

A Bioinformaticians' Guide to Python



HELLO, WORLD!

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Preparing for Launch



<http://bit.ly/2kgkYfm>



Installing Anaconda

A Python distribution for Data Science.

1

DOWNLOAD ANACONDA NOW

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Supercharge your Data Science team with tickets to **AnacondaCON
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GET SUPERPOWERS WITH **ANACONDA**

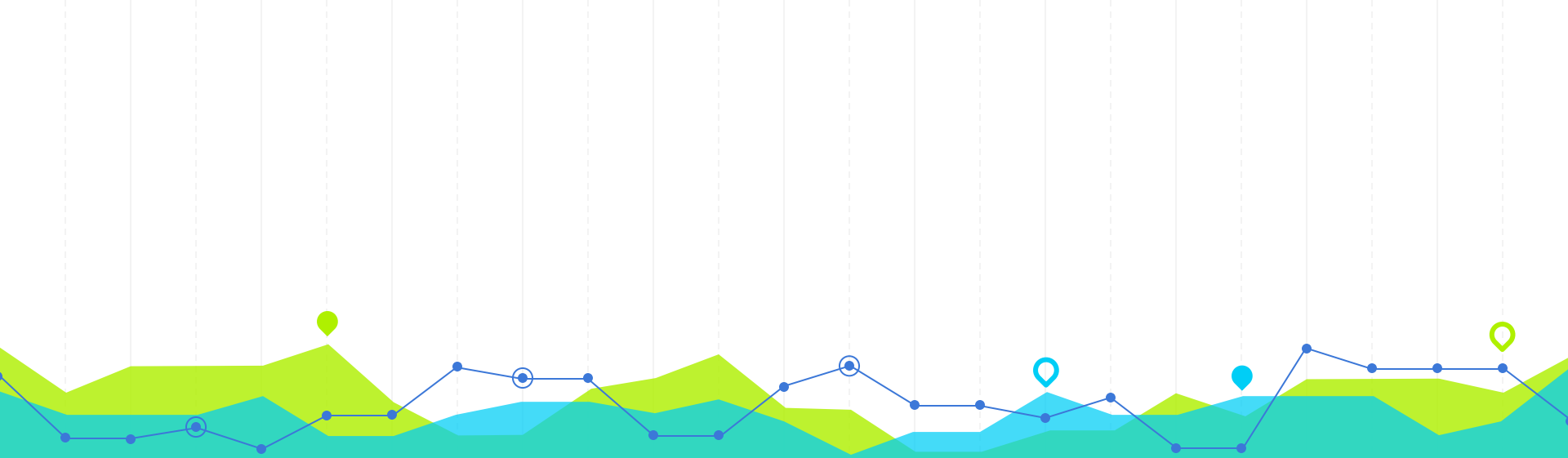
Anaconda is the leading open data science platform powered by Python. The open source version of Anaconda is a high performance distribution of Python and R and includes over 100 of the most popular Python, R and Scala packages for data science.

Additionally, you'll have access to over 720 packages that can easily be installed with conda, our renowned package, dependency and environment manager, that is included in Anaconda. See the [packages](#) included with Anaconda and the Anaconda [changelog](#)

Which version should I download and install?

With Anaconda you can run multiple versions of Python in isolated environments, so choose the download with the Python version that you use more often, as that will be your default Python version.

If you don't have time or disk space for the entire distribution, try [Miniconda](#) which contains only conda and Python. Then install just the individual packages you want through the conda command.

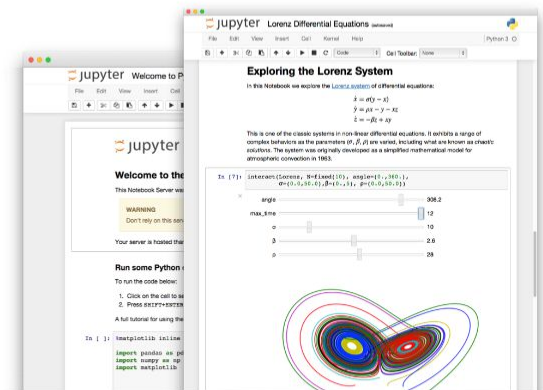


Running Jupyter

An interactive notebook for Python.

2

Ready to get started?

[Try it in your browser](#)
[Install the Notebook](#)


The Jupyter Notebook

The Jupyter Notebook is a web application that allows you to create and share documents that contain live code, equations, visualizations and explanatory text. Uses include: data cleaning and transformation, numerical simulation, statistical modeling, machine learning and much more.



