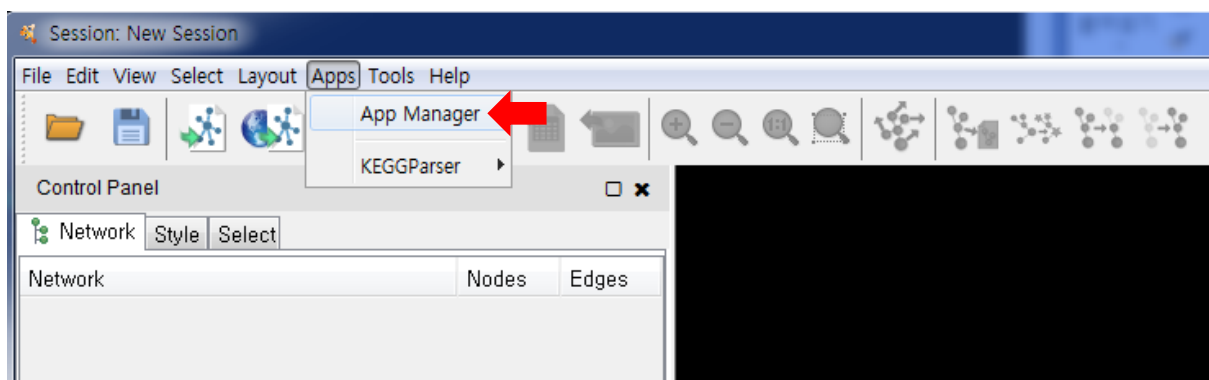


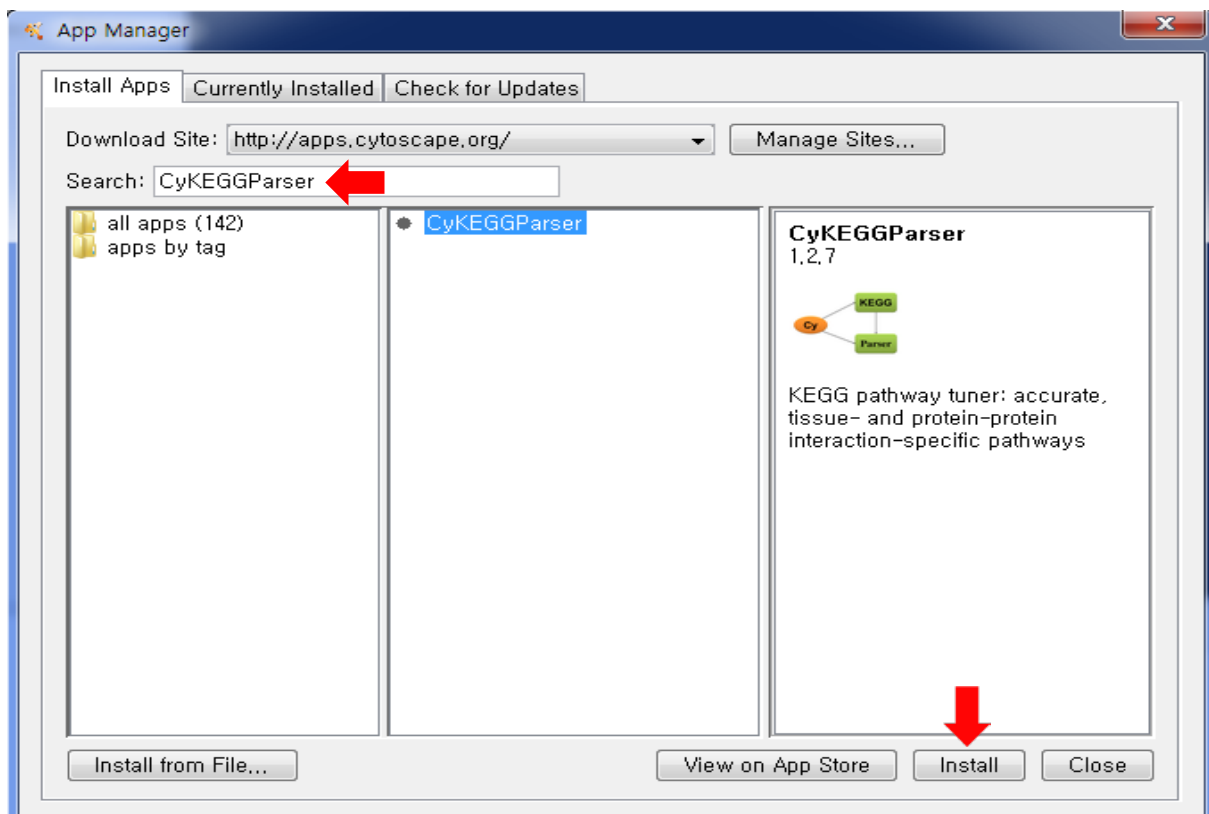
[Manual for Subpath Visualization with Cytoscape]

