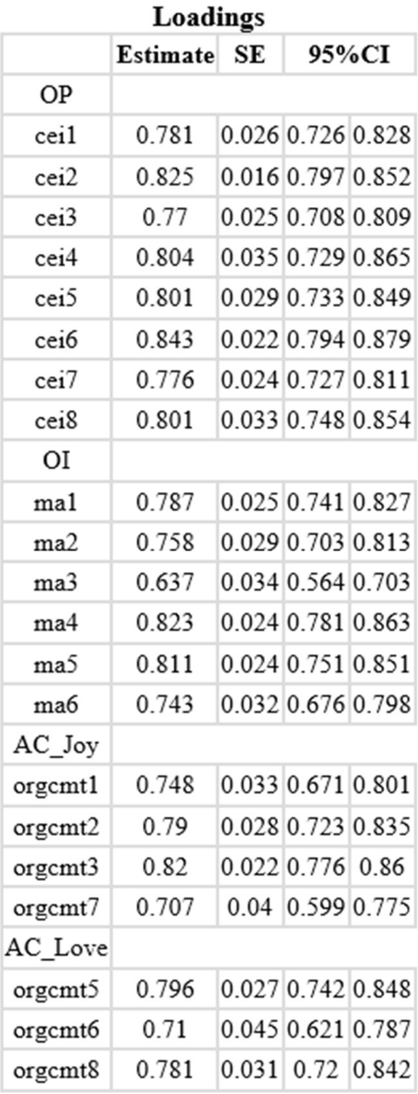
    - When sample size > 100, a GFI ≥ .93 or an SRMR ≤ .08 indicates an acceptable fit. In this case, there is no preference for one index over the other, or for using a combination of the indexes over using them separately. Each index's suggested cutoff value may be used independently to assess the model fit.

- **OPE** (out-of-sample prediction error) indicates the prediction power of a specified model for unseen observations (Cho, Jung, & Hwang, 2019). The OPE can be used for comparing different models in terms of prediction power.
- **OPE_S** indicates the prediction power of a specified structural model and **OPE_M** indicates the prediction power of a specified measurement model.



Weights

	Estimate	SE	95%CI	
OP				
cei1	0.15	0.008	0.132	0.163
cei2	0.16	0.01	0.139	0.181
cei3	0.157	0.009	0.137	0.173
cei4	0.147	0.008	0.131	0.164
cei5	0.162	0.01	0.146	0.186
cei6	0.168	0.009	0.15	0.187
cei7	0.15	0.008	0.134	0.165
cei8	0.154	0.008	0.139	0.172
OI				
ma1	0.219	0.017	0.183	0.249
ma2	0.211	0.02	0.164	0.25
ma3	0.194	0.018	0.158	0.231
ma4	0.261	0.02	0.222	0.3
ma5	0.237	0.021	0.205	0.279
ma6	0.184	0.021	0.134	0.223
AC_Joy				
orgcmt1	0.302	0.019	0.266	0.342
orgcmt2	0.33	0.017	0.297	0.363
orgcmt3	0.364	0.02	0.33	0.4
orgcmt7	0.304	0.022	0.253	0.343
AC_Love				
orgcmt5	0.453	0.025	0.412	0.502
orgcmt6	0.388	0.025	0.329	0.437
orgcmt8	0.466	0.022	0.421	0.509



Loadings

	Estimate	SE	95%CI	
OP				
cei1	0.781	0.026	0.726	0.828
cei2	0.825	0.016	0.797	0.852
cei3	0.77	0.025	0.708	0.809
cei4	0.804	0.035	0.729	0.865
cei5	0.801	0.029	0.733	0.849
cei6	0.843	0.022	0.794	0.879
cei7	0.776	0.024	0.727	0.811
cei8	0.801	0.033	0.748	0.854
OI				
ma1	0.787	0.025	0.741	0.827
ma2	0.758	0.029	0.703	0.813
ma3	0.637	0.034	0.564	0.703
ma4	0.823	0.024	0.781	0.863
ma5	0.811	0.024	0.751	0.851
ma6	0.743	0.032	0.676	0.798
AC_Joy				
orgcmt1	0.748	0.033	0.671	0.801
orgcmt2	0.79	0.028	0.723	0.835
orgcmt3	0.82	0.022	0.776	0.86
orgcmt7	0.707	0.04	0.599	0.775
AC_Love				
orgcmt5	0.796	0.027	0.742	0.848
orgcmt6	0.71	0.045	0.621	0.787
orgcmt8	0.781	0.031	0.72	0.842

The above two tables display the estimates of component weights and component loadings of indicators per component. They also show the bootstrap standard errors (SE) and bootstrap 95% confidence intervals (95% CI) of the weight and loading estimates. The 95% confidence intervals can be used for testing the significance of an estimate (i.e., an estimate may be considered statistically significant at a .05 level if its confidence interval does not include 0). When a component is specified as a canonical component, its indicators' loadings will not be reported. Note that GSCA Pro does not provide a t-test (Estimate/SE) and its p-value because this test is a parametric test assuming the normality of a parameter estimate. Such a parametric test is not consistent with GSCA which typically does not require a distributional assumption. No literature is available that shows that GSCA's estimates are normally distributed.

Path coefficients

	Estimate	SE	95%CI	
OP→OI	0.362	0.059	0.234	0.476
OI→AC_Joy	0.614	0.035	0.559	0.686

OI→AC_Love	-0.404	0.051	-0.515	-0.307

This table shows the estimates of path coefficients and their bootstrap standard errors (SE) and 95% confidence intervals (95% CI).

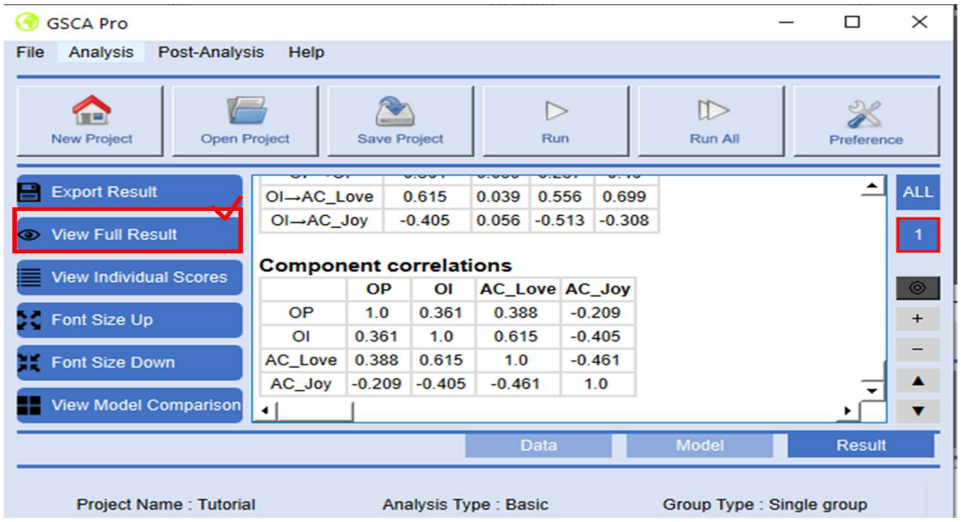
Component correlations

	OP	OI	AC_Joy	AC_Love
OP	1.1	0.362	0.388	-0.209
OI	0.362	1.1	0.614	-0.404
AC_Joy	0.388	0.614	1.1	-0.461
AC_Love	-0.209	-0.404	-0.461	1.1

This table shows the correlations among components.

4. View and Interpret Full Results

- To view more detailed results, click on [**View Full Result**] on the left-hand window. Then, more detailed analysis results are displayed.



OI→AC_Love	0.615	0.039	0.556	0.699
OI→AC_Joy	-0.405	0.056	-0.513	-0.308

Component correlations

	OP	OI	AC_Love	AC_Joy
OP	1.0	0.361	0.388	-0.209
OI	0.361	1.0	0.615	-0.405
AC_Love	0.388	0.615	1.0	-0.461
AC_Joy	-0.209	-0.405	-0.461	1.0

Project Name : Tutorial
Analysis Type : Basic
Group Type : Single group

- Below are the additional results that are not displayed in the "**Result**" tab.

HTMT

OP ↔ OI	0.409
OP ↔ AC_Joy	0.467
OP ↔ AC_Love	0.26
OI ↔ AC_Joy	0.753
OI ↔ AC_Love	0.527
AC_Joy ↔ AC_Love	0.641

This table shows the heterotrait-monotrait (HTMT) ratio per pair of components, which is defined as the mean value of the item correlations across constructs relative to the (geometric) mean of the average correlations for the items measuring the same construct. Discriminant validity problems are present when HTMT values are high. Henseler et al. (2015) propose a threshold value of 0.90 for structural models with constructs that are conceptually very similar. In such a setting, an HTMT value above 0.90 would suggest that discriminant validity is not present. But when constructs are conceptually more distinct, a lower, more conservative, threshold value is suggested, such as 0.85 (Henseler, Ringle, & Sarstedt, 2015).

Rönkkö and Cho (2020) show that the HTMT ratio is based on the parallel assumption of each block of indicators, i.e., the variances of the indicators are the same and the covariances of indicators are the same. The parallel assumption is not made in GSCA and is hardly met in practice. In addition, the HTMT ratios may not be suitable for assessing the discriminant validity of a model with components only. Thus, in general, we do not recommend relying on the HTMT ratios in GSCA. Instead, they may be used for factors when applying GSCA$_M$ (p. 36) or IGSCA (p. 37).

Construct quality measures

	OP	**OI**	**AC_Joy**	**AC_Love**
PVE	0.641	0.581	0.589	0.583
Alpha	0.92	0.854	0.766	0.642
Rho	0.934	0.892	0.851	0.807
Dimensionality	1.1	1.1	1.1	1.1

The **PVE** (Proportion of Variance Explained) is the average amount of the total variance of indicators that is explained by their corresponding component, as in principal components analysis. If a single component explains 70% or higher of the total variance of a block of indicators, this may be indicative of unidimensionality for the block (Jolliffe & Cadman, 2016). The **Alpha** indicates Cronbach's alpha. The **Rho** is Dillon-Goldstein's rho or the composite reliability. Note that although Cronbach's alpha is used for assessing the reliability of sum scores, this metric assumes the equal covariances of a block of indicators, i.e., tau-equivalence (Benitez et al., 2020), which is not made in GSCA. Dillon-Goldstein's rho should be calculated based on factor loadings rather than component loadings (Benitez et al., 2020). Thus, this metric is not suitable for GSCA. Instead, the Rho can be used for factors when applying GSCA$_M$ or IGSCA. The **Dimensionality** indicates the number of eigenvalues greater than 1 for a set of indicators per component. If Dimensionality > 1, more than one component may be considered for a set of indicators.

Fornell-Larcker criterion values

	OP	**OI**	**AC_Joy**	**AC_Love**
OP	0.8	0.0	0.0	0.0
OI	0.362	0.762	0.0	0.0
AC_Joy	0.388	0.614	0.767	0.0
AC_Love	-0.209	-0.404	-0.461	0.763

Fornell and Larcker (1981) proposed the traditional metric and suggested that each factor's AVE (average variance extracted) should be compared to the squared inter-factor correlation (as a measure of shared variance) of that same factor and all other factors in the structural model. The shared variance for all factors should not be larger than their AVEs. However, AVE and the Fornell-Larcker criterion do not apply to GSCA because they are calculated based on factor loadings (Benitez et al., 2020). Instead, these metrics may be used for factors when applying $GSCA_M$ or IGSCA.

R squared values of indicators in the measurement model

cei1	cei2	cei3	cei4	cei5	cei6	cei7	cei8	ma1	ma2	ma3	ma4	ma5	ma6	orgcmt1	orgcmt2	orgcmt3	orgcmt7	orgcmt5	orgcmt6	orgcmt8
0.609	0.68	0.593	0.646	0.642	0.711	0.603	0.642	0.619	0.575	0.405	0.678	0.657	0.552	0.559	0.624	0.672	0.5	0.633	0.504	0.61

This table shows how much variance of each indicator is explained by the indicator's component. When a canonical component is chosen for a set of indicators, the indicators' R-squared values are not provided.

R squared values of components in the structural model

OP	OI	AC_Joy	AC_Love
0.0	0.131	0.377	0.163

This table shows how much variance of each component is explained by its independent components. When a component is exogenous (e.g., OP in the present example), its R-squared value is equal to zero.

GSCA Pro also provides the **variance inflation factor (VIF)** for the structural model if any component is affected by more than one component. Although no clear rule of thumb is available, a VIF value greater than 5 (Hair, Ringle, & Sarstedt, 2011) or 10 (Myers, 1990, p. 369) has often been taken as evidence to raise some concern. Also, if the measurement model contains a "canonical component", the VIF values of its corresponding indicators are calculated.

F squared values

	OP	OI	AC_Joy	AC_Love
OP	0.0	0.15	0.0	0.0
OI	0.0	0.0	0.604	0.195
AC_Joy	0.0	0.0	0.0	0.0
AC_Love	0.0	0.0	0.0	0.0

This table shows the f^2 effect size of each predictor component. As a rule of thumb, the f^2 values of 0.02, 0.15 and 0.35 may be considered small, medium, and large effect sizes, respectively (Cohen, 1988).

