

NetLCP GUI Tutorial

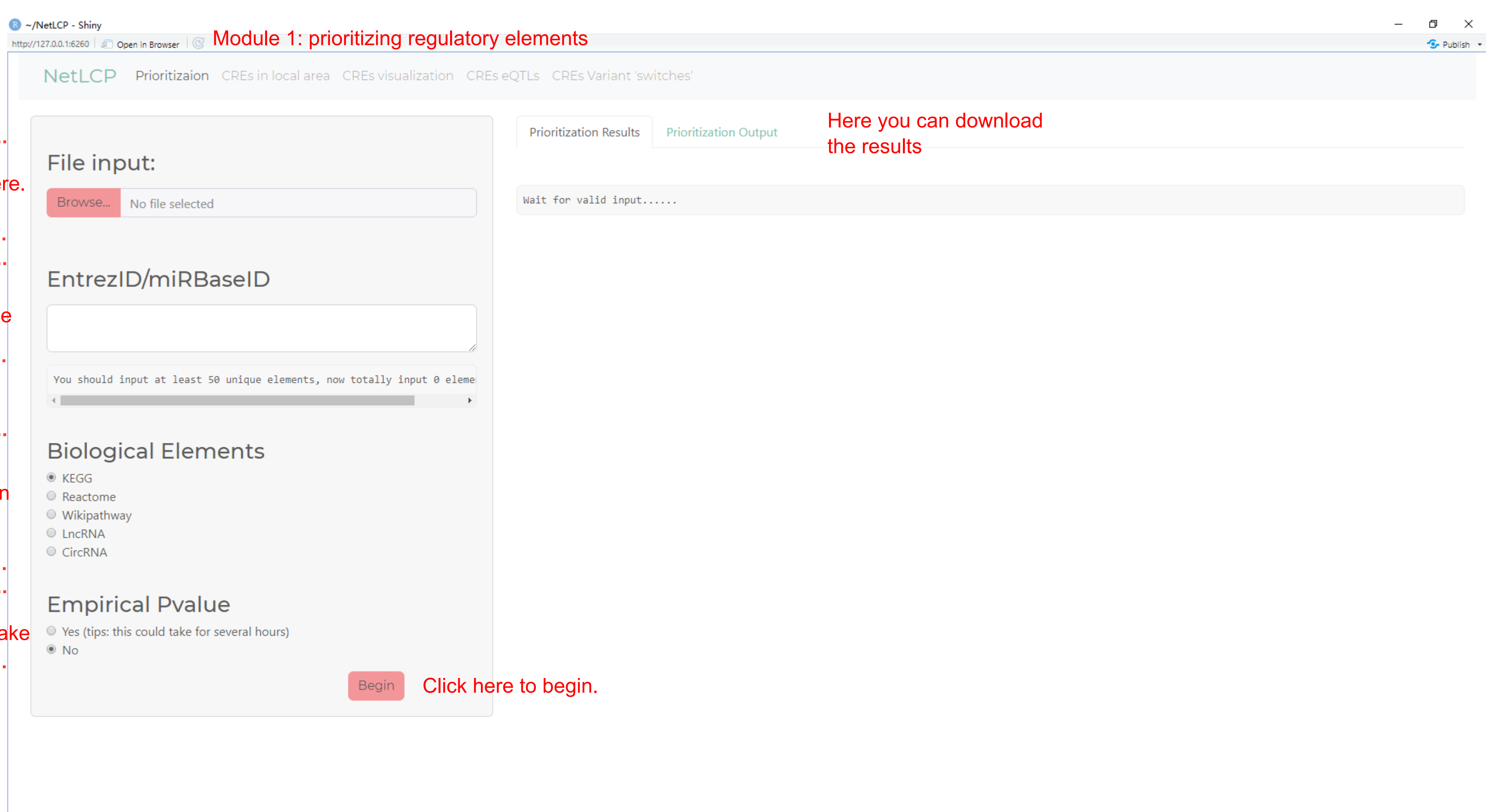
input_file_example.txt - 记事本
文件(F) 编辑(E) 格式(O) 查看(V) 帮助(H)
5155
5291
5300
5371
5580
5663
5728
2185
5054
25942
6647
6774
6776
6777
6794
6872
6929
7027
7153
MIMAT0000423
MIMAT0000449
MIMAT0002809
MIMAT0000765
MIMAT0000261
MIMAT0000441
MIMAT0000279
MIMAT0000438
MIMAT0000262
MIMAT00002875
MIMAT0000081

You can input miRNA/
mRNA through a file here.
Example file is given.