This is manual for visualization of subpaths determined by MIDAS using Cytoscape.

1. Download & Install Cytoscape (<http://www.cytoscape.org/>).
2. Open Cytoscape
3. Go to Apps → App Manager



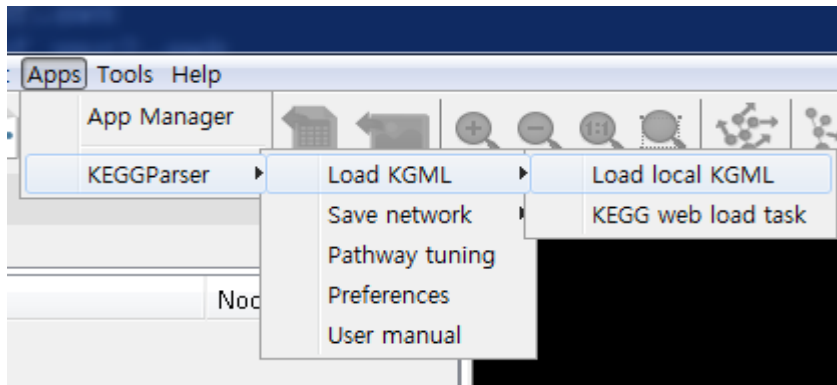
4. Search “CyKEGGParser” & Install



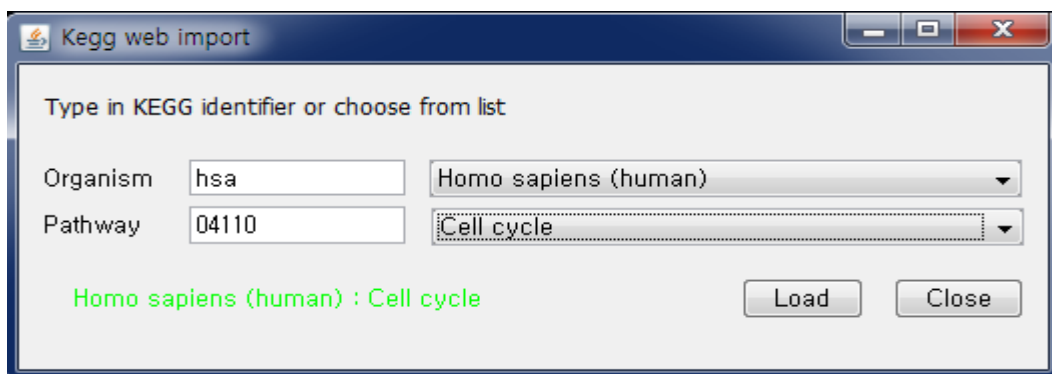
5. Load KEGG pathway from KGML file.

Select “Load local KGML” file if you have KGML file in your local repository.