Unstandardized component means

OP	OI	AC_Joy	AC_Love
4.078	3.663	3.164	2.79

This table shows the averages of unstandardized components in the same scales as their original indicators.

Unstandardized component variances

OP	OI	AC_Joy	AC_Love
0.411	0.427	0.409	0.377

This table shows the variances of unstandardized components in the same scales as their original indicators.

Sample correlations (lower diagonal) & Residual correlations (upper diagonal)

	cei1	cei2	cei3	cei4	cei5	cei6	cei7	cei8	ma1	ma2	ma3	ma4	ma5	ma6	orgcmt1	orgcmt2	orgcmt3	orgcmt7	orgcmt5	orgcmt6	orgcmt8
cei1	0.0	-0.0	-0.317	0.035	0.234	-0.35	-0.46	-0.137	0.091	0.139	0.103	-0.282	-0.069	0.037	-0.012	-0.047	-0.017	0.072	0.143	-0.035	-0.102
cei2	0.644	0.0	0.21	-0.225	-0.366	-0.129	-0.25	-0.226	0.048	-0.025	0.052	0.045	-0.093	-0.037	0.097	-0.066	-0.147	0.114	0.03	-0.161	0.123
cei3	0.475	0.711	0.0	-0.193	-0.507	-0.147	0.147	-0.26	-0.028	-0.127	-0.053	0.049	0.073	0.095	0.12	-0.019	-0.02	-0.075	-0.017	-0.031	0.045
cei4	0.64	0.587	0.545	0.0	0.275	-0.244	-0.43	-0.16	-0.068	0.054	0.006	0.061	-0.091	0.037	-0.071	0.001	0.029	0.037	-0.134	0.08	0.051
cei5	0.713	0.537	0.423	0.742	0.0	-0.065	-0.402	-0.162	-0.038	0.052	-0.003	-0.14	-0.033	0.193	-0.14	-0.027	0.163	-0.002	0.124	0.043	-0.157
cei6	0.54	0.656	0.598	0.599	0.655	0.0	0.181	-0.224	-0.083	-0.072	0.031	0.094	-0.023	0.047	-0.039	0.076	0.0	-0.035	0.034	0.022	-0.052
cei7	0.425	0.551	0.657	0.463	0.471	0.716	0.0	0.179	-0.036	-0.004	-0.066	0.104	0.135	-0.153	0.033	0.094	-0.023	-0.096	-0.105	0.019	0.082
cei8	0.574	0.584	0.517	0.587	0.584	0.603	0.689	0.0	0.112	-0.011	-0.063	0.082	0.087	-0.23	0.007	-0.01	0.008	-0.005	-0.085	0.065	0.019
ma1	0.278	0.294	0.272	0.204	0.251	0.272	0.257	0.293	0.0	-0.052	-0.226	-0.41	-0.22	-0.023	0.159	-0.093	-0.073	0.01	-0.009	0.016	-0.007
ma2	0.273	0.238	0.202	0.223	0.256	0.243	0.242	0.219	0.576	0.0	-0.154	-0.313	-0.305	-0.153	-0.103	0.061	-0.15	0.185	0.053	-0.038	-0.014
ma3	0.239	0.239	0.196	0.18	0.205	0.247	0.18	0.167	0.394	0.405	0.0	-0.229	-0.363	-0.114	-0.034	-0.014	0.013	0.032	0.026	-0.037	0.01
ma4	0.073	0.219	0.235	0.177	0.147	0.255	0.241	0.208	0.504	0.508	0.424	0.0	0.147	-0.289	0.032	0.022	0.087	-0.135	-0.068	-0.02	0.083
ma5	0.182	0.209	0.277	0.16	0.217	0.255	0.287	0.246	0.559	0.498	0.352	0.716	0.0	-0.281	0.035	0.005	0.057	-0.093	-0.039	0.043	-0.003
ma6	0.188	0.188	0.252	0.173	0.269	0.239	0.136	0.087	0.575	0.496	0.414	0.502	0.492	0.0	-0.096	0.017	0.063	0.012	0.044	0.047	-0.086
orgcmt1	0.232	0.266	0.281	0.255	0.215	0.256	0.261	0.226	0.371	0.271	0.275	0.394	0.348	0.258	0.0	-0.237	-0.366	-0.356	-0.103	0.025	0.074
orgcmt2	0.215	0.201	0.219	0.282	0.259	0.292	0.281	0.215	0.307	0.376	0.318	0.431	0.374	0.343	0.495	0.0	-0.341	-0.389	0.015	-0.022	0.006
orgcmt3	0.182	0.128	0.174	0.246	0.279	0.219	0.191	0.174	0.362	0.342	0.369	0.502	0.44	0.404	0.474	0.528	0.0	-0.309	-0.061	0.082	-0.02
orgcmt7	0.288	0.297	0.216	0.317	0.288	0.277	0.223	0.243	0.328	0.418	0.322	0.343	0.313	0.323	0.362	0.39	0.455	0.0	0.141	-0.083	-0.055
orgcmt5	-0.039	-0.114	-0.162	-0.201	-0.075	-0.166	-0.16	-0.14	-0.214	-0.178	-0.179	-0.352	-0.328	-0.147	-0.369	-0.321	-0.393	-0.185	0.0	-0.437	-0.533
orgcmt6	-0.016	-0.088	-0.071	-0.018	-0.004	-0.061	-0.017	0.015	-0.14	-0.155	-0.157	-0.258	-0.22	-0.086	-0.151	-0.163	-0.157	-0.137	0.379	0.0	-0.529
orgcmt8	-0.203	-0.154	-0.205	-0.205	-0.25	-0.269	-0.156	-0.173	-0.255	-0.245	-0.22	-0.341	-0.357	-0.242	-0.3	-0.327	-0.381	-0.272	0.42	0.322	0.0

The lower diagonal of this table shows the correlations among all indicators, whereas the upper diagonal shows the differences between the sample correlations and model-implied correlations.

Correlations between indicators and components

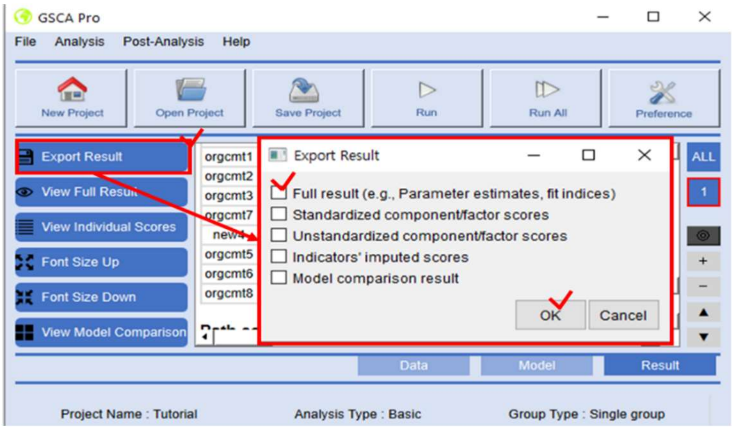
	OP	OI	AC_Joy	AC_Love
cei1	0.781	0.262	0.295	-0.119
cei2	0.825	0.302	0.283	-0.157
cei3	0.77	0.314	0.286	-0.196
cei4	0.804	0.243	0.356	-0.193
cei5	0.801	0.288	0.34	-0.152
cei6	0.843	0.33	0.338	-0.224
cei7	0.776	0.299	0.309	-0.152
cei8	0.801	0.271	0.277	-0.138
ma1	0.332	0.787	0.445	-0.27
ma2	0.296	0.758	0.457	-0.255
ma3	0.259	0.637	0.42	-0.244
ma4	0.244	0.823	0.548	-0.419
ma5	0.287	0.811	0.484	-0.4
ma6	0.241	0.743	0.436	-0.213
orgcmt1	0.311	0.425	0.748	-0.365
orgcmt2	0.307	0.473	0.79	-0.361
orgcmt3	0.249	0.533	0.82	-0.416

orgcmt7	0.335	0.446	0.707	-0.264
orgcmt5	-0.165	-0.316	-0.417	0.796
orgcmt6	-0.041	-0.229	-0.198	0.71
orgcmt8	-0.253	-0.369	-0.42	0.781

This table shows the correlations between each indicator and all components. This information may be used for re-specifying the relationships between indicators and components (measurement model).

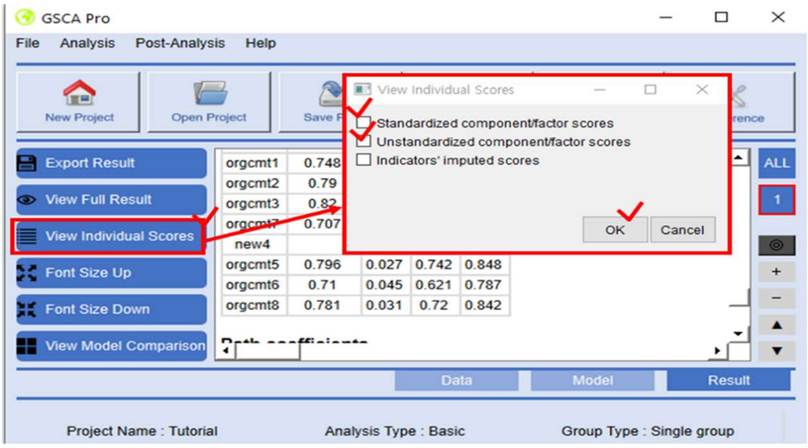
4. Export Results

- Users can export and store full results in CSV format by clicking on [**Export Result**], checking the Full result box in the "Export Result" window, and clicking on [OK].



5. View Individual Scores

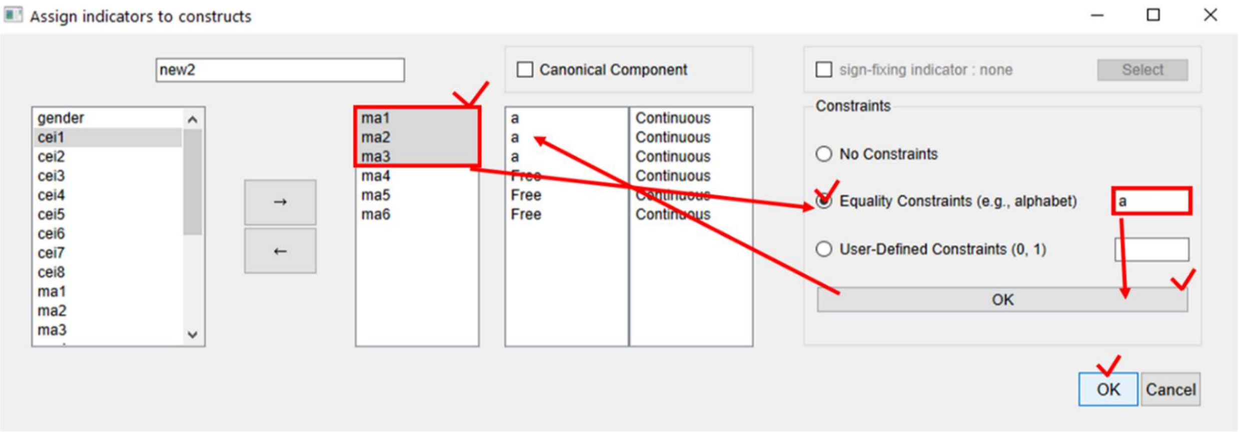
- Users can view individual scores (i.e., standardized construct scores, unstandardized construct scores, or indicator scores with missing values imputed) by clicking on [**View Individual Scores**].



Analysis – Basic GSCA with Constrained Parameters

1. How to impose equality constraints on loadings

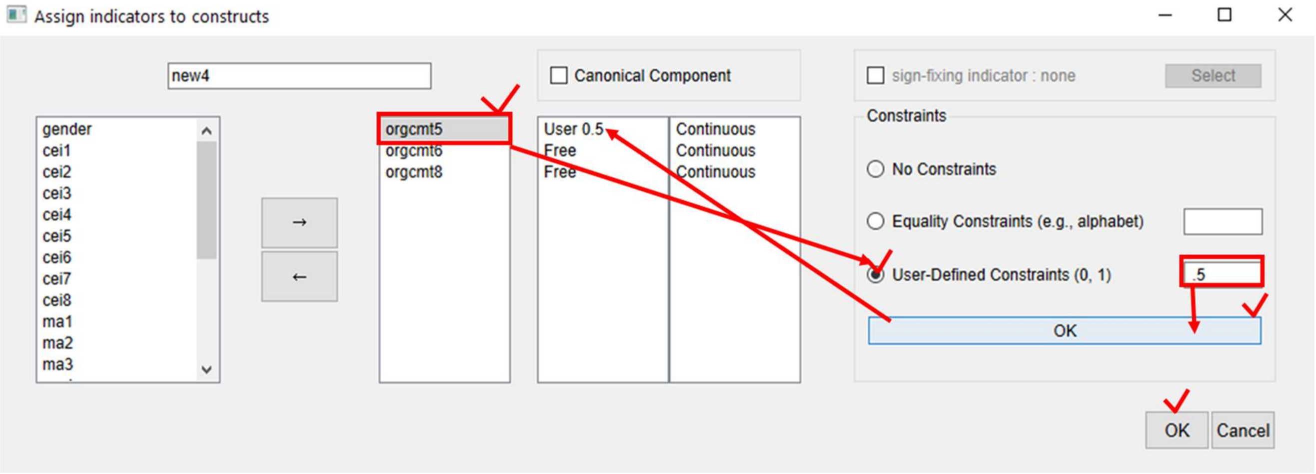
- In the "**Assign Indicators to Constructs**" window, select indicators whose loadings are constrained to be equal.
- Constrain the loadings of the selected indicators to be identical by inserting a label (e.g., an alphabet letter or number) in the "**Equality Constraints**" dialog box. Then, click on "**OK**".



