Tutorial 1.6: Export heatmap image and table results

Export the results of the enrichment analysis as an image and as a table containing the details of the statistic results

GiTools 1.5.7

File Edit Data Analysis Help

File menu:
- New
- Open
- Save
- Save As ...
- Close
- Import
- Export
  - Export labels ...
  - Export matrix ...
  - Export table ...
  - Export heatmap as an image ...
  - Export scale as an image ...
  - Export heatmap as html ...
  - Export PDF report ...
- Exit

Export the heatmap as an image file

Tabs: Welcome | tutorial.enrichme... | tutorial-results-0.heatmap

Callout:

STEP 1

Click on Export heatmap as an image...

☑ Show rows gri...

Col... Size

☑ Show columns

Col... Size

Scale

P-Value scale

Value Right P-Value

☐ Filter sig. by

Corrected right P-Value

Sig. level 0.05 Empty

Columns (heatmap labels):
testis, mouth, nos, cervix uteri, hematopoietic and reticuloendothelial systems, breast, kidney, thyroid gland, prostate gland, brain, nos, adrenal cortex, bones and joints, pancreas, liver, ovary, lung, skin, lymph nodes, colon, nos, urinary bladder, stomach

Rows:
- Staphylococcus aureus infection - Homo sapiens (hu
- ECM-receptor interaction - Homo sapiens (human)
- Complement and coagulation cascades - Homo sapiens
- p53 signaling pathway - Homo sapiens (human)
- Cell cycle - Homo sapiens (human)
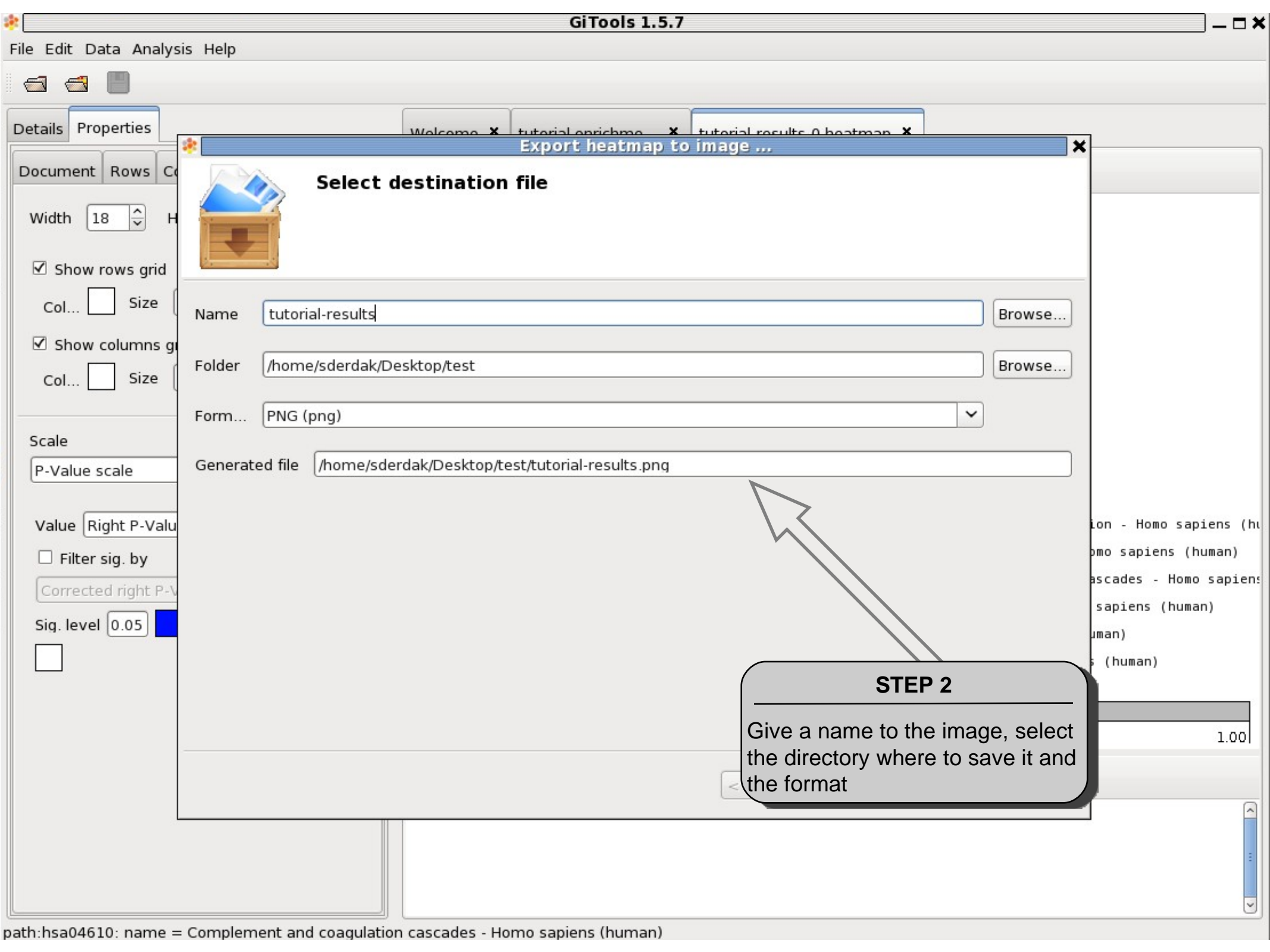- Focal adhesion - Homo sapiens (human)

0.00 0.05   1.00

Data Results Automatic update Update

path:hsa04610: name = Complement and coagulation cascades - Homo sapiens (human)

GiTools 1.5.7

File Edit Data Analysis Help

Details | **Properties**

Document | Rows | Co...

Welcome ✖ tutorial enrichme... ✖ tutorial results 0 heatmap ✖

Export heatmap to image ...

Select destination file

Width 18

☑ Show rows grid

Col... ☐ Size

☑ Show columns g...

Col... ☐ Size

Name   tutorial-results   Browse...

Folder   /home/sderdak/Desktop/test   Browse...

Form...   PNG (png) ▼

**Generated file**   /home/sderdak/Desktop/test/tutorial-results.png

Scale

P-Value scale

Value Right P-Valu...

☐ Filter sig. by

Corrected right P-V...

Sig. level 0.05 ☐

☐

ion - Homo sapiens (hu...
omo sapiens (human)
ascades - Homo sapiens
sapiens (human)
uman)
s (human)

STEP 2

Give a name to the image, select
the directory where to save it and
the format

1.00

<

path:hsa04610: name = Complement and coagulation cascades - Homo sapiens (human)

home/sderdak/Desktop/test/tutorial-results.png

After the export you will have a new file with the image in the directory that you indicated.

GiTools 1.5.7
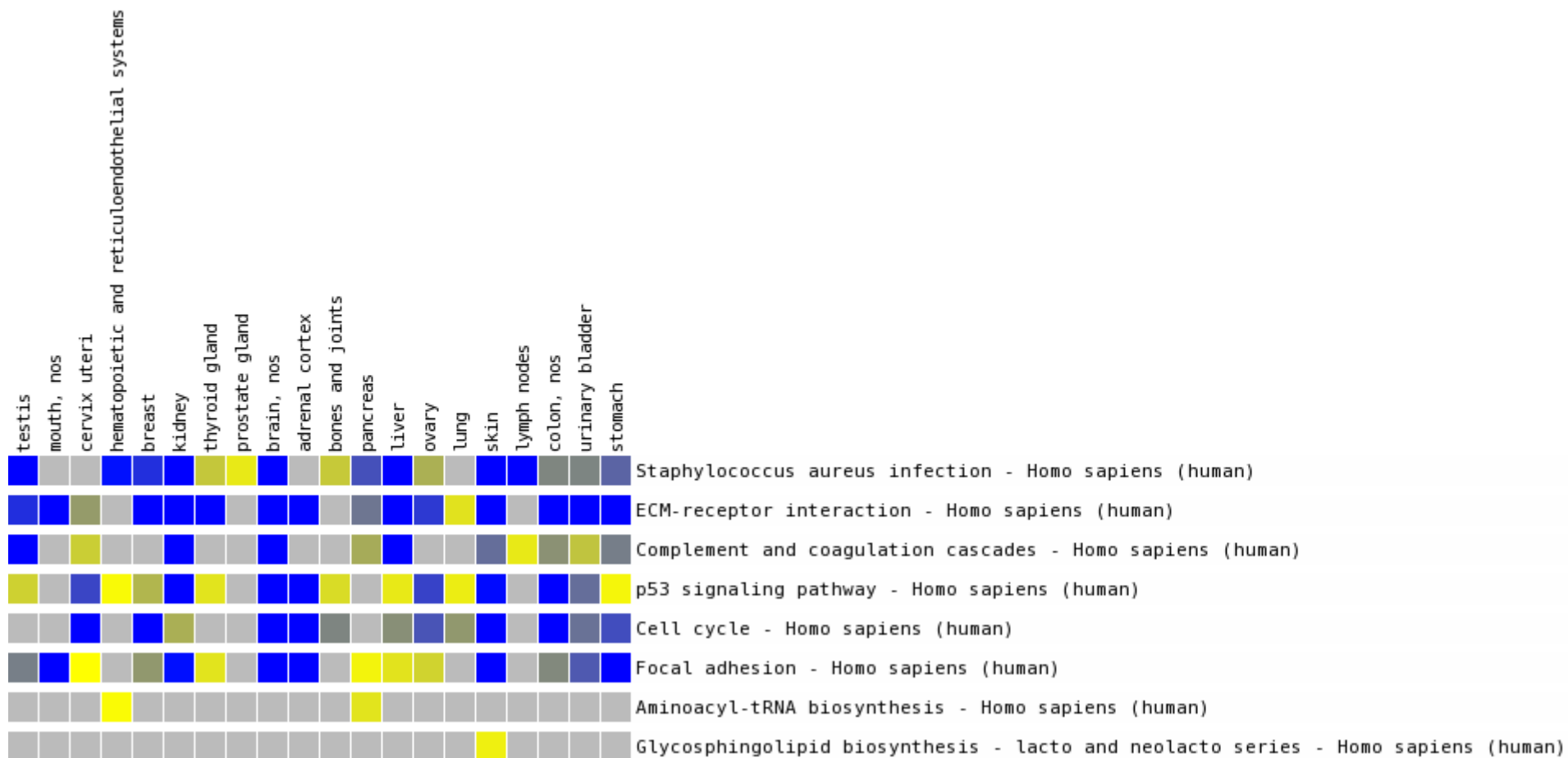
File Edit Data Analysis Help

New
Open
Save
Save As ...
Close
Import
Export
Exit

Export labels ...
Export matrix ...
Export table ...
Export heatmap as an image ...
Export scale as an image ...
Export heatmap as html ...
Export PDF report ...

Export a table

Welcome   tutorial.enrichme...   tutorial-results-0.heatmap

Columns   Cells

Annotations

Load...   Import

Headers

Text: name

Add   Remove   E...   Up   Down

Size 600   ☑ Visible

hematopoietic and reticuloendothelial systems

testis
mouth, nos
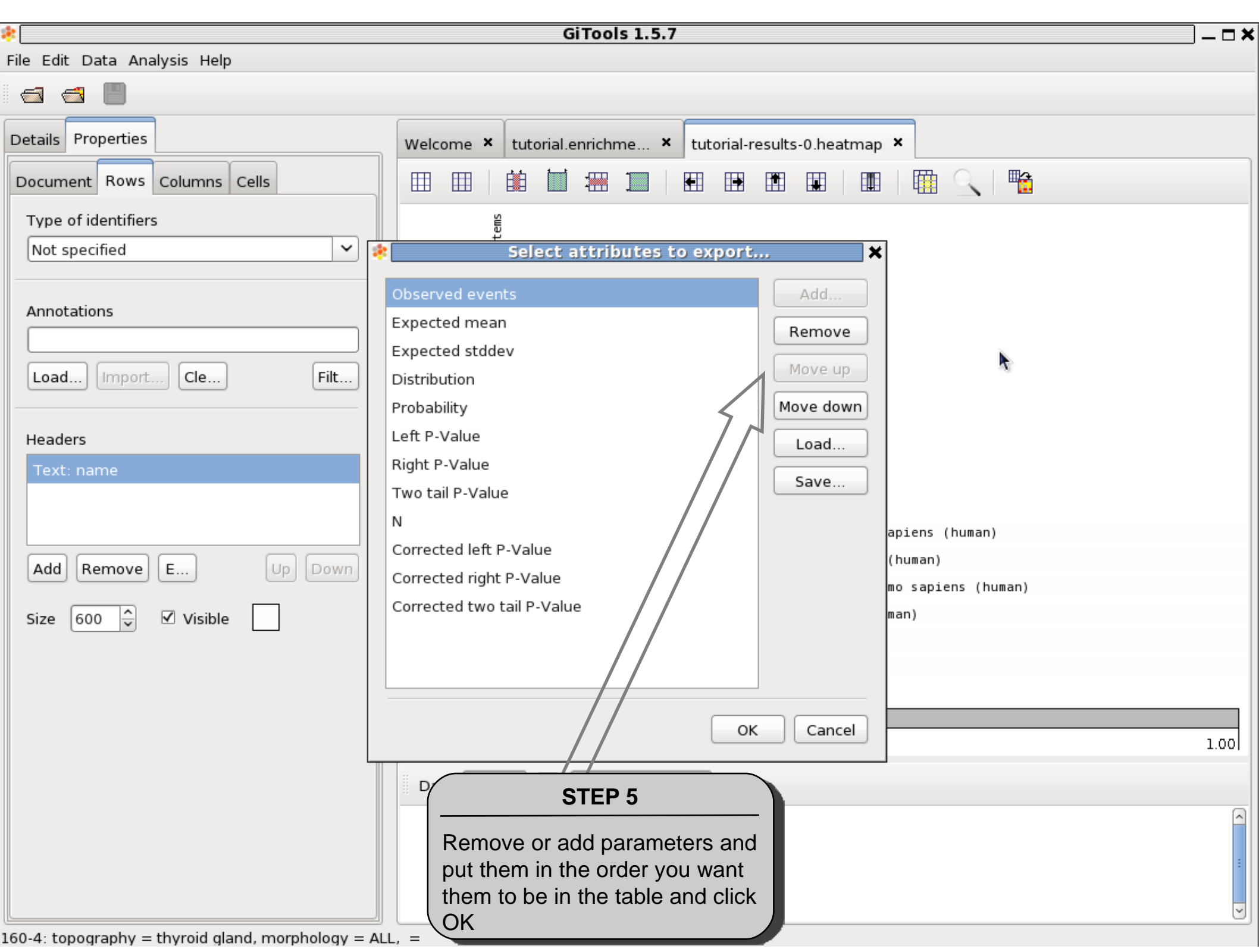cervix uteri
breast
kidney
thyroid gland

Staphylococcus aureus infection - Homo sapiens (human)
ECM-receptor interaction - Homo sapiens (human)
Complement and coagulation cascades - Homo sapiens (human)
p53 signaling pathway - Homo sapiens (human)
Cell cycle - Homo sapiens (human)
Focal adhesion - Homo sapiens (human)

0.00 0.05   1.00

Data   Results

STEP 4

Click Export table ... to export a table with the parameters of the enrichment analysis results

145-4, path:hsa04510: Observed events = 36, Expected mean = 16.153006389370795, Expected stddev = 3.851652963850875, Distribution = BINOMIAL, Probability = 0...

GiTools 1.5.7

File Edit Data Analysis Help
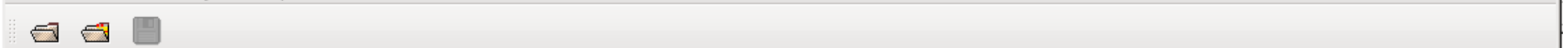
Details | Properties

Document | Rows | Columns | Cells

Type of identifiers

Not specified ▼

Annotations

[   ]

Load... Import... Cle... Filt...

Headers

Text: name

Add Remove E... Up Down

Size 600 ⬍ ☑ Visible

Welcome ✕ tutorial.enrichme... ✕ tutorial-results-0.heatmap ✕

Select attributes to export...

Observed events
Expected mean
Expected stddev
Distribution
Probability
Left P-Value
Right P-Value
Two tail P-Value
N
Corrected left P-Value
Corrected right P-Value
Corrected two tail P-Value

Add...
Remove
Move up
Move down
Load...
Save...

OK Cancel

apiens (human)
(human)
mo sapiens (human)
man)

1.00

STEP 5

Remove or add parameters and put them in the order you want them to be in the table and click OK