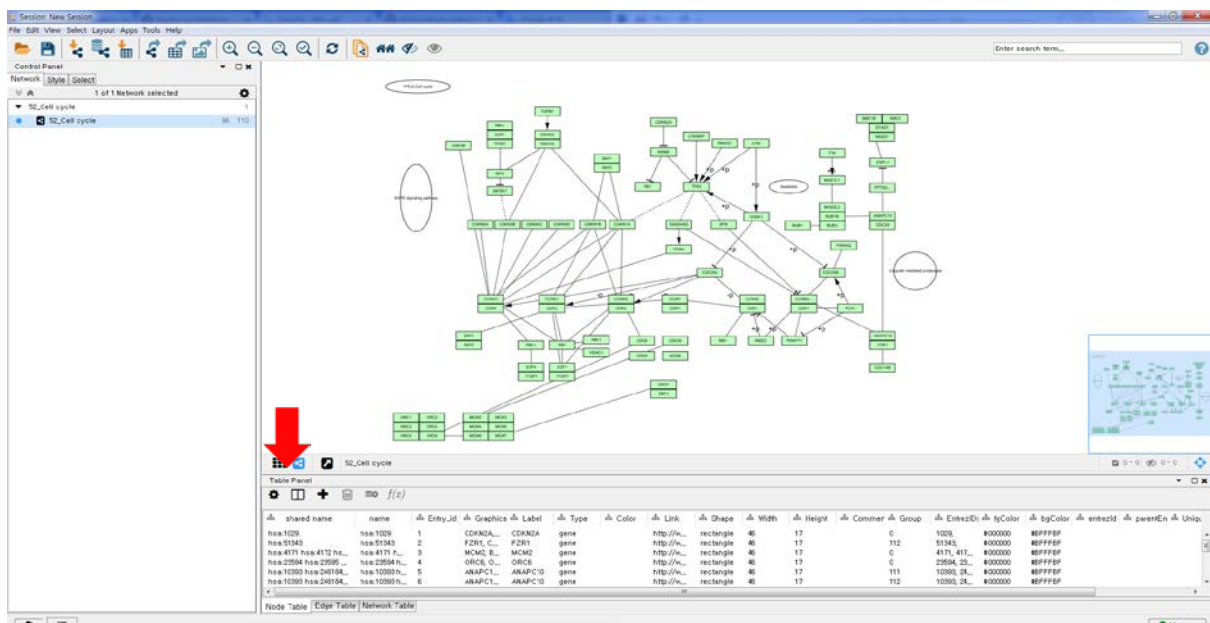
You can download KGML files from MIDAS in [Output Directory]/kegg_pathways/kgml/



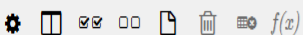
Or, select “KEGG web load task” and select proper target pathway.



Example) Loaded network from hsa04110 “Cell cycle”




6. Move to “Edge Table” panel in Table panel

Table Panel															
															
shared...	shared...	name	interacti...	Type	SubTyp...	SubTyp...	ArrowS...	LineStyle	EdgeLa...	Relatio...	Relatio...	Comm...	Entry1	Entry2	kegg.type
				pd	express...		None	Dash		-->			49	34	GErel
				pd	express...		None	Dash		-->			49	47	GErel
				pd	express...		None	Dash		-->			49	32	GErel
				pp	activation		Delta	Solid		-->			47	23	PPrel
				pp	inhibition		T	Solid		--			36	48	PPrel
				pp	inhibition		T	Solid		--			36	49	PPrel
				pp	activation		Delta	Solid		-->			37	49	PPrel
				pp	activation	phosph...	Delta	Solid	+p	-->	+p		35	49	PPrel
				pp	activation	phosph...	Delta	Solid	+p	-->	+p		33	49	PPrel

Node Table | **Edge Table** | Network Table

7. Select “name” column and click $f(x)$

Table Panel					
					
shared name	shared interaction	name	interaction	Type	SubType
				pd	expressi...
				pd	expressi...
				pd	expressi...
				pp	activation
				pp	inhibition
				pp	inhibition
				pp	activation

Node Table | Edge Table | **Network Table**

8. Using “CONCATENATE” function, make Edge ID

Create Function For: name

Functions

- ABS
- ACOS
- AND
- ASIN
- ATAN2
- AVERAGE
- BLIST
- COMBIN
- CONCATENATE**
- COS
- COSH
- COUNT
- DEGREE
- DEGREES
- EXP

Returns a string (a.k.a, text object).
Call with CONCATENATE([strings]).

Next Argument:

Entry1

Add

Add

Undo

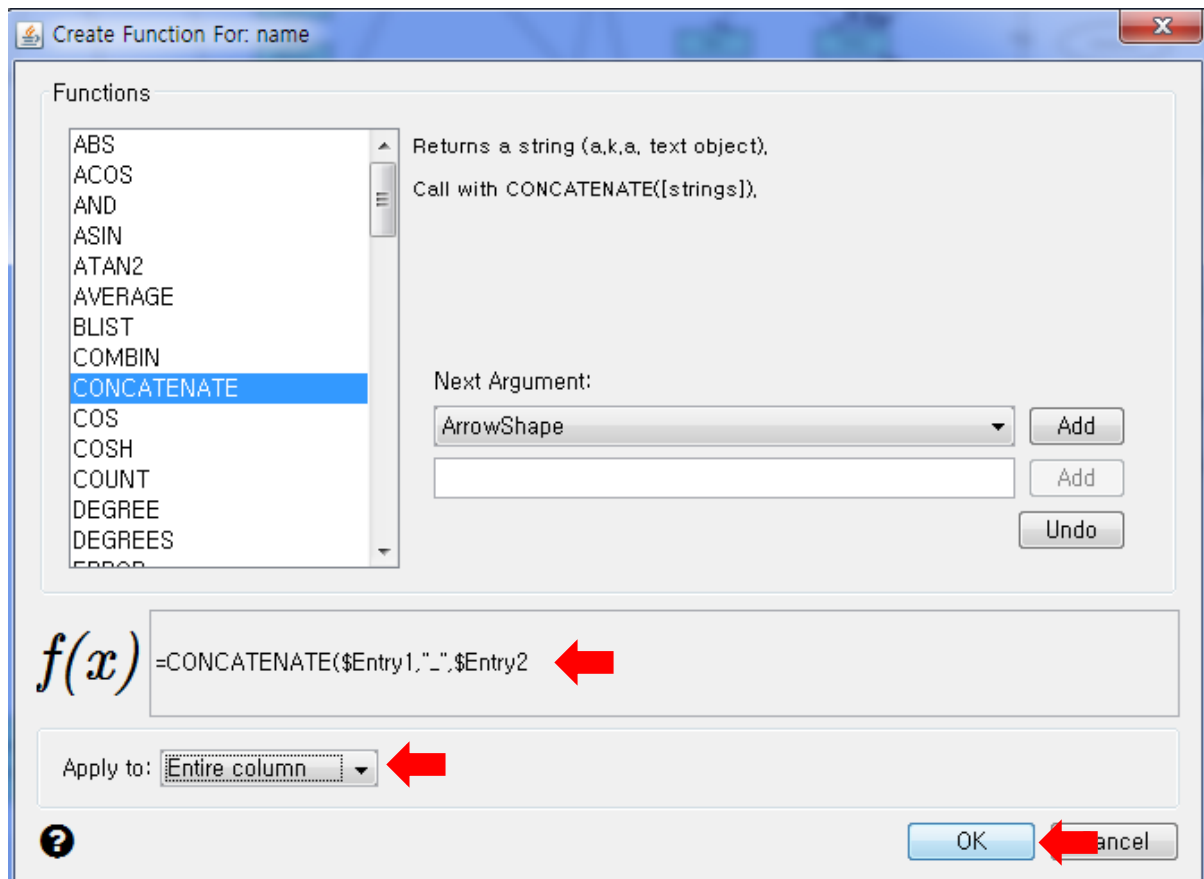
$f(x)$ =CONCATENATE(

Apply to: Current cell only

OK Cancel

Add arguments with proper order: Entry1 (select dropdown menu) → “_” (typing in the white blank box) → Entry2 (select dropdown menu)

This is proper setting of applying function. Change “Apply to”: “Current cell only” → “Entire column”



Function applied result

Table Panel				
<div> ⚙️ 📖 + 🗑️ 🔗 $f(x)$ </div>				
shared name	shared interaction	name	interaction	Type
49_34		49_34		pd
49_47		49_47		pd
49_32		49_32		pd
47_23		47_23		pp
36_48		36_48		pp
36_49		36_49		pp
37_49		37_49		pp

Node Table
Edge Table
Network Table

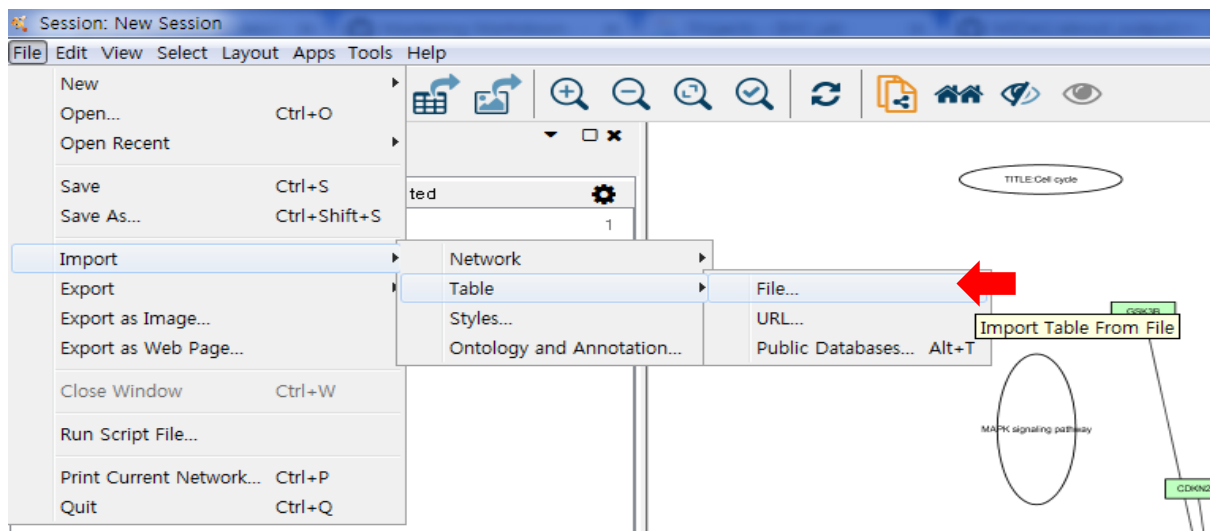
9. Import subpath color & width file from MIDAS result

You can find the file in the [Output Directory]/Summary_result/cytoscape/~.

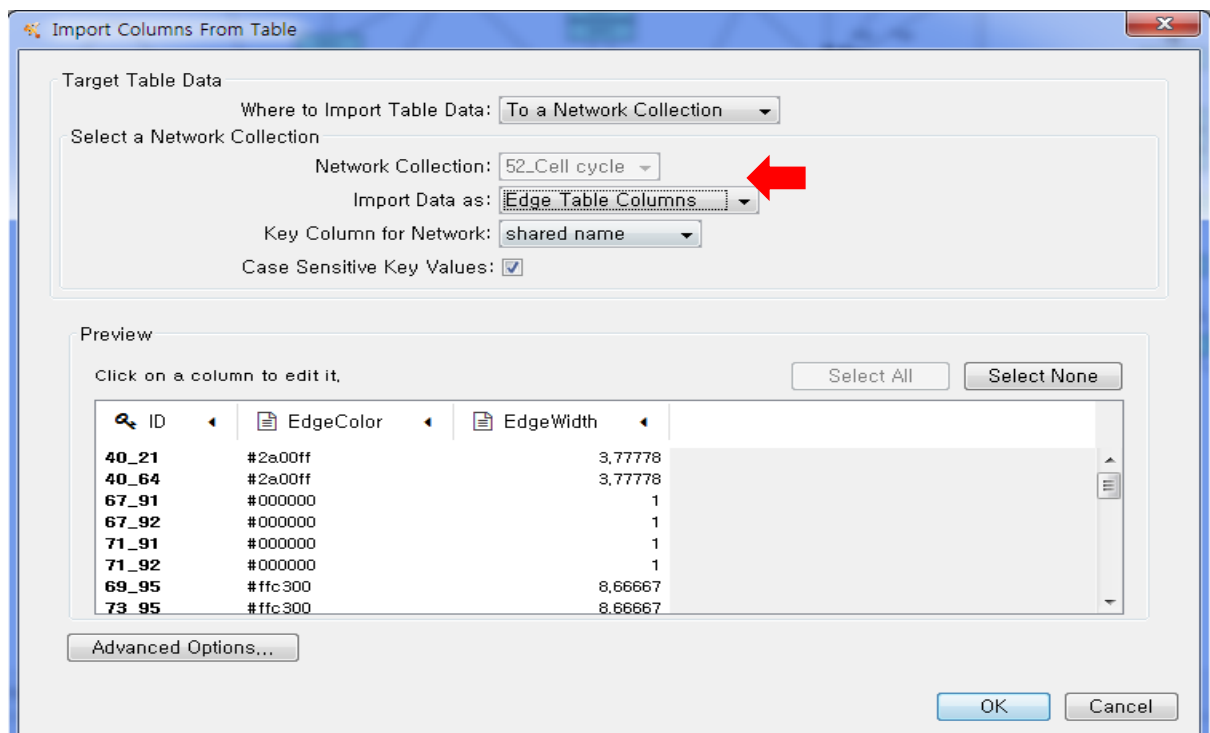
For example)