* Note that any loadings with the same label will be constrained to be equal. In the above example, three indicators (ma1 – ma3) are chosen and labeled "a", indicating that the loadings for these indicators are constrained to be equal.

2. How to constrain loadings to user-defined values

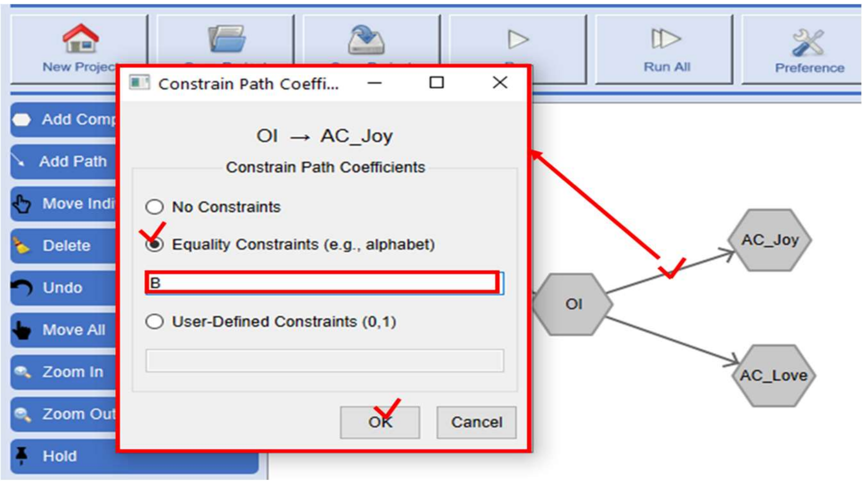
- In the "**Assign Indicators to Constructs**" window, select an indicator whose loading is to be fixed to a user-defined value.
- Constrain the loading of the selected indicator to a user-defined value by inserting that value in the "**User-Defined Constraints**" dialog box. Then, click on "**OK**".



* Note that user-defined values should be between 0 and 1 (**exclusive**).

3. How to impose equality constraints on path coefficients

- Double-click on the middle point of an individual path to be constrained in the model.
- In the "**Constrain Path Coefficients**" window, constrain the selected path coefficient by inserting a label (alphabet or number) in the "**Equality Constraints**" dialog. Then, click on "**OK**".



Constrain Path Coeffi...

OI → AC_Joy

Constrain Path Coefficients

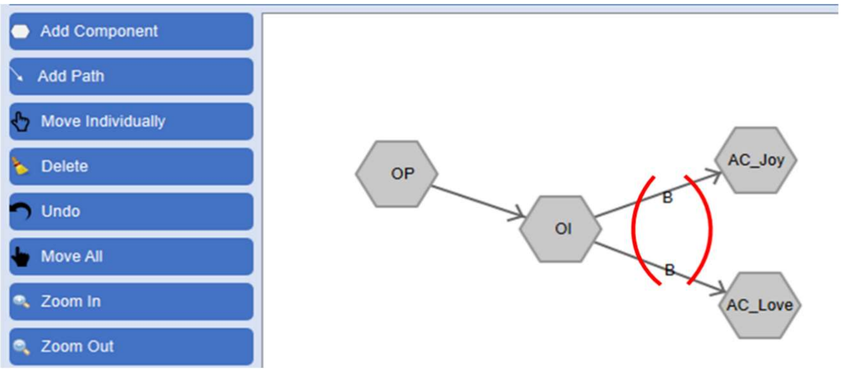
○ No Constraints

● Equality Constraints (e.g., alphabet)

B

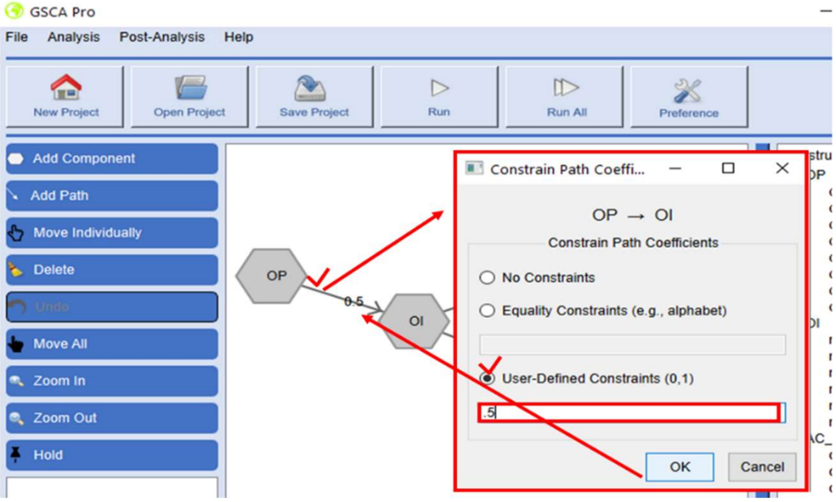
○ User-Defined Constraints (0,1)

- Repeat the above step for other path coefficients that are to be held equal to the first path coefficient, using the same label.
- In the model, subsequently, users can see all chosen paths labeled the same ("B"), indicating that they are constrained to be equal.



4. How to impose a user-defined constraint on path coefficients

- Double-click on the middle point of an individual path to be constrained in the model.
- In the "**Constrain Path Coefficients**" window, constrain the selected path coefficient to a user-defined value (between 0 and 1) by inserting that value in the "**User-Defined Constraints**" dialog. Then, click on "**OK**".



OP → OI

Constrain Path Coefficients

○ No Constraints

○ Equality Constraints (e.g., alphabet)

● User-Defined Constraints (0,1)

.5

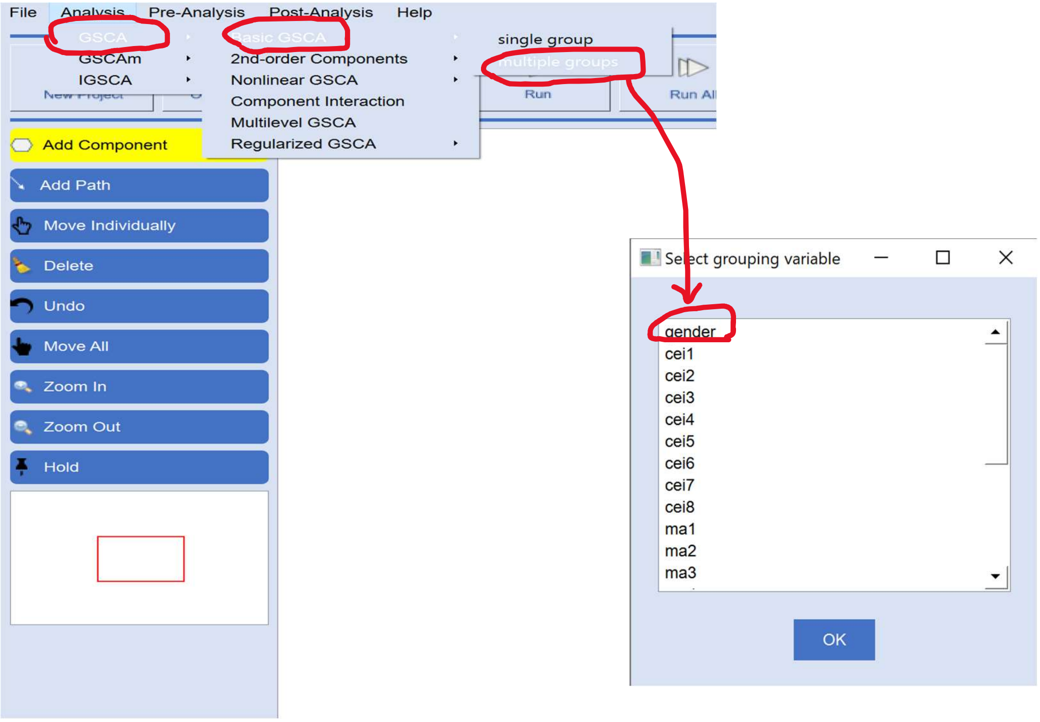
- In the model, subsequently, users can see the path fixed to the defined value.
- <u>Note that user-defined values should be between 0 and 1 (**exclusive**).</u>

Analysis – Basic GSCA: Multigroup Analysis

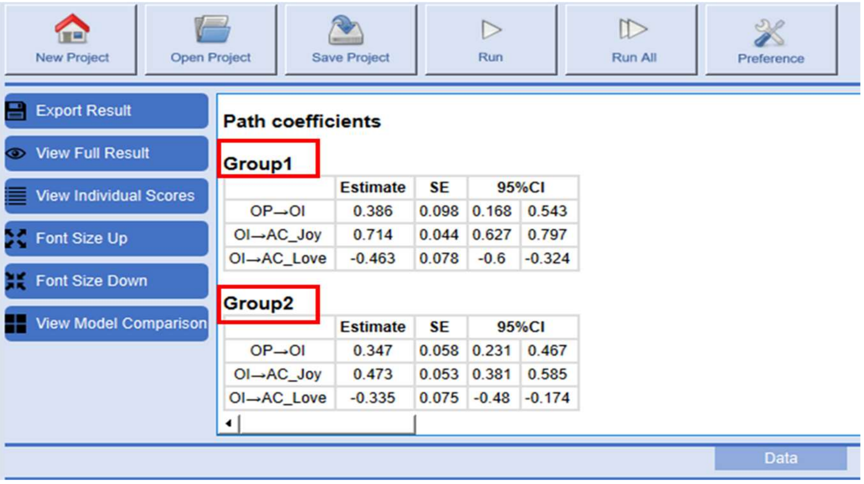
* Note: To conduct a multiple-group analysis, users must include a categorical/grouping variable in the data, which indicates group memberships of cases. Group memberships must be denoted by positive integers (e.g., sex: 1 = male & 2 = female) and arranged in ascending order (from smallest to largest), always using 1 as the smallest one (e.g., 1, 2, 3,…).

1. How to conduct a multi-group analysis without cross-group equality constraints

- To begin, select "**Analysis** → **GSCA** → **Basic GSCA** → **multiple groups**" under the [**Analysis**] menu.
- Select a grouping variable in the list of indicators in a dialog box. Then, click on "**OK**". In this example, "gender" was chosen.



- Users then specify their measurement and structural models in the same way as described for basic, single-group analysis.
- Once the above steps are complete, users can run *GSCA Pro* for fitting the specified model to multiple groups simultaneously. This is done by clicking on the **[Run]** shortcut.
- As shown below, all multi-group analysis results are displayed in the "**Results**" window. In this example, the same model was applied to two groups (males and females) at the same time. Thus, all parameter estimates are provided for each of the two groups labeled Group 1 and Group 2.



Path coefficients

Group1

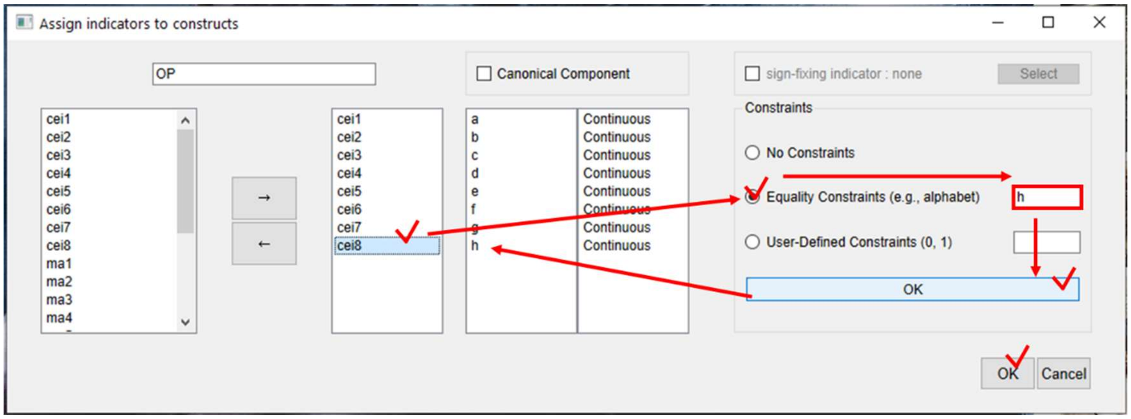
	Estimate	SE	95%CI	
OP→OI	0.386	0.098	0.168	0.543
OI→AC_Joy	0.714	0.044	0.627	0.797
OI→AC_Love	-0.463	0.078	-0.6	-0.324

Group2

	Estimate	SE	95%CI	
OP→OI	0.347	0.058	0.231	0.467
OI→AC_Joy	0.473	0.053	0.381	0.585
OI→AC_Love	-0.335	0.075	-0.48	-0.174

2. How to conduct a multi-group analysis with cross-group equality constraints

- To impose cross-group equality constraints on loadings, select indicators whose loadings are constrained to be equal across groups in the "**Assign Indicators to Constructs**" window. Then, constrain the loadings of the selected indicators to be identical across groups by inserting a label (alphabet or number) in the "**Equality Constraints**" dialog box. Then, click on "**OK**".

