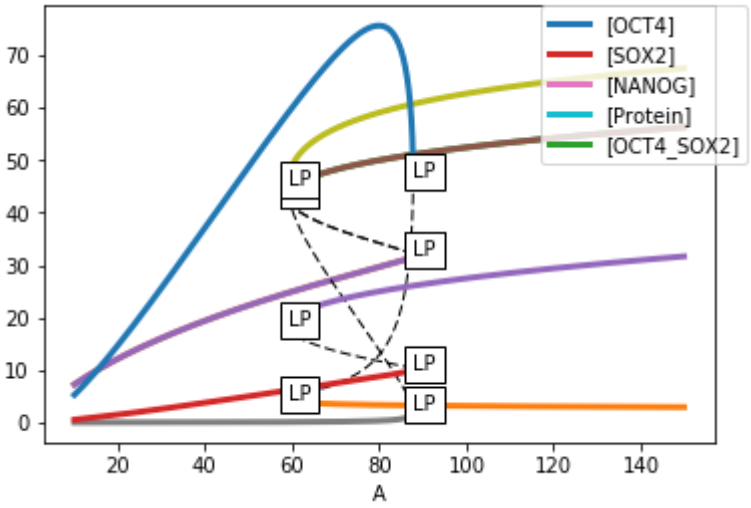
[1]

```
%matplotlib inline
"""
This script performs bifucation analysis on embryonic stem cell model
"""
import platform

if 'darwin' in platform.system().lower():
    from rrplugins import *
else:
    from teplugins import *
import matplotlib.pyplot as plt

sbmlModel ="/Users/phantom/devel/src/tellurium-
examples/BIOMD0000000203.xml"
auto = Plugin("tel_auto2000")

# Setup properties
auto.setProperty("SBML", readAllText(sbmlModel))

# Bifurcation specific properties
auto.setProperty("ScanDirection", "Positive")
auto.setProperty("PrincipalContinuationParameter", "A")
auto.setProperty("PCPLowerBound", 10)
auto.setProperty("PCPUpperBound", 150)

# Set maximum numberof points
auto.setProperty("NMX", 5000)

# execute the plugin
auto.execute()

# plot Bifurcation diagram
pts      = auto.BifurcationPoints
lbls     = auto.BifurcationLabels
biData   = auto.BifurcationData
biData.plotBifurcationDiagram(pts, lbls)
```


[OCT4]
[SOX2]
[NANOG]
[Protein]
[OCT4_SOX2]
LP
LP
LP
LP
LP
LP
LP
70
60
50
40
30
20
10
0
20
40
60
80
100
120
140
A

```
[ ]
```