You can also input
miRNA/mRNA here, one
per line.

Choose the prioritization
module.

Choose the empirical
pvalue or not (it could take
for several hours).



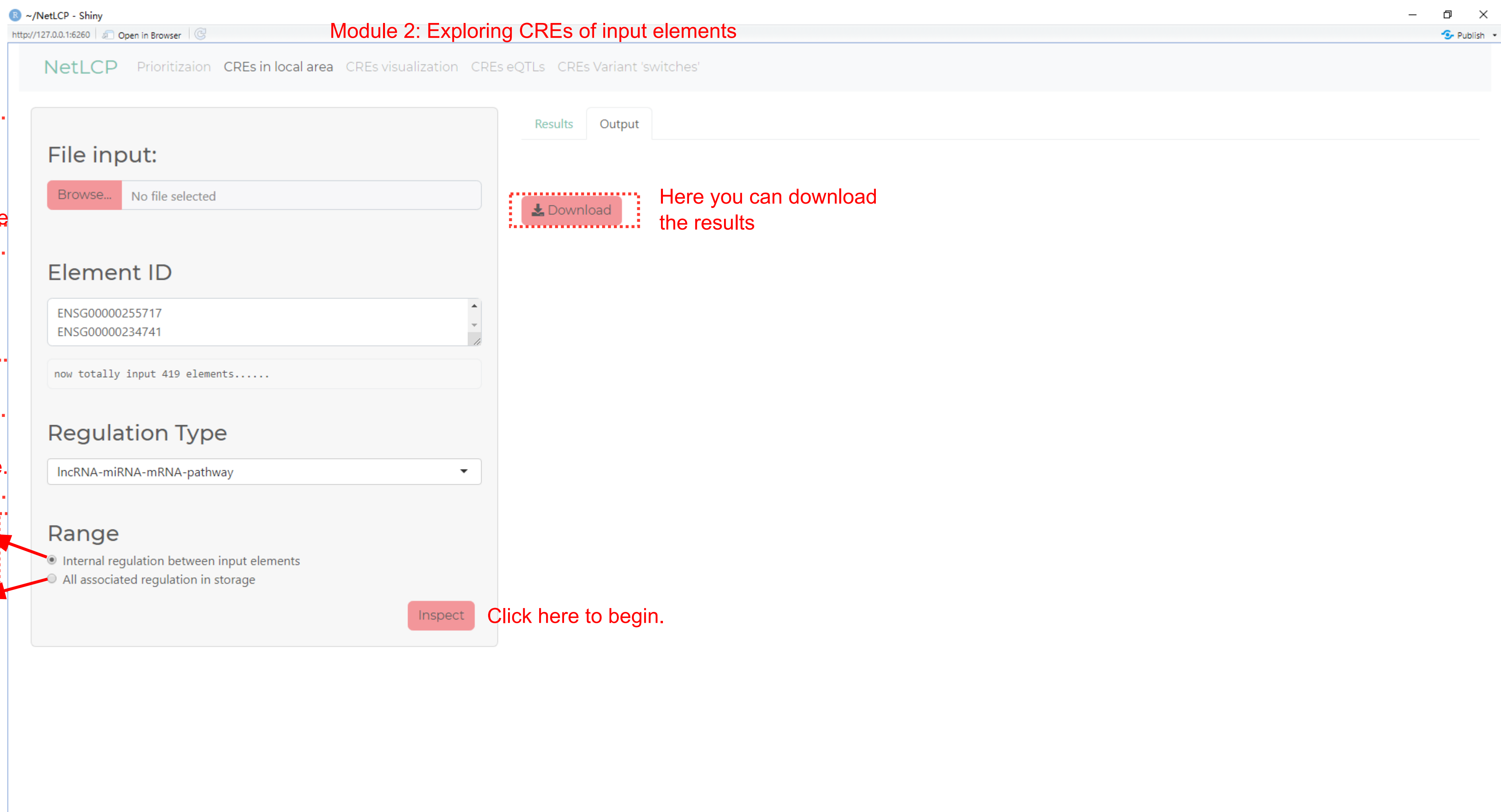
Click here to begin.