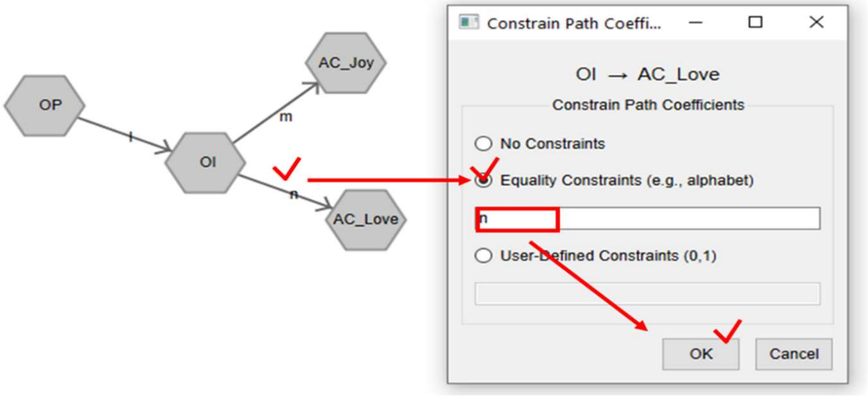


OP

cei1	a	Continuous
cei2	b	Continuous
cei3	c	Continuous
cei4	d	Continuous
cei5	e	Continuous
cei6	f	Continuous
cei7	g	Continuous
cei8	h	Continuous

● Equality Constraints (e.g., alphabet): h

- To impose cross-group equality constraints on path coefficients, clicking on the middle point of a path in the model. Then, constrain the selected path coefficient to be identical across groups by inserting a label in the "**Equality Constraints**" dialog box. Then, click on "**OK**".



● Equality Constraints (e.g., alphabet)

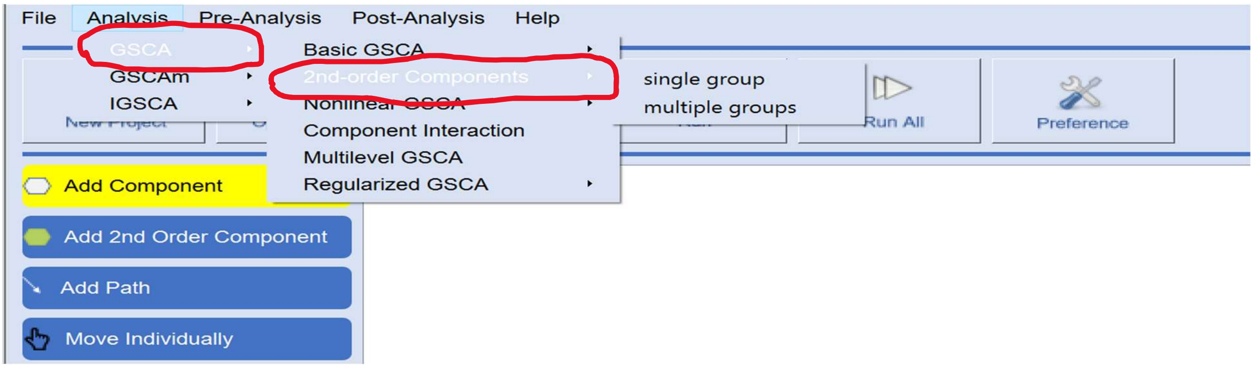
n

- <u>Note that any loadings and path coefficients with the same label will be constrained to be equal across groups</u>.

Analysis – GSCA with 2nd-order Components

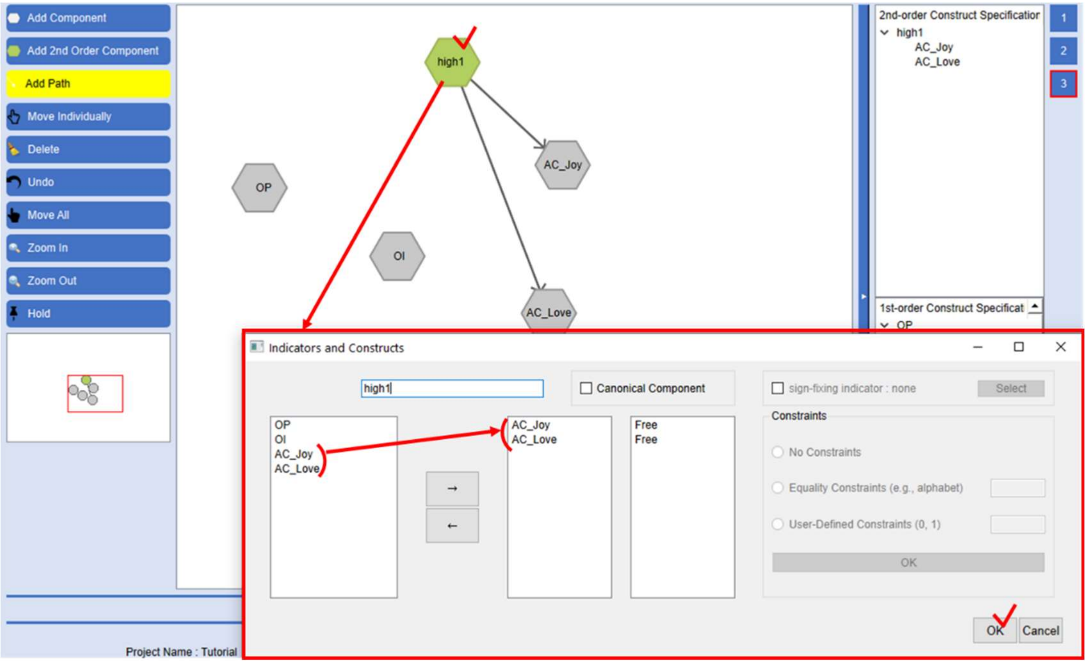
Users can specify and examine a model that involves second-order components (Hwang & Takane, 2014, Chapter 3).

- To begin, select "**Analysis → GSCA → 2nd-order Components → single group or multiple groups**" under the [**Analysis**] menu.



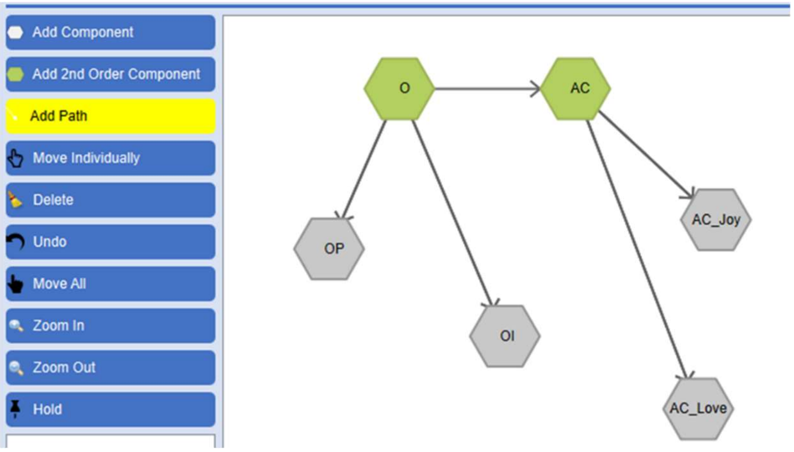
- Users specify (first-order) components as described earlier.

- Subsequently, users specify second-order components as follows:
    - Click once on **[Add 2nd-Order Component]** in the Tool Panel. Click the left mouse button with the cursor placed in the Main Window as many times as the number of second-order components, which appear as green hexagons. In the example below, a second-order component, labeled *high1*, is assumed to be linked to *AC_Joy* and *AC_Love*.
    - After drawing all second-order components, double-click on an individual second-order component.



- In the "**Assign Indicators to Constructs**" window,
  - Users can rename the second-order component by typing a new name.
  - Users select the (first-order) components in the list and move them to the right-hand dialog window ("Free" means a free loading to be estimated).
  - Then, arrows connecting second-order components to their first-order components will appear in the model.
  - Optionally,
    - ✓ Users can specify the second-order component as a canonical component, which does not involve loadings. In this case, the second-order component is connected to its first-order component by a straight line.
    - ✓ If users want to align the sign of each first-order component's weight with the correlation of a certain first-order component (a sign-fixing indicator) with the second-order component, they can indicate which first-order component is used as the sign-fixing indicator.
    - ✓ Users can impose constraints on loadings for 2nd-order components. This can be done in the "**Constrain Path Coefficients**" window. Users can access this window by double-clicking on the middle point of an individual arrow from a 2nd order component to (first-order) components.
  - Click on OK.
- Repeat the above steps for the remaining second-order components.

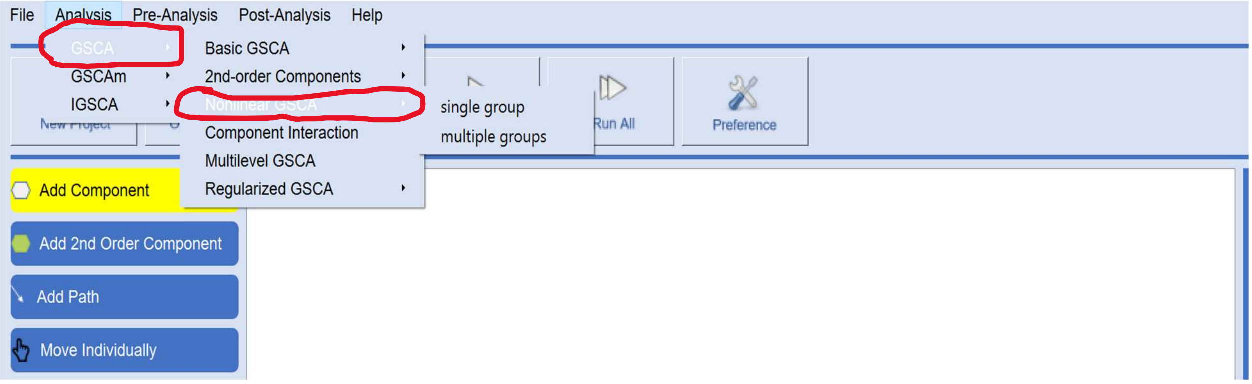
- Users draw path coefficients to complete their structural model.


Add Component
Add 2nd Order Component
Add Path
Move Individually
Delete
Undo
Move All
Zoom In
Zoom Out
Hold
O
AC
OP
OI
AC_Joy
AC_Love

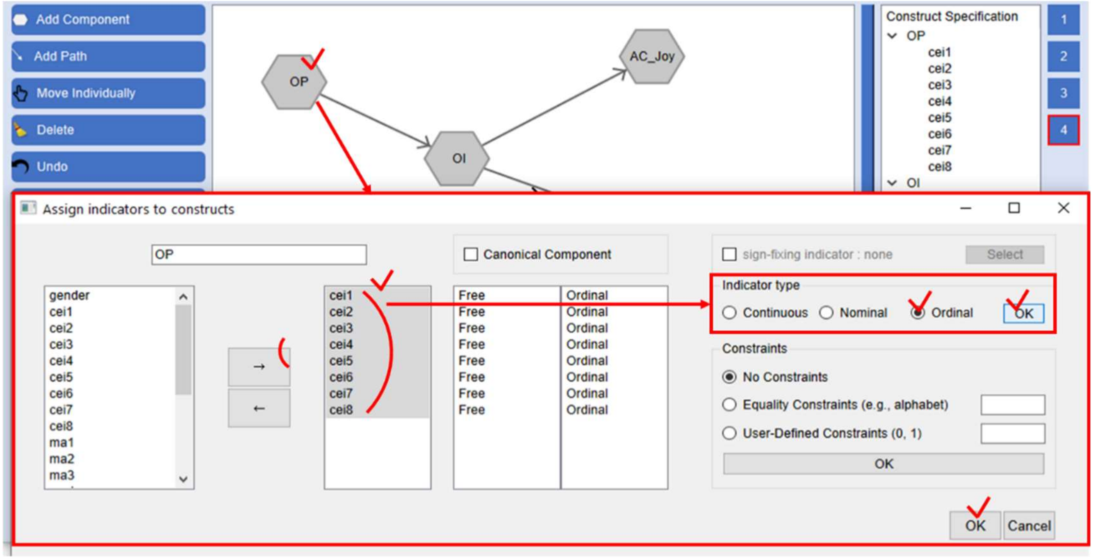
Analysis – Nonlinear GSCA

Users can apply nonlinear GSCA when indicators are not continuous (i.e., nominal or ordinal) (Hwang & Takane, 2014, Chapter 5).