Language of choice

The Notebook has support for over 40 programming languages, including those popular in Data Science such as Python, R, Julia and Scala.



Share notebooks

Notebooks can be shared with others using email, Dropbox, GitHub and the [Jupyter Notebook Viewer](#).



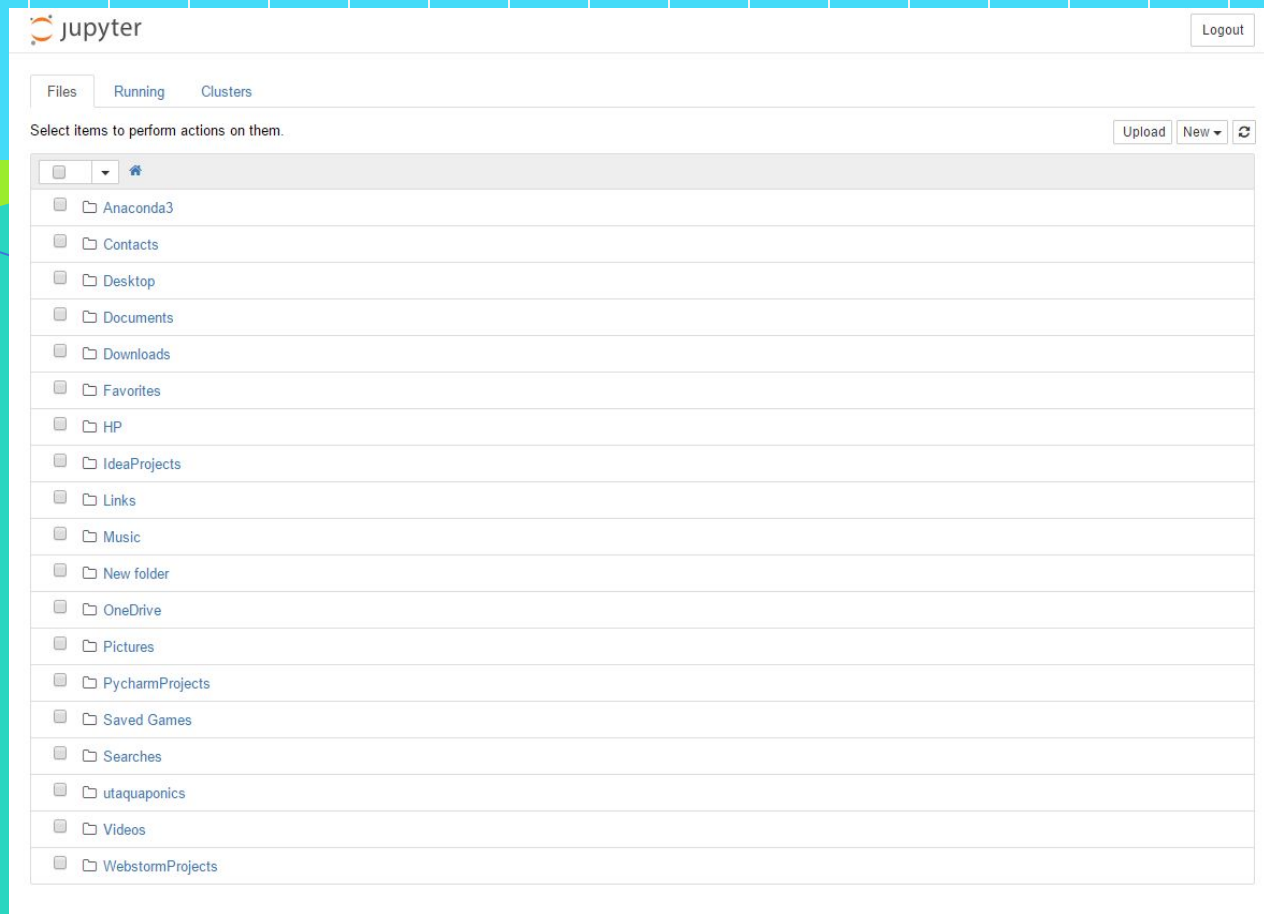
Interactive widgets

Code can produce rich output such as images, videos, LaTeX, and JavaScript. Interactive widgets can be used to manipulate and visualize data in realtime.

