

# Practical Bioinformatics

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# String tricks

```
# Join a list of strings  
x = []  
for i in s1:  
    x.append(f(i))  
return "".join(x)
```

```
# Work with a string directly  
s2 = ""  
for i in s1:  
    s2 += f(i)  
return s2
```

# Indexing tricks

*# 0 to n-1*

**range(n)**

*# m to n-1*

**range(m, n)**

*# n to m+1*

**range(n, m, -1)**

*# 0, 2, 5, 8*

**range(0, 9, 3)**

- Try sorting today's heatmap on different principal components. Look at the output in JavaTreeView by exporting the sorted heatmap in CDT format.
- *Optional*: try sorting on the polar angle formed by two principal components:

```
np.arctan2(pc1, pc2)
```

(Where  $pc1$  and  $pc2$  are the PC projections for a single gene)