- To begin, select "**Analysis → GSCA → Nonlinear GSCA → single group or multiple groups**" under the [**Analysis**] menu.



- Users then specify their measurement and structural models as in basic analysis, as described earlier.
- Double-click on an individual component (a hexagon). Then, the "**Assign Indicators to Constructs**" window will appear.
- In the "**Assign Indicators to Constructs**" window, users select an indicator and then choose the indicator's type in a right-hand dialog box called "**Indicator Type**" and click on "OK" in the box.

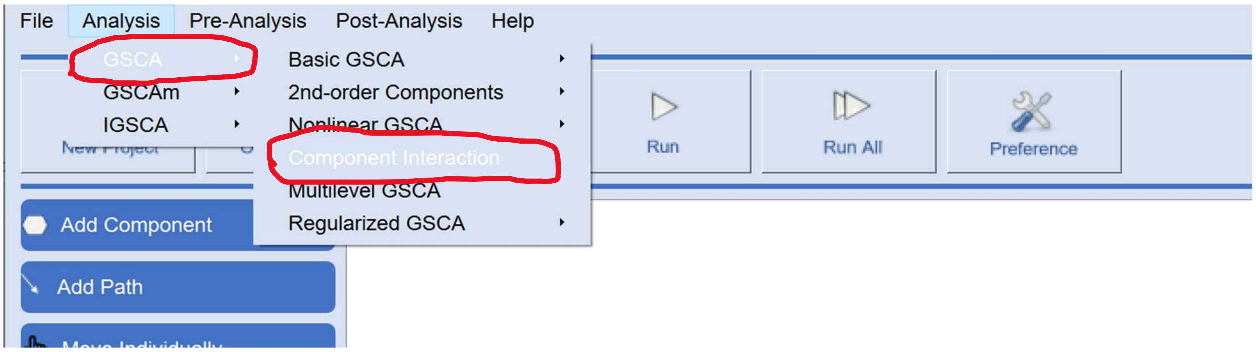


cei1	Free	Ordinal
cei2	Free	Ordinal
cei3	Free	Ordinal
cei4	Free	Ordinal
cei5	Free	Ordinal
cei6	Free	Ordinal
cei7	Free	Ordinal
cei8	Free	Ordinal

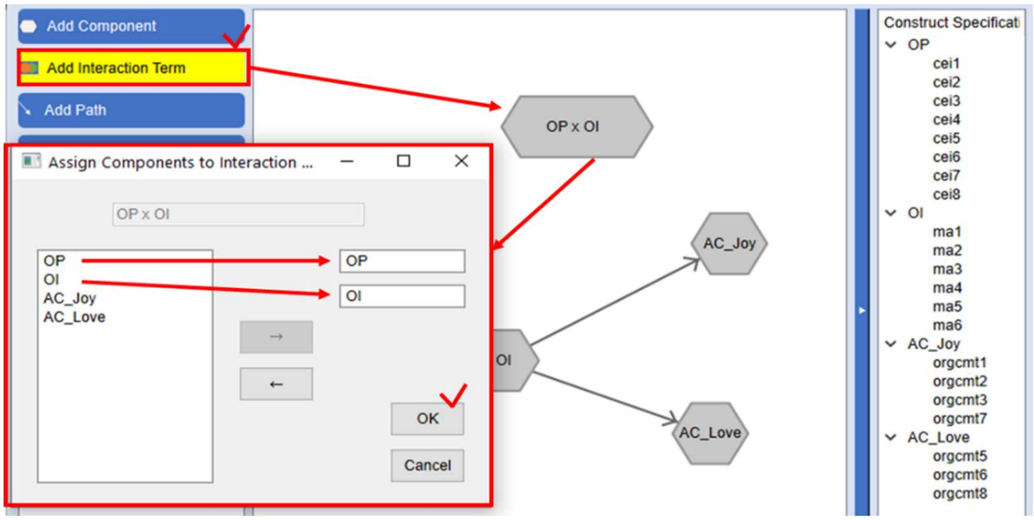
Analysis – GSCA with Component Interactions

Users can specify and examine interaction terms of components (Hwang et al., 2021; Hwang, Ho, & Lee, 2010; Hwang & Takane, 2014, Chapter 6).

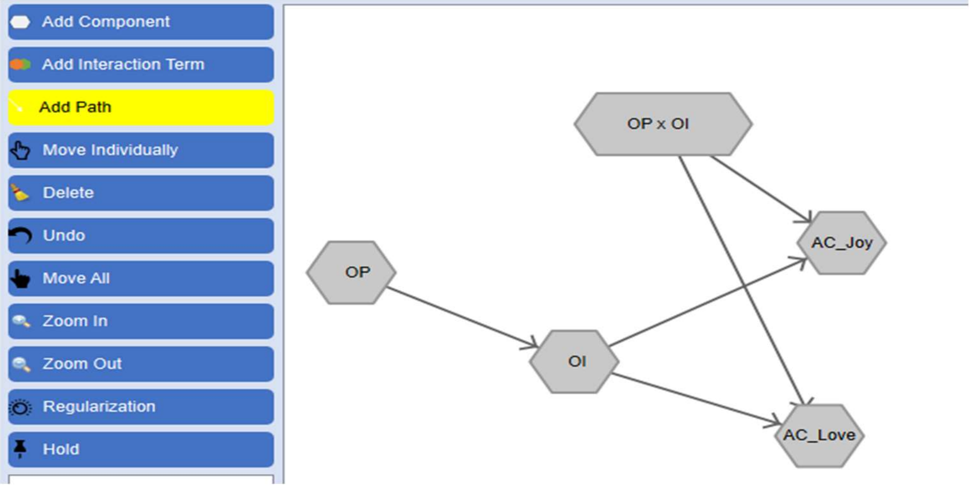
- To begin, select “**Analysis → GSCA → Component Interaction**” under the [**Analysis**] menu.



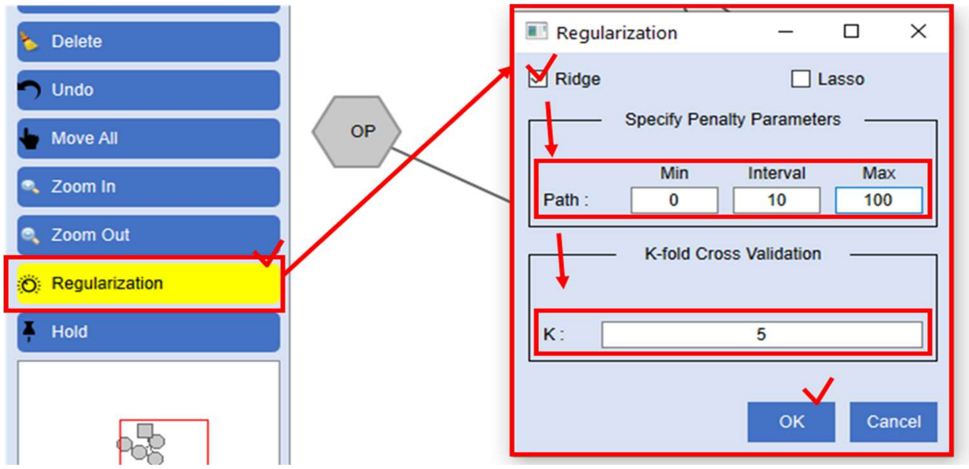
- Users then specify their measurement and structural models without component interaction terms as in basic analysis, as described earlier.
- To add component interaction terms, click once on **[Add Component Interaction]** in the Tool Panel.
- Click the left mouse button with the cursor placed in the Main Window as many times as the number of component terms. In the present example, one interaction term between OP and OI is specified.
- Double-click on a component interaction term. Then, in the “**Assign Components to Interaction Terms**” window, move each component of the interaction term and click on “OK.”



- Repeat the above step for the remaining interaction terms.
- Add the paths of the interaction terms.



- Optionally, users can conduct a **regularized** estimation of path coefficients to avoid potential multicollinearity in the structural model. Such multicollinearity may occur because component interaction terms tend to be highly correlated with their components.
    - To apply regularization, click once on **[Regularization]** in the Tool Panel.
    - In the "**Regularization**" window, users can choose either ridge or lasso regularization. Also, they can choose the range of candidate penalty parameters and the number of data splits for cross validation (i.e., K).



☑ Ridge ☐ Lasso

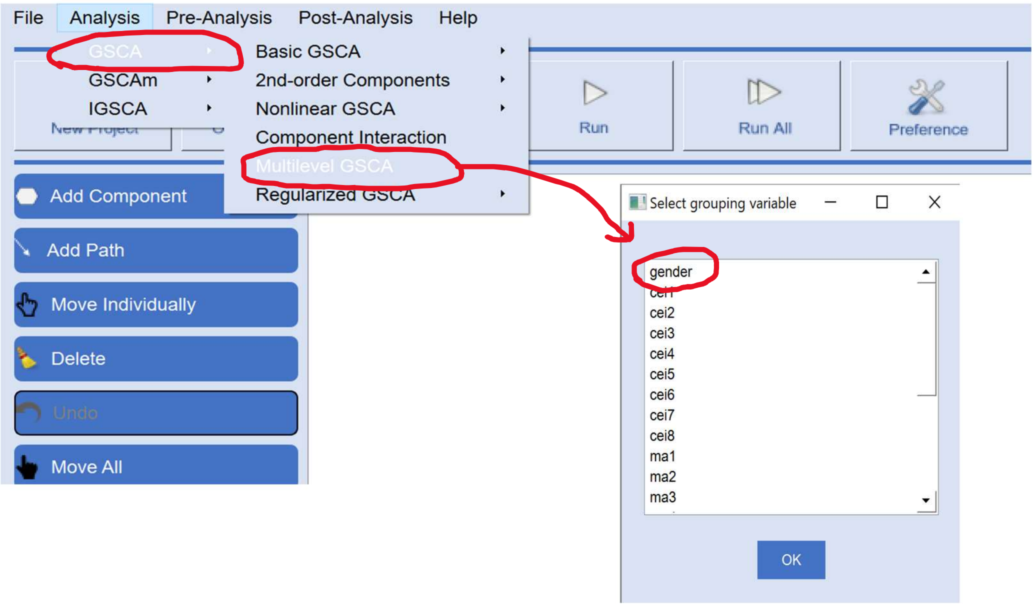
	Min	Interval	Max
Path :	0	10	100

K : 5

Analysis – Multilevel GSCA

Note: To apply multilevel GSCA, users must include a categorical, grouping variable in the data, which indicates second-level units. GSCA Pro currently provides a two-level analysis only (Hwang & Takane, 2014, Chapter 7; Hwang, Takane, & Malhotra, 2007).

- To begin, select "**Analysis → GSCA → Multilevel GSCA**" under the [**Analysis**] menu.
- Select a second-level variable in the list of indicators in the data file in a dialog box. Then, click on "**OK**".

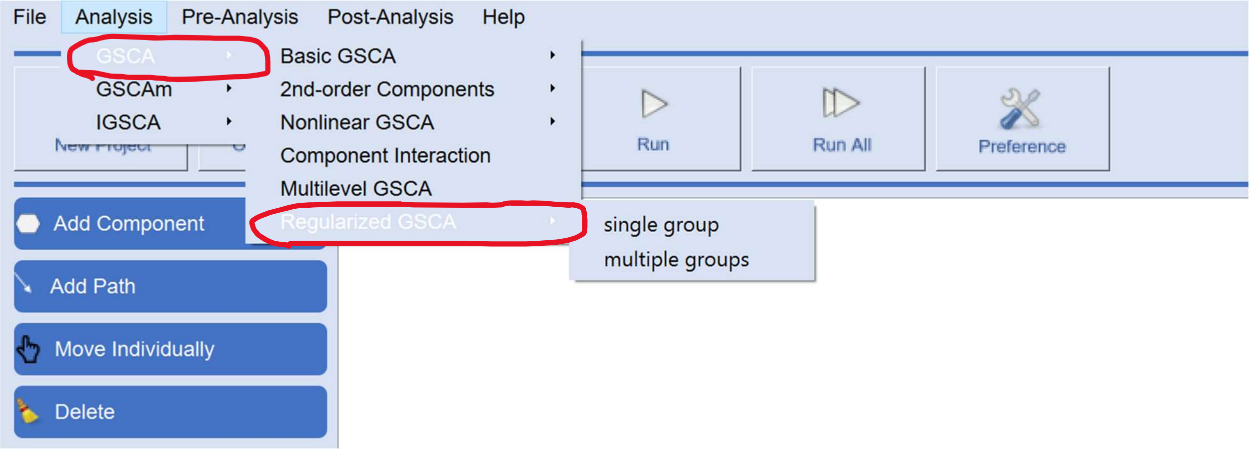


- Then, specify both measurement and structural models as described earlier.

