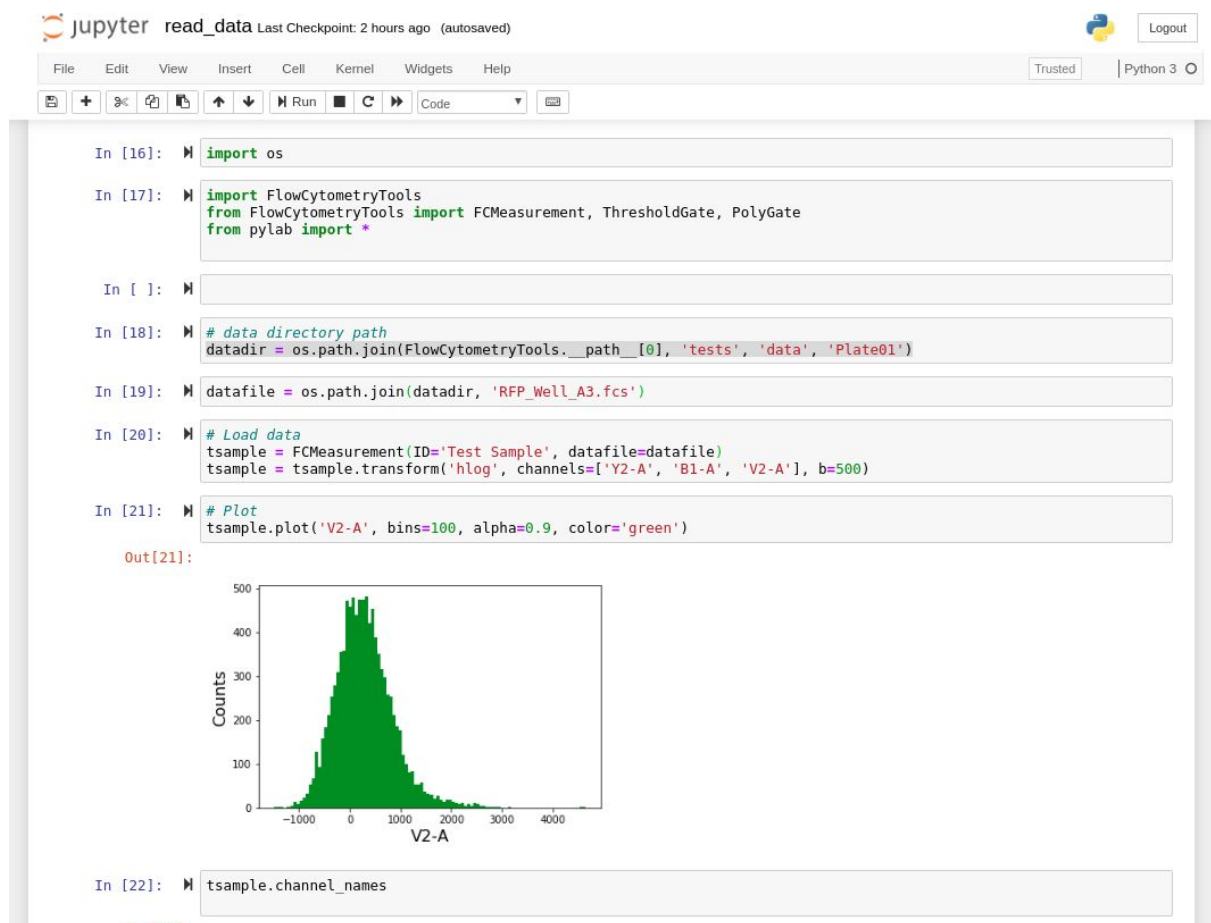


Python for fcs files analysis

We have started learning and practicing the Python libraries for analysis of prostate cancer cells.

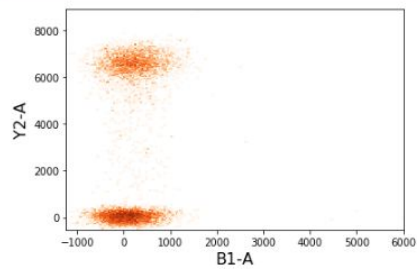
We have selected jupyter notebook to start with because it gives online access to all the team members. So far we have used the tutorial with sample data, reading, visualizing, gating etc.



Run Code

```
In [25]: tsample.plot(['B1-A', 'Y2-A'], cmap=cm.Oranges, colorbar=False)
```

Out[25]:



```
In [52]: # Create Threshold gate with Y2-A value below 1000
y2_gate_below = ThresholdGate(300.0, ['Y2-A'], region='below')
y2_gate_above = ThresholdGate(-300.0, ['Y2-A'], region='below')

# Gate for event B1-A value above 2000.0
b1_gate = ThresholdGate(2000.0, ['B1-A'], region='above')
```

```
In [53]: # Use interactive GUI
# tsample.view_interactively(backend='webagg')
```

```
In [54]: # Apply gates
figure()
tsample.plot(['Y2-A'], gates=[y2_gate_below, y2_gate_above], bins=100)
title('Gate Plotted')
```

Out[54]: Text(0.5, 1.0, 'Gate Plotted')