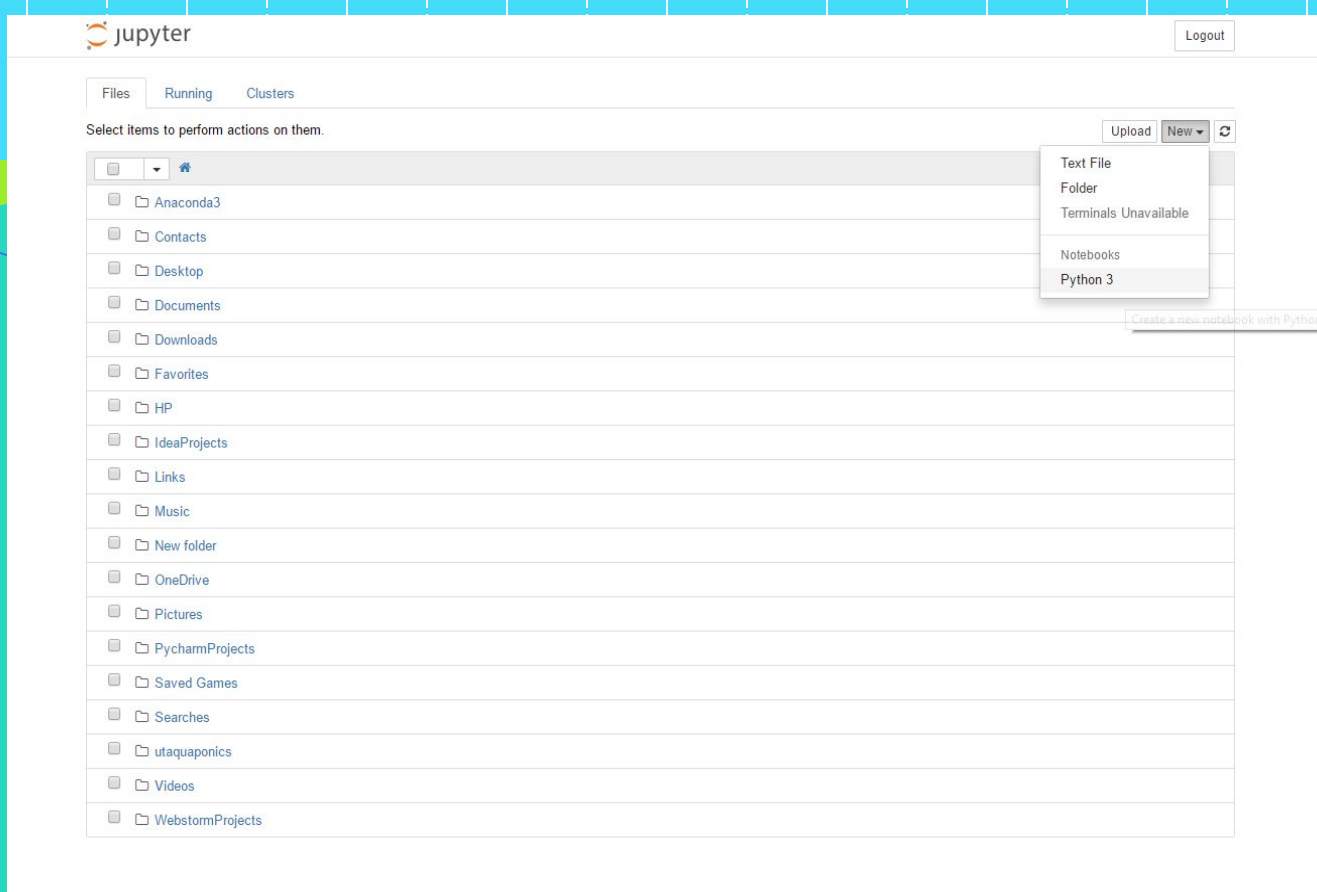


Big data integration

Leverage big data tools, such as Apache Spark, from Python, R and Scala. Explore that same data with pandas, scikit-learn, ggplot2, dplyr, etc.

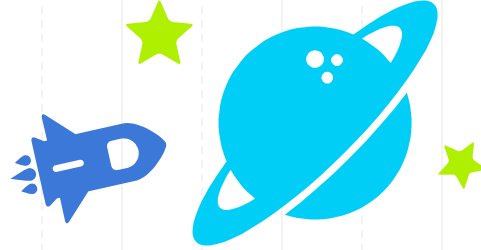


```
trenton@linux:~$ jupyter notebook
```