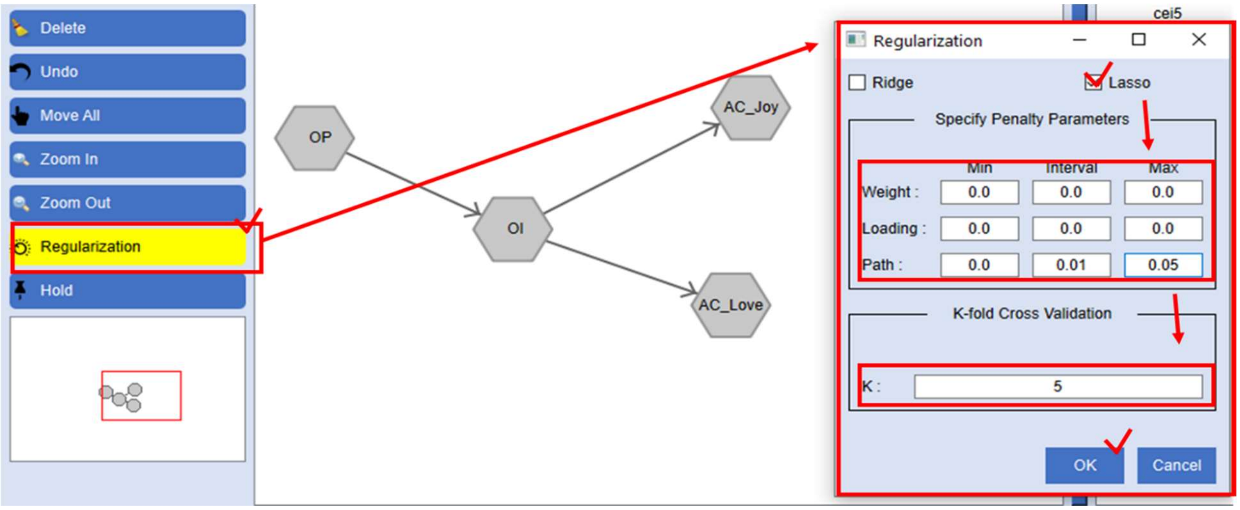
Analysis – Regularized GSCA

Users can obtain regularized parameter estimates for addressing multicollinearity or selecting variables (Hwang, 2009; Hwang & Takane, 2014, Chapters 8, 9).

- To begin, select "**Analysis → GSCA → Regularized GSCA → single group or multiple groups**" under the [**Analysis**] menu.



- Specify both measurement and structural models.
- Then, click once on **[Regularization]** in the Tool Panel.
- In the "**Regularization**" window, users can choose either ridge or lasso regularization. Also, they can choose the range of candidate parameters of each penalty term for each parameter set (weight, loading, and path coefficient) and the number of data splits for cross validation (i.e., K).



☐ Ridge ☑ Lasso

Specify Penalty Parameters

	Min	Interval	Max
Weight :	0.0	0.0	0.0
Loading :	0.0	0.0	0.0
Path :	0.0	0.01	0.05

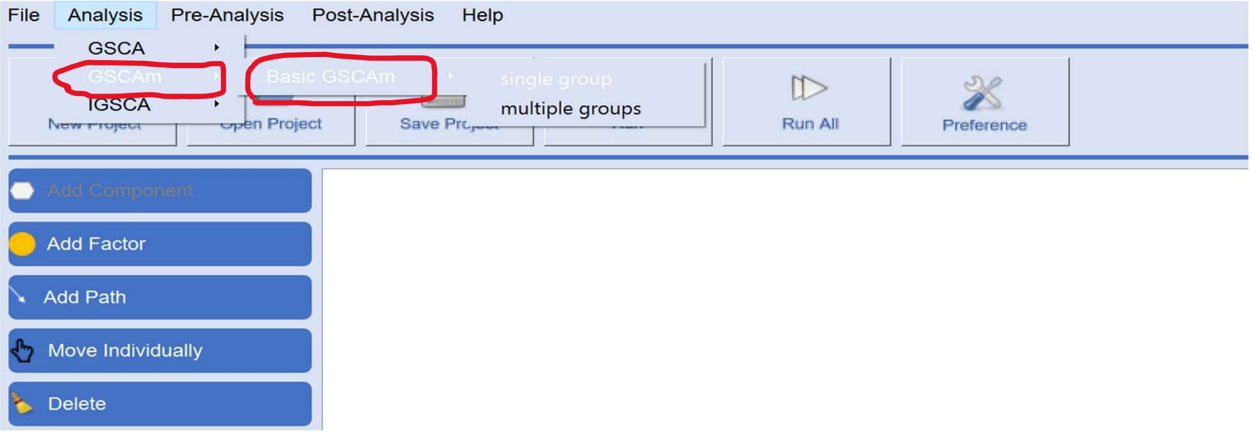
K-fold Cross Validation

K : 5

GSCA$_M$ (generalized structured component analysis with measurement errors incorporated) (Hwang, Takane, & Jung, 2017) can be used for estimating models with (common) factors or latent variables only. GSCA Pro uses a circle to denote a factor in a path diagram.

Analysis – GSCA$_M$

- To begin, select "**Analysis → GSCAm → Basic GSCAm → single group or multiple groups**" under the [**Analysis**] menu.



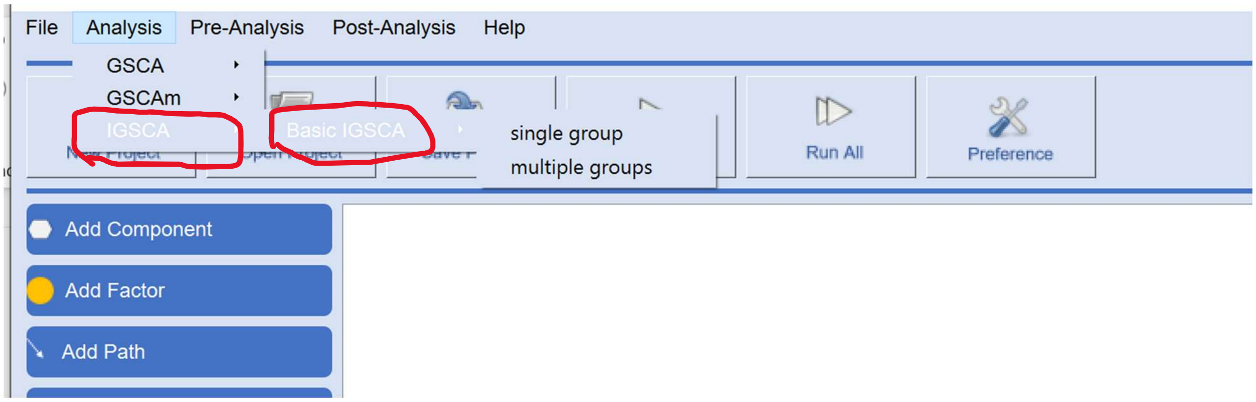
- To add factors, click once on **[Add Factor]** in the Tool Panel. Click the left mouse button with the cursor placed in the Main Window as many times as the number of factors. Each factor is displayed by a circle.
- Then, double-click on an individual factor to assign indicators to the factor.

- Specify the structural model.

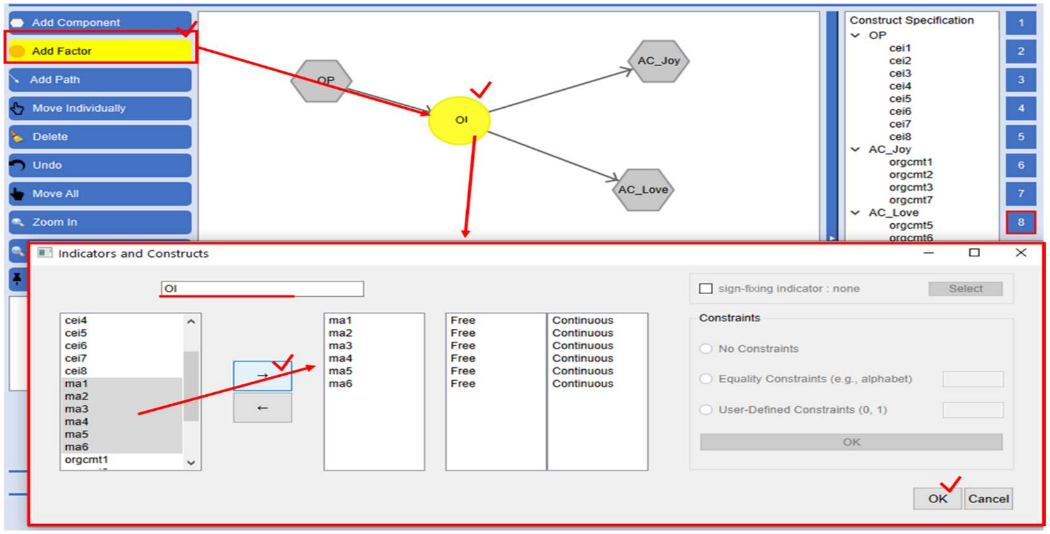
IGSCA (integrated generalized structured component analysis) (Hwang, Cho, Jung, Falk, Flake, Jin, & Lee, 2021) can be used for estimating <u>models with both factors and components</u>.

Analysis – IGSCA

- To begin, select "**Analysis → IGSCA → Basic IGSCA → single group or multiple groups**" under the [**Analysis**] menu.



- Click once on **[Add Component]** to add components and click once on **[Add Factor]** to add factors in the Tool Panel.
- Then, assign indicators to each component or factor by double-clicking on it.



- Specify the structural model.

Rule-of-thumb cutoff values for GFI and SRMR in IGSCA (Cho et al., 2022)

- If N = 50, GFI = .84 and SRMR = .13 may be used to indicate an acceptable level of model fit. However, using the SRMR cut-off over the GFI cut-off is recommended.
- If N = 100, GFI = .88 and SRMR = .10 may be chosen to indicate an acceptable level of model fit. If N = 200, GFI = .91 and SRMR = .08 can be chosen. Although both indexes can be used to assess model fit in these sample sizes, using the suggested SRMR cut-off values may still be preferable to using the GFI cut-off values.
- If N > 500, GFI = .95 and SRMR = .06 may be chosen. In this case, each index's suggested cut-off value can be used independently to assess the model fit. That is, a GFI ≥ .95 or an SRMR ≤ .06 may indicate an acceptable fit.

Post-Analysis – Model Comparison

Users can compare competing models (e.g., constrained and unconstrained models) after fitting the models to the same data (Cho et al., 2019; Hwang & Takane, 2014, Chapter 3).

- Specify a model or open an existing model from a project.
- Users can specify as many competing models as they want by clicking on the [+] box in the Model Bar.
- In the "**Add Model**" window, click on "New Model" and then a new blank page appears in the Main Window for specifying another model (refer to Figure (1)).
- In the "**Add Model**" window, users can also copy and paste an existing model by clicking on the "copy" dialog box. Then, the model appears on a new page in the Main Window and users can modify it (refer to Figure (2)).

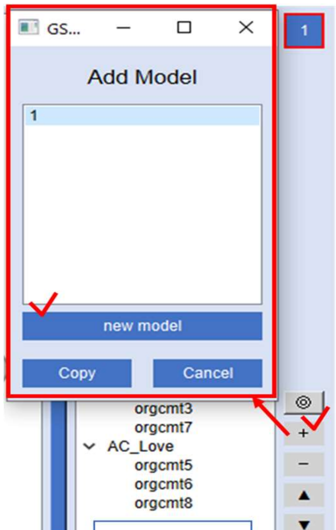


Figure (1)

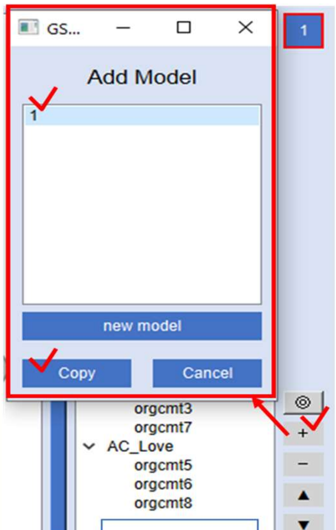
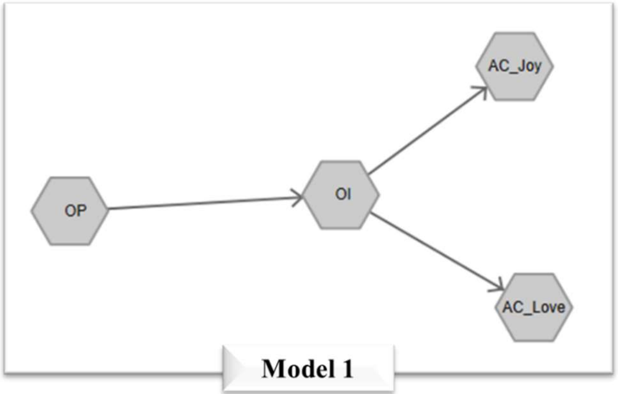
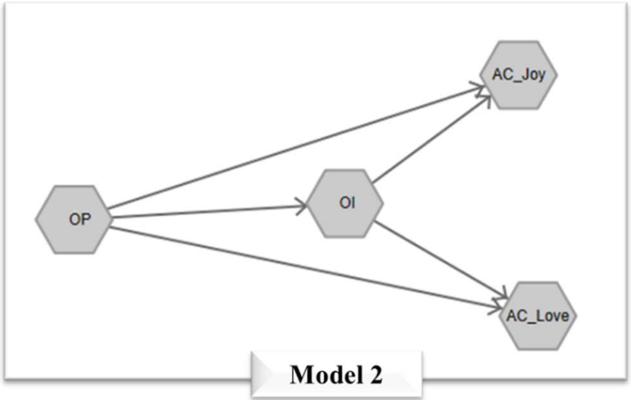


Figure (2)

- Likewise, users can delete any model by clicking on the [-] box in the Model Bar.
  - In the present example, we specified the following competing models.