Here you can download
the results

You can input the element IDs to see the
regulation between/associating them.
Example file and input are given above.

Choose the regulation type

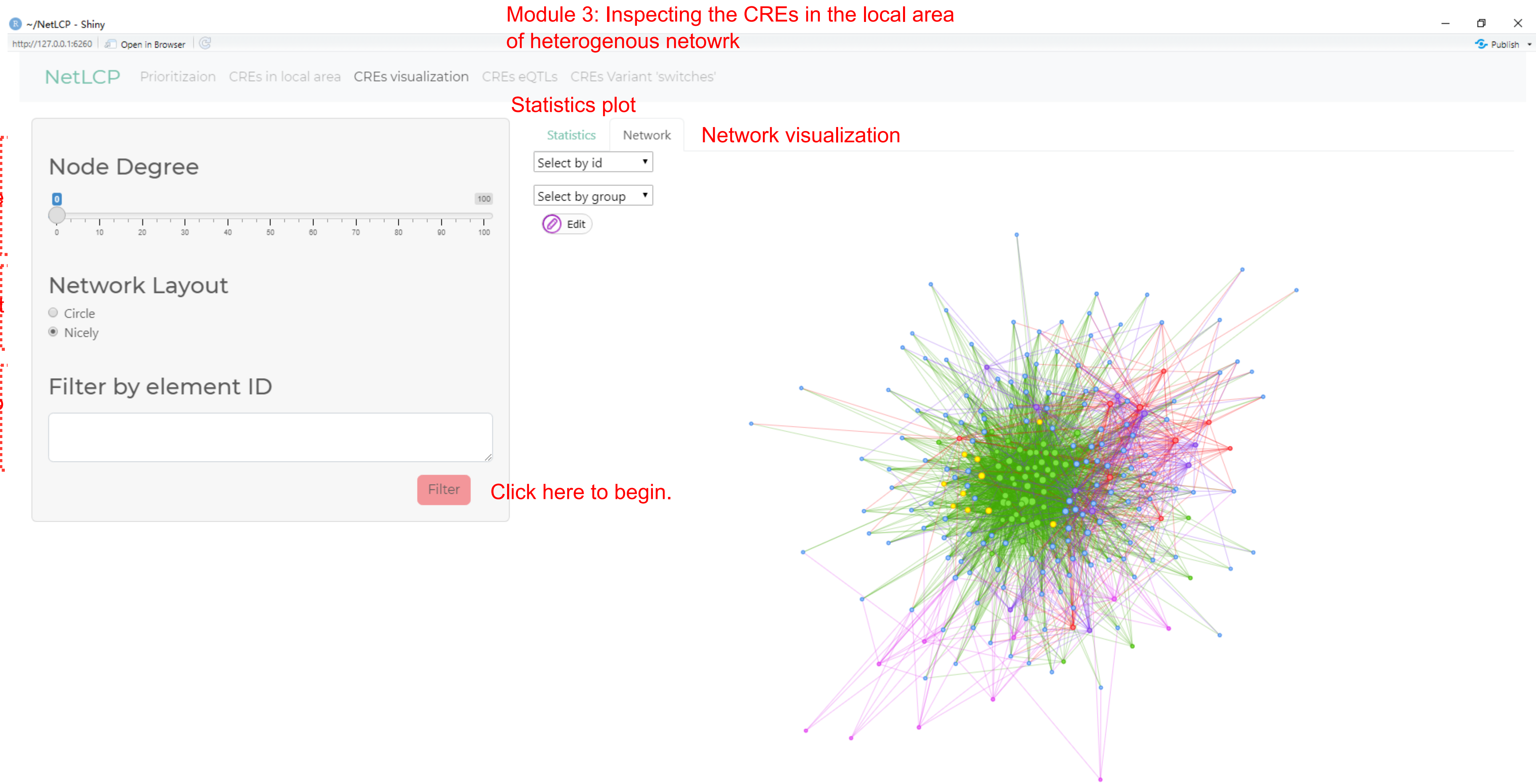
It returns the regulation between input
elements. Commonly used.
It returns all associated regulation which
may include other elements. It usually
returns large data.



