

Python for scientific research

Flow control

Bram Kuijper

University of Exeter, Penryn Campus, UK

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Researcher
Development



What we've done so far

- 1 Declare variables using built-in data types and execute operations on them
- 2 **Next:** Controlling the flow of a program

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- **Flow control** commands lets us dictate the **order** in which commands are run:
 - 1 **If-else**: to change what commands are executed under certain conditions
 - 2 **For loops**: to repeat the same thing N times
 - 3 **While loops**: to repeat the same thing until a specific condition is met

- Print whether the integer x is positive, negative or zero

```
1 if x > 0:
2     print("x is positive")
3 elif x < 0:
4     print("x is negative")
5 else:
6     print("x is zero")
```

- Note the lack of `{ }` used in many other languages (R, C/C++); in Python **indentation** is everything!

For loops

- Print the integers 1 to 5

```
1 for x in range(5):  
2     print(x+1)
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- Loop through a list of gene names and print them in upper case

```
1 geneNames = ["Irf1", "Ccl3", "Il12rb1", "Ifng", "Cxcl10"  
2             ""]  
2 for gene in geneNames:  
3     print(gene.upper())
```

While loops

- Print the integers 10 to 1

```
1 x = 10
2 while x > 0:
3     print(x)
4     x = x - 1
```

- **Note:**

- 1 Use for loops over while loops where possible
- 2 Ensure that the while condition evaluates to False at some point to avoid an infinite loop

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1 geneNames = ["Irf1", "Ccl3", "Il12rb1", "Ifng", "Cxcl10",  
               ""]  
2 for gene in geneNames:  
3     print(gene.upper())
```

- What if I want to store the upper case gene names in another variable, called `x` for simplicity?

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1 Using for loops:

```
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2 for gene in geneNames:
3     x.append(gene.upper())
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2 Using list comprehension:

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1 x = [gene.upper() for gene in geneNames]
```

3 What if I want to ignore gene Ifng?

```
1 x = [gene.upper() for gene in geneNames if gene != "Ifng"]
```

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- Print the index next to upper cased gene name
 - ❶ Using a standard for loop:

```
1 i = 0 # index counter
2 for gene in geneNames:
3     print("{0}. {1}\n".format(i+1, gene.upper()))
4     i = i + 1
```

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1 i = 0 # index counter
2 for gene in geneNames:
3     print("{0}. {1}\n".format(i+1, gene.upper()))
4     i = i + 1
```

2 Using enumerate:

```
1 for i, gene in enumerate(geneNames):
2     print("{0}. {1}\n".format(i+1, gene.upper()))
```