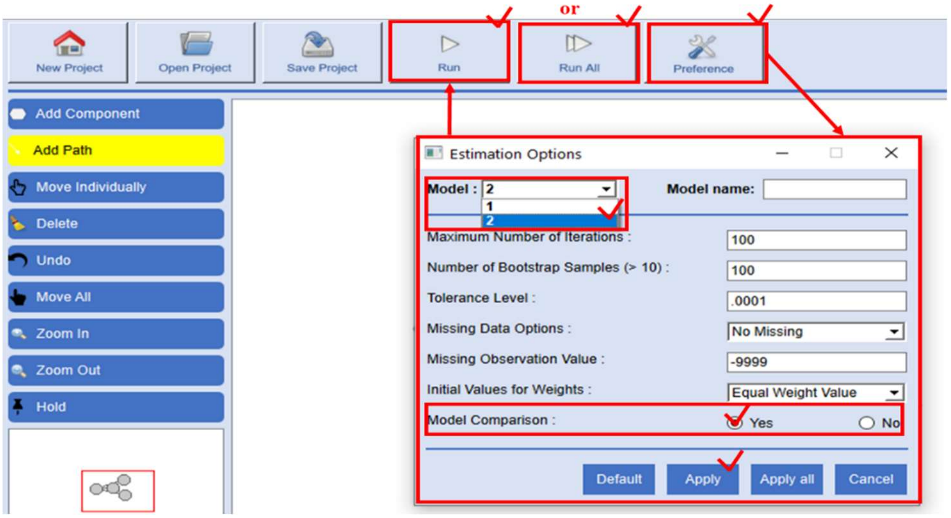


Model 1



Model 2

- Users can fit specified models individually by clicking on the [**Run**] shortcut for each model or fit all models simultaneously by clicking on the [**Run All**] shortcut.
  - **IMPORTANT:** Before fitting models, users should indicate which models they plan to compare. To do this, select the [**Preference**] shortcut and select "Yes" in the bottom option of <u>**Model Comparison**</u> per model and click on "**Apply**". If you click on "**Apply all**", all the preference options that you set up for a model will also be applied to the other models.



Estimation Options

Model : 2 (1, 2) Model name:

Maximum Number of Iterations : 100

Number of Bootstrap Samples (> 10) : 100

Tolerance Level : .0001

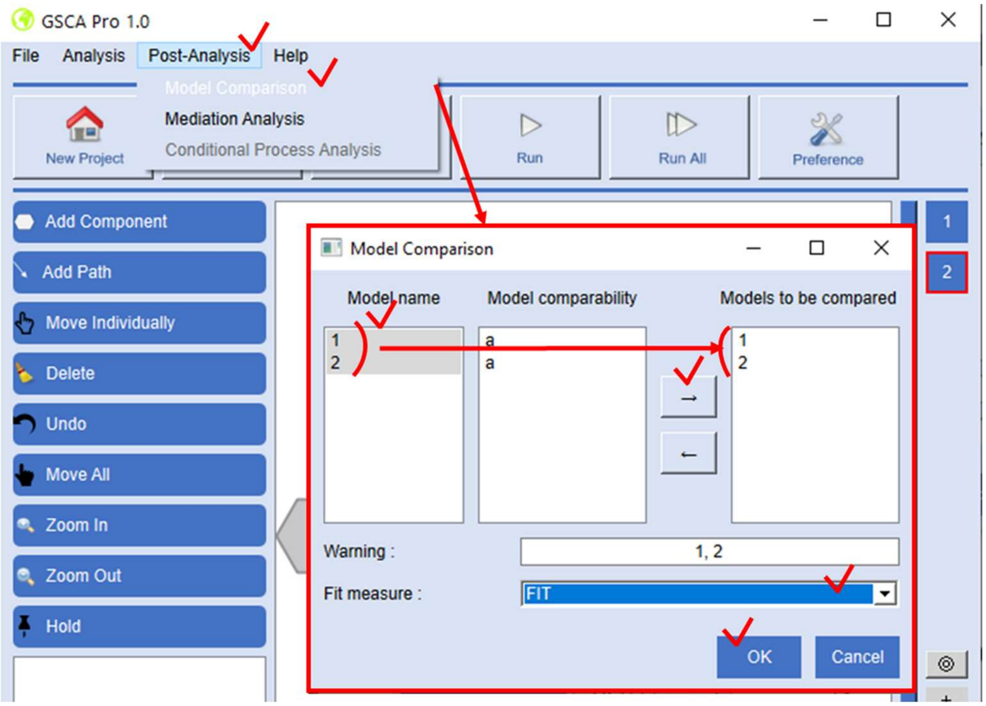
Missing Data Options : No Missing

Missing Observation Value : -9999

Initial Values for Weights : Equal Weight Value

Model Comparison : ● Yes ○ No

- After fitting all models, select "**Post-Analysis → Model Comparison**" under the [**Analysis**] menu.
- In the left-hand "**Model Name"** dialog box of the [**Model Comparison**] window, move all the models that users want to compare to the right-hand "**Models to be compared**" dialog box. Note that the middle "**Model comparability"** dialog box shows which models are directly comparable. Only the models with the same label can be compared in a pair-wise manner.
- Users can choose which model fit index(es) they will use for comparing models in the bottom dialog box "**Fit measures**."



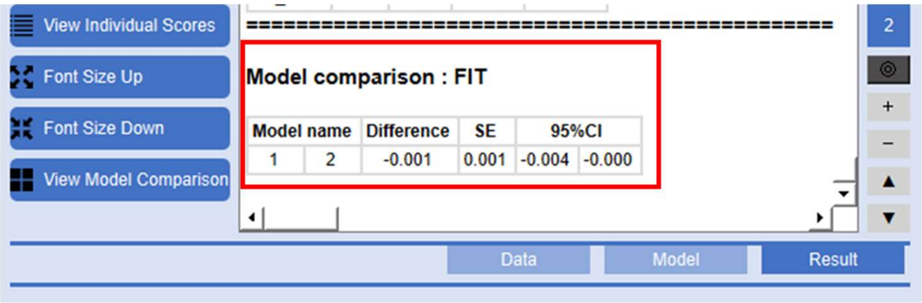
Model Comparison

Model name	Model comparability	Models to be compared
1	a	1
2	a	2

Warning : 1, 2

Fit measure : FIT

- In the “**Result**” window, each pair of the selected competing models is compared based on each fit index. For example, if the FIT difference between two models is statistically significant (i.e., its 95% confidence interval does not contain a zero), the model with the larger FIT value may be preferred in terms of the explanation power of the sample at hand. If the OPE difference between the two models is statistically significant, the model with the smaller OPE may be preferred in terms of the prediction power of unseen samples.



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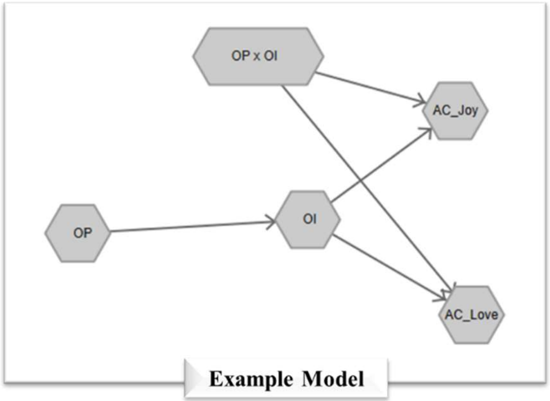
Model comparison : FIT

Model name		Difference	SE	95%CI	
1	2	-0.001	0.001	-0.004	-0.000

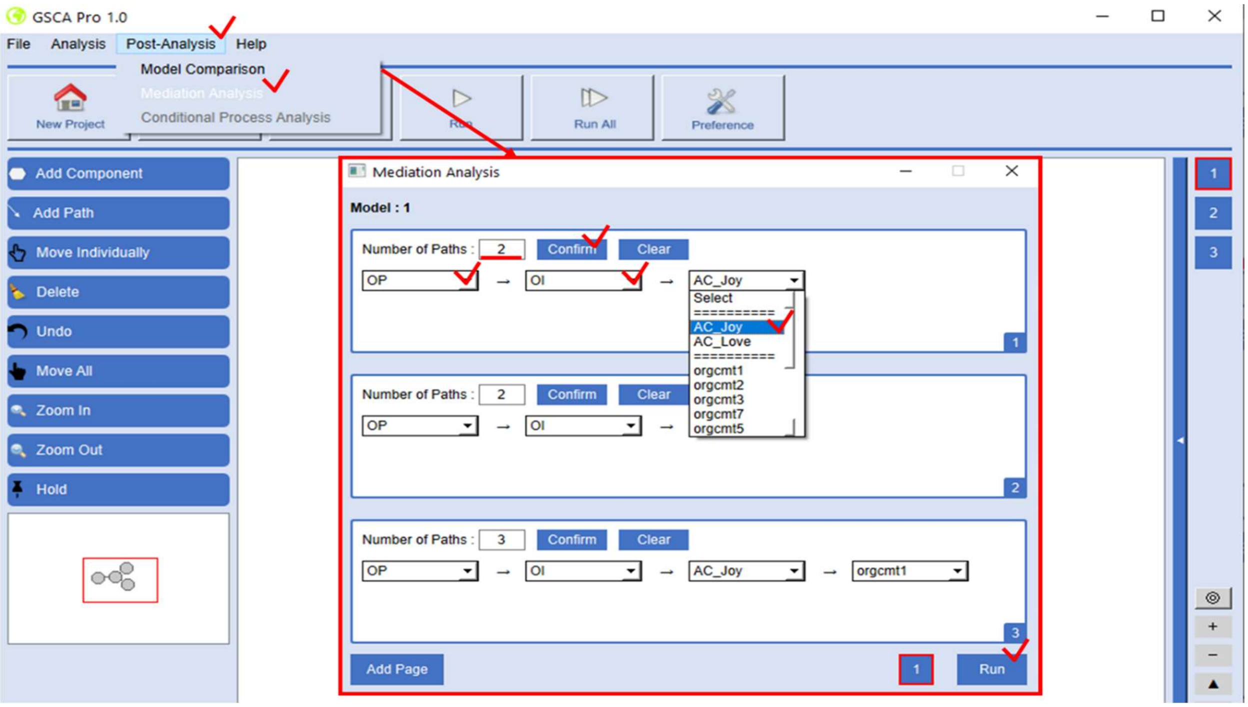
Post-Analysis – Mediation Analysis

After fitting a model, users can calculate an indirect effect of a variable (component or indicator) and examine its statistical significance (Hwang & Takane, 2014, Chapter 3).



Example Model

- After fitting a model, select "**Post-Analysis → Mediation Analysis**" under the menu of [**Analysis**].
- In the "**Mediation Analysis**" window, indicate how many paths are involved in an indirect effect of interest in the "**Number of Paths**" box and click on "**Confirm**."
    - In the present example, if users want to test the indirect effect of OP on AC_Joy through OI, there are two paths involved (i.e., OP → OI and OI → AC_Joy). Thus, they can put 2 in the Number of Paths box.
- Then, assign a variable (component or indicator) to each of the small boxes and click on "**Run**" at the bottom.
    - In the present example, if users want to test the indirect effect of OP on AC_Joy through OI, they assign OP to the first box, OI to the second, and AC_Joy to the third box.
- Users can test a maximum of three indirect effects per page. If they want to test more indirect effects, they can add an extra page by clicking on "**Add Page**" at the bottom.



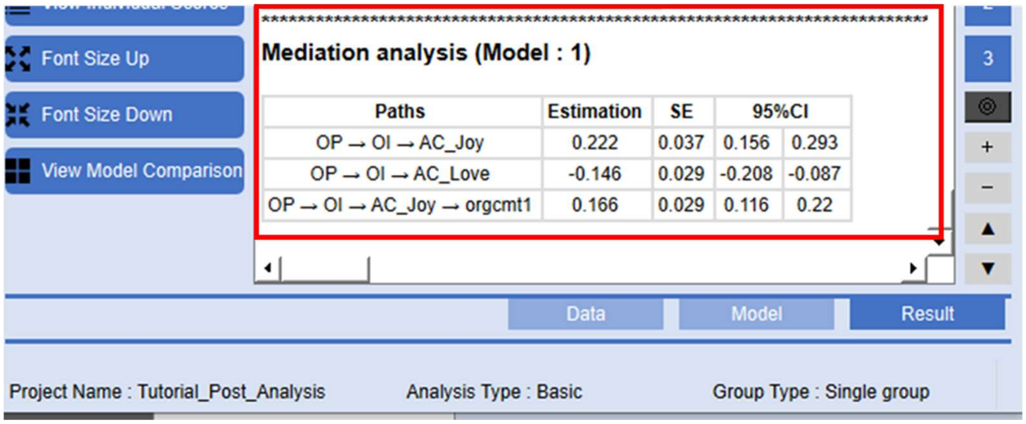
Model : 1

Number of Paths : 2
OP → OI → AC_Joy

Number of Paths : 2
OP → OI →

Number of Paths : 3
OP → OI → AC_Joy → orgcmt1

- In the “**Result**” window, users can view each indirect effect’s estimate and its standard error and 95% confidence interval.