Click here to begin.

Here you can download
the results

If you input a single element, it returns
associated regulation. If you input a group
of elements, it returns regulation between
them.



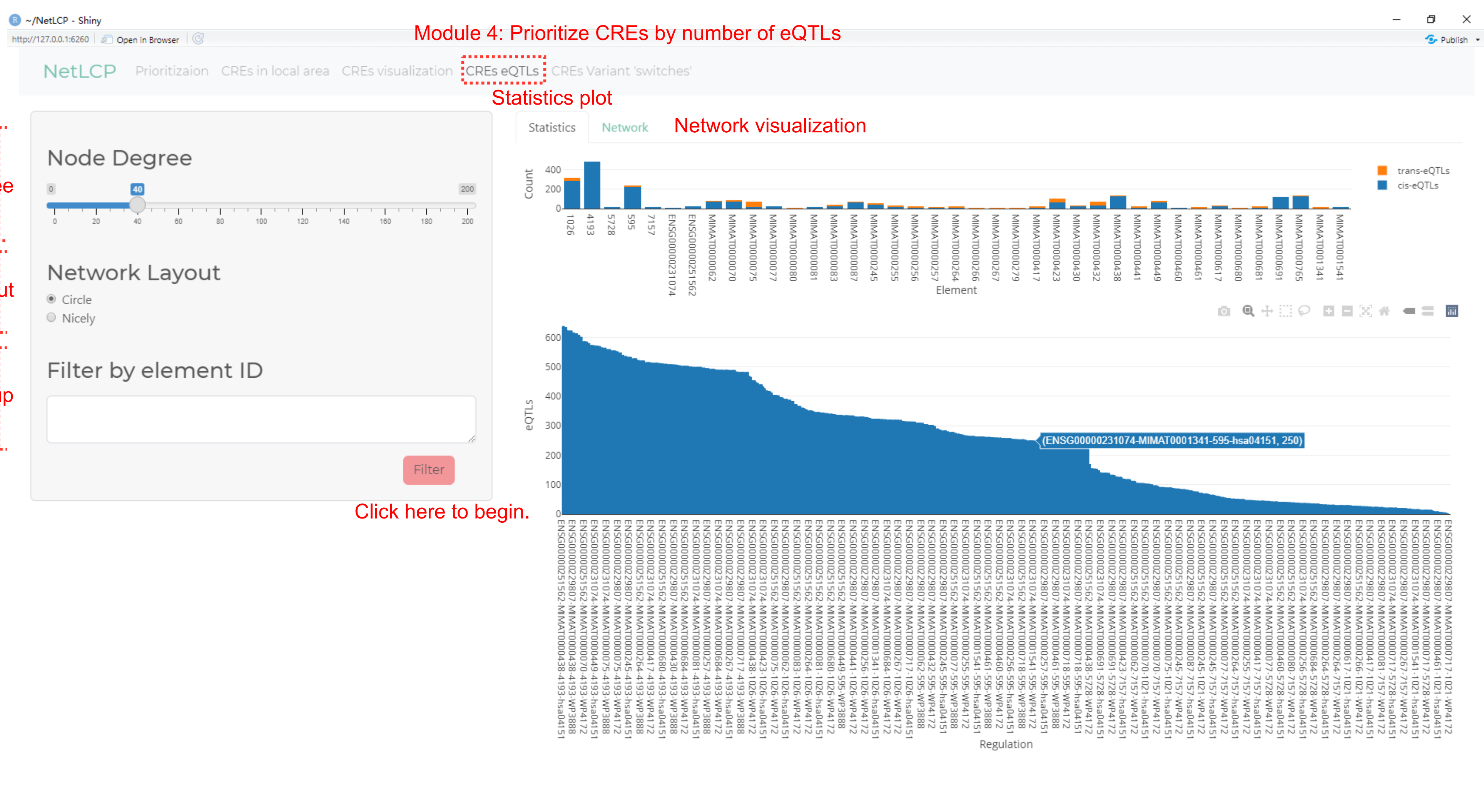
Filter the node degree

Change the network layout

Click here to begin.