160-4: topography = thyroid gland, morphology = ALL, =

home/sderdak/Desktop/test/table.txt

After the export you will have a new file that contains the table with the parameters that you selected.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	column	row	observed	expected-mean	expected-stdev	distribution	probability	left-p-value	right-p-value	two-tail-p-value	N	corrected-left-p-value	corrected-right-p-value	corrected-two-tail-p-value
2	110-4	path:hsa05150	29	5.04	2.14	BINOMIAL	0.1	1	1.79E-016	1	53	1	3.52E-014	1
3	118-4	path:hsa05150	4	1.64	1.26	BINOMIAL	0.03	0.98	0.08	1	50	1	0.57	1
4	120-4	path:hsa05150	6	3.03	1.69	BINOMIAL	0.06	0.97	0.08	1	51	1	0.52	1
5	131-4	path:hsa05150	12	2.5	1.54	BINOMIAL	0.05	1	5.20E-006	1	53	1	0	1
6	140-4	path:hsa05150	10	1.91	1.36	BINOMIAL	0.04	1	1.71E-005	1	53	1	6.79E-004	1
7	145-4	path:hsa05150	32	4.16	1.95	BINOMIAL	0.08	1	1.50E-022	1	51	1	2.97E-020	1
8	160-4	path:hsa05150	7	2.18	1.45	BINOMIAL	0.04	1	0.01	1	52	1	0.17	1
9	169-4	path:hsa05150	6	2.19	1.45	BINOMIAL	0.04	0.99	0.02	1	53	1	1	1
10	173-4	path:hsa05150	27	5.05	2.13	BINOMIAL	0.1	1	1.59E-014	1	51	1	3.14E-012	1
11	18-4	path:hsa05150	8	7.63	2.55	BINOMIAL	0.15	0.65	0.5	1	51	1	0.79	1
12	189-4	path:hsa05150	11	4.75	2.07	BINOMIAL	0.09	1	0.01	1	50	1	0.07	1
13	190-4	path:hsa05150	8	1.36	1.15	BINOMIAL	0.03	1	6.01E-005	1	53	1	0.01	1
14	202-4	path:hsa05150	19	4.98	2.11	BINOMIAL	0.1	1	1.15E-007	1	48	1	5.68E-006	1
15	203-4	path:hsa05150	11	4.17	1.96	BINOMIAL	0.08	1	0	1	50	1	0.04	1
16	42-4	path:hsa05150	2	1.29	1.12	BINOMIAL	0.02	0.86	0.37	1	53	1	1	1
17	44-4	path:hsa05150	32	6.32	2.35	BINOMIAL	0.12	1	4.10E-017	1	51	1	8.11E-015	1
18	49-4	path:hsa05150	16	4.11	1.94	BINOMIAL	0.08	1	1.47E-006	1	51	1	9.71E-005	1
19	84-4	path:hsa05150	13	4.61	2.05	BINOMIAL	0.09	1	4.90E-004	1	53	1	0.01	1
20	09/04/11	path:hsa05150	11	3.4	1.78	BINOMIAL	0.07	1	4.58E-004	1	51	1	0.01	1
21	94-4	path:hsa05150	10	2.44	1.52	BINOMIAL	0.05	1	1.33E-004	1	52	1	0	1
22	110-4	path:hsa04512	21	7.7	2.64	BINOMIAL	0.1	1	1.64E-005	1	81	1	1.53E-004	1
23	118-4	path:hsa04512	20	2.66	1.6	BINOMIAL	0.03	1	1.45E-012	1	81	1	2.83E-010	1
24	120-4	path:hsa04512	13	4.88	2.14	BINOMIAL	0.06	1	0	1	82	1	0.04	1
25	131-4	path:hsa04512	2	3.91	1.93	BINOMIAL	0.05	0.24	0.91	1	83	0.91	1	1
26	140-4	path:hsa04512	14	3.02	1.71	BINOMIAL	0.04	1	1.79E-006	1	84	1	8.89E-005	1
27	145-4	path:hsa04512	22	6.69	2.48	BINOMIAL	0.08	1	4.53E-007	1	82	1	7.47E-006	1

STEP 7

Select one parameter to show in the matrix and click OK.

home/sderdak/Desktop/test/matrix.txt

After the export you will have a new file with a matrix of values for the parameter that you selected.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	
		110-4	118-4	120-4	131-4	140-4	145-4	160-4	169-4	173-4	18-4	189-4	190-4	202-4	203-4	42-
	path:hsa05150	1.79E-016	0.08	0.08	5.20E-006	1.71E-005	1.50E-022	0.01	0.02	1.59E-014	0.5	0.01	6.01E-005	1.15E-007	0	
	path:hsa04512	1.64E-005	1.45E-012	0	0.91	1.79E-006	4.53E-007	1.30E-006	0.13	1.63E-011	2.50E-008		0.65	2.64E-004	6.79E-007	2.49E-005
	path:hsa04610	2.24E-007	0.66	0.01	0.84	0.1	4.49E-010	0.07	0.32	1.28E-010	0.33	0.79	0	4.13E-012	0.51	
	path:hsa04115	0.01	0.17	4.02E-005	0.04	0	2.94E-007	0.02	0.78	5.10E-010	8.42E-009	0.01	0.25	0.02	3.59E-005	
	path:hsa04110	0.14	0.56	3.23E-020	0.13	1.10E-007	0	0.88	0.75	8.00E-008	3.20E-020	4.69E-004	0.1	6.90E-004	7.03E-005	9.4
	path:hsa04510	3.68E-004	7.70E-011	0.05	0.83	9.47E-004	4.73E-006	0.02	0.43	9.75E-008	1.14E-006	0.65	0.03	0.02	0.01	
	path:hsa00970	0.88	0.7	0.43	0.04	0.78	0.85	0.41	1	1	0.87	0.17	0.02	1	0.93	
	path:hsa00601	1	0.2	0.44	0.7	1	0.88	0.28	1	1	0.98	0.9	1	0.49	1	

THANKS FOR USING GITOOLS

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