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Mediation analysis (Model : 1)

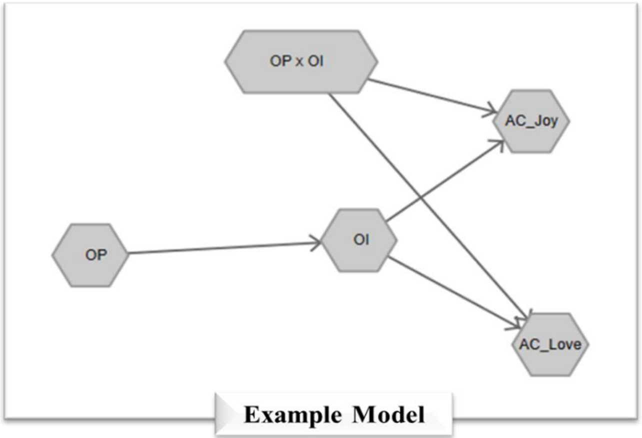
Paths	Estimation	SE	95%CI	
OP → OI → AC_Joy	0.222	0.037	0.156	0.293
OP → OI → AC_Love	-0.146	0.029	-0.208	-0.087
OP → OI → AC_Joy → orgcmt1	0.166	0.029	0.116	0.22

Project Name : Tutorial_Post_Analysis	Analysis Type : Basic	Group Type : Single group

Post-Analysis – Conditional Process Analysis

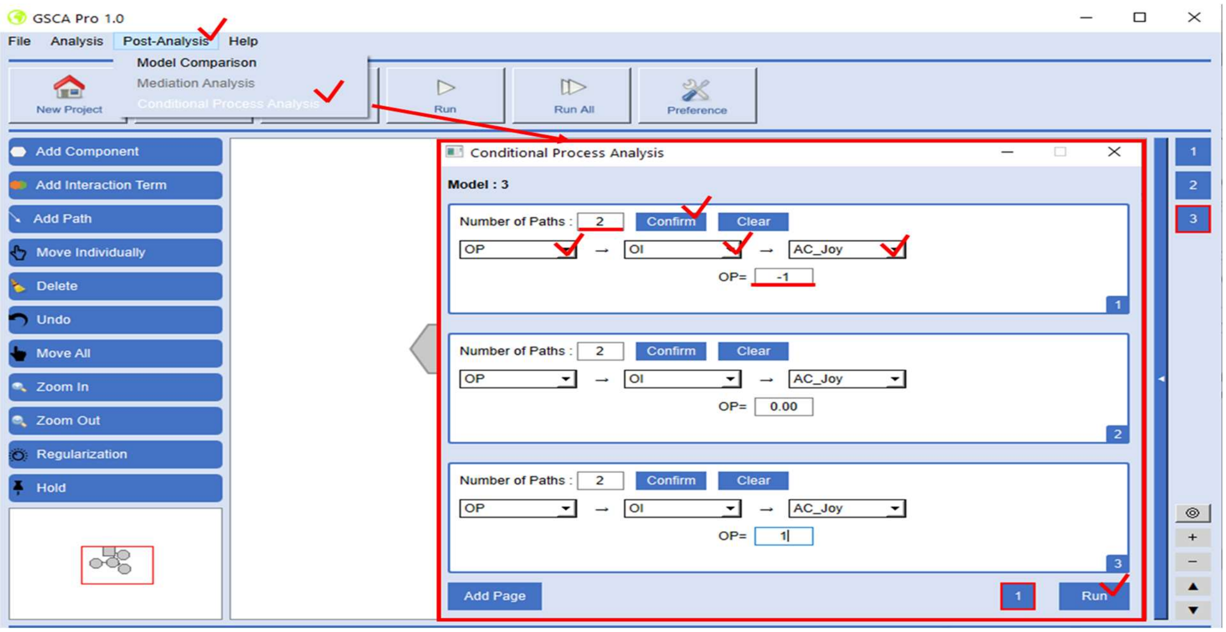
Conditional process analysis refers to an analytic approach that encompasses mediation, moderation, moderated mediation, and mediated moderation analyses (Hayes, 2013; Hayes & Preacher, 2013). *GSCA Pro* enables users to conduct a conditional process analysis that involves components or indicators. Before conducting this analysis, users first specify and fit a model with component interaction terms. Hwang et al. (2021) provide an example of conditional process analysis in GSCA.

Below, we explain how to compute and test the indirect effect of a variable (component or indicator) at user-defined, specific values of moderators. For illustration, we consider the following model.



Example Model

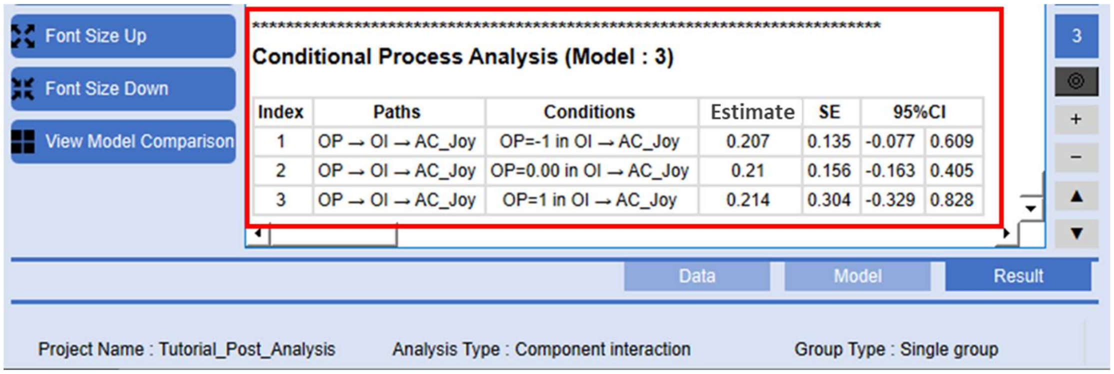
- After fitting a model, select "**Post-Analysis → Conditional Process Analysis**" under the **[Analysis]** menu.
- In the "**Conditional Process Analysis**" window, indicate how many paths are involved in a (conditional) direct or indirect effect of interest in the "**Number of Paths**" box and click on "**Confirm**."
  - In the present example, if users want to test the indirect effect of OP on AC_Joy mediated through OI at a certain value of OP, there are two paths involved (i.e., OP → OI and OI → AC_Joy). Thus, they can put 2 in the Number of Paths box.
- Then, assign a variable (component or indicator) to each of the small boxes. Then, *GSCA Pro* automatically searches for moderators that are involved in a mediating pathway of interest and ask users to add the values of the moderators. Then, click on "**Run**" at the bottom.
  - In the example, if users want to test the indirect effect of OP on AC_Joy through OI at OP = -1, they assign OP to the first box, OI to the second, and AC_Joy to the third box. Then, they add -1 to the box appearing below the second path.



Model : 3

1	Number of Paths : 2	OP	→ OI	→ AC_Joy	OP= -1
2	Number of Paths : 2	OP	→ OI	→ AC_Joy	OP= 0.00
3	Number of Paths : 2	OP	→ OI	→ AC_Joy	OP= 1

- Users can test three indirect effects per page. If they want to test more effects, they can add an extra page by clicking on "**Add Page**" at the bottom.
- In the "**Result**" window, users can view each effect's estimate and its standard error and 95% confidence interval.



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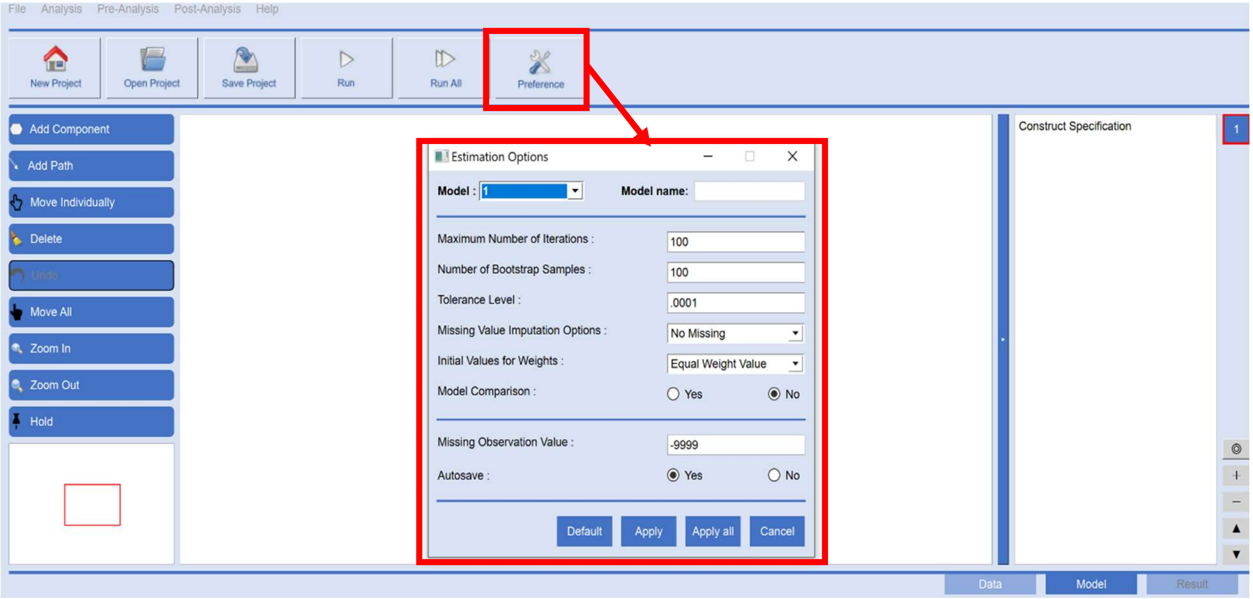
Conditional Process Analysis (Model : 3)

Index	Paths	Conditions	Estimate	SE	95%CI	
1	OP → OI → AC_Joy	OP=-1 in OI → AC_Joy	0.207	0.135	-0.077	0.609
2	OP → OI → AC_Joy	OP=0.00 in OI → AC_Joy	0.21	0.156	-0.163	0.405
3	OP → OI → AC_Joy	OP=1 in OI → AC_Joy	0.214	0.304	-0.329	0.828

Project Name : Tutorial_Post_Analysis Analysis Type : Component interaction Group Type : Single group

Preference – Estimation Options

- Users can set up their estimation options. This can be done by clicking on the [**Preference]** shortcut.



Estimation Options

Model : 1
Model name:

Maximum Number of Iterations : 100
Number of Bootstrap Samples : 100
Tolerance Level : .0001
Missing Value Imputation Options : No Missing
Initial Values for Weights : Equal Weight Value
Model Comparison : ○ Yes ● No

Missing Observation Value : -9999
Autosave : ● Yes ○ No

- As GSCA utilizes an iterative algorithm for parameter estimation, users need to decide on the maximum number of iterations, a tolerance level (of the optimization function difference between two consecutive iterations), and initial values for weights. By default, the maximum number of iterations = 100, tolerance level = .0001, and equal initial values are used for weights. Users can change the maximum number of iterations and tolerance level and assign random initial values to weights.
- As GSCA uses the bootstrap method (Efron, 1982) to obtain the standard errors and 95% confidence intervals of parameter estimates, users need to prescribe the number of bootstrap samples. The default number of bootstrap samples is 100.
- *GSCA Pro* currently provides three options for handling missing values: (1) listwise deletion, (2) mean substitution, and (3) least-squares imputation (Hwang & Takane, 2014, Chapter 3). If the uploaded data contain missing observations, users choose one of the options and specify which numeric value indicates missing observations. The default value indicating missing observations is -9999. Users can change it to a user-defined value in the box of **[Missing Observation Value]**.
- If users consider comparing a group of models, they should select "Yes" in the [Model Comparison] option for each model in the comparison group. Then, *GSCA Pro* will save all necessary information on each fitted model for a post-analysis of model comparison. This option may have *GSCA Pro* use a high amount of RAM, tending to decrease computational speed particularly when the sample size and/or the number of models to be compared is large.

- Users can set up their preference options for each model separately by clicking on the **[Apply]** button per model number. Also, they can apply the same preference options to all models at once by clicking on the **[Apply all]** button.
- The option **Autosave** (default = Yes) is available that automatically saves the current changes or progress in the program.

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