[Output Directory]/

Summary_result/cytoscape/hsa04110_for_cytoscape.txt.no_group.txt

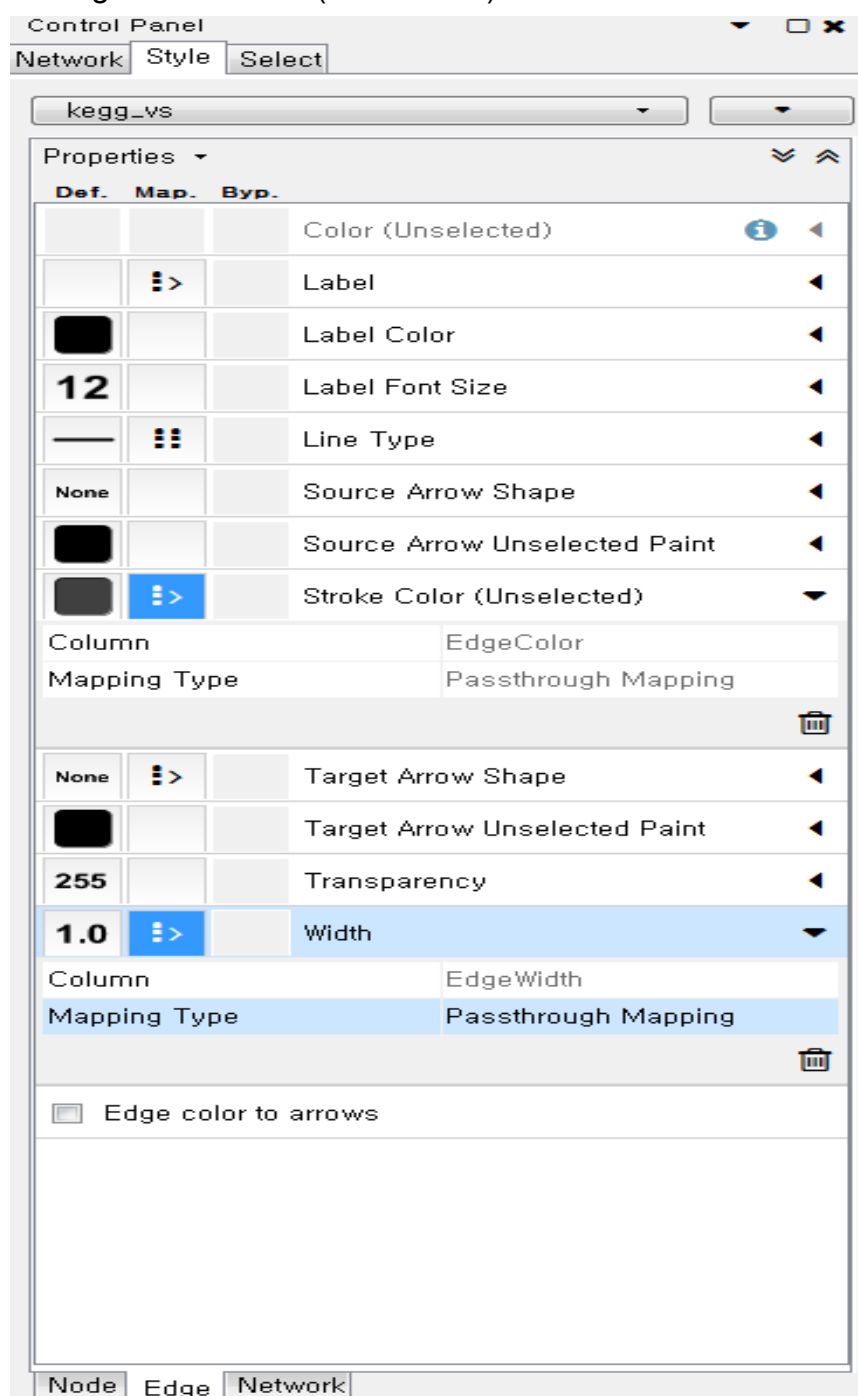


10. Change Import Data as to “Edge Table Columns”



11. Move to Control panel & Edge Tab

Setting “Stroke Color (Unselected)” & “Width” like below.



12. Visualization of subpaths is done.