Network visualization

You can input a single element or a group
of elements.



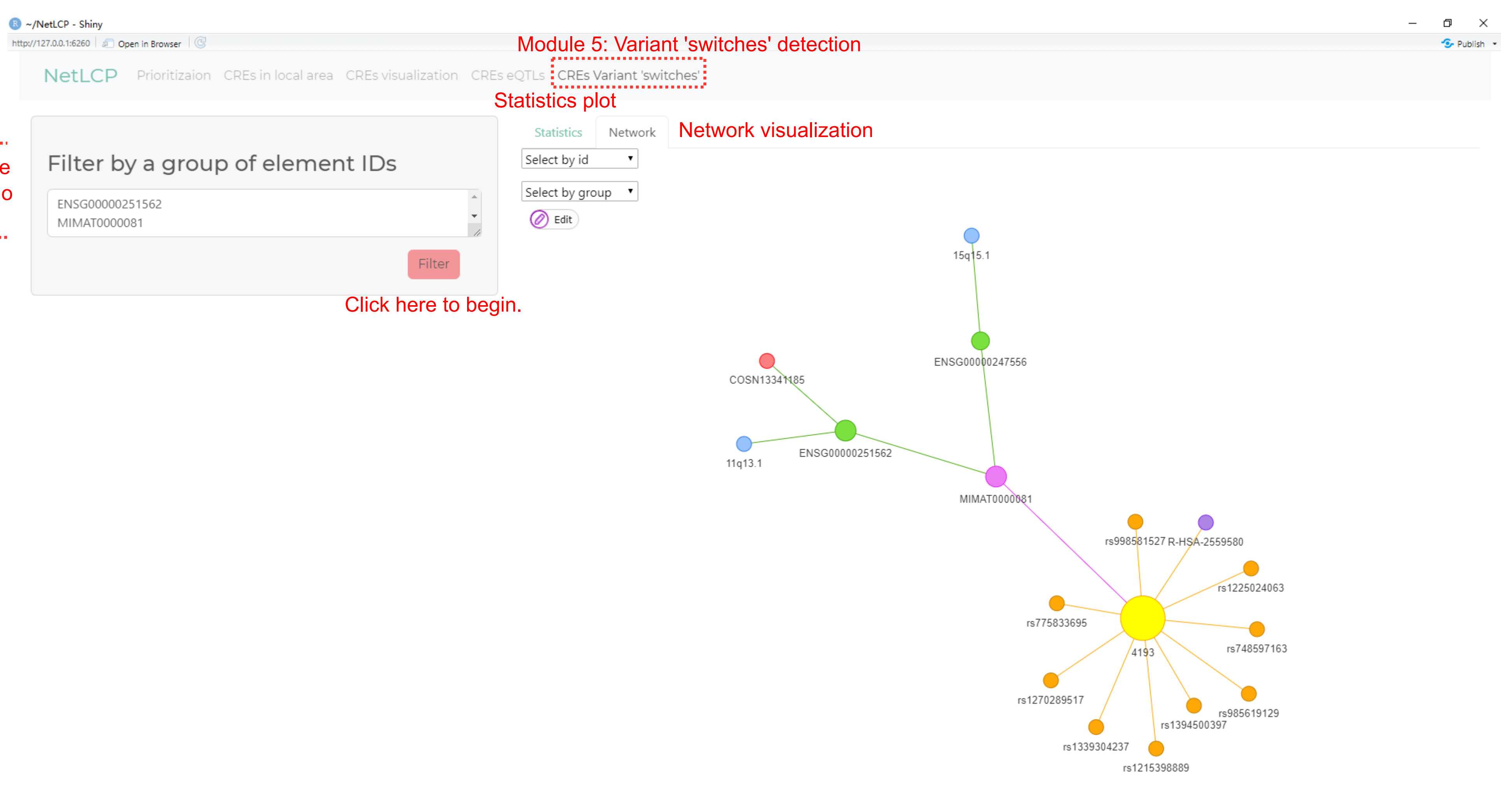
Filter the node degree

Change the network layout

Click here to begin.

Network visualization

You can input a group of elements. Note
that if won't exhibit anything until you do
this.



Click here to begin.

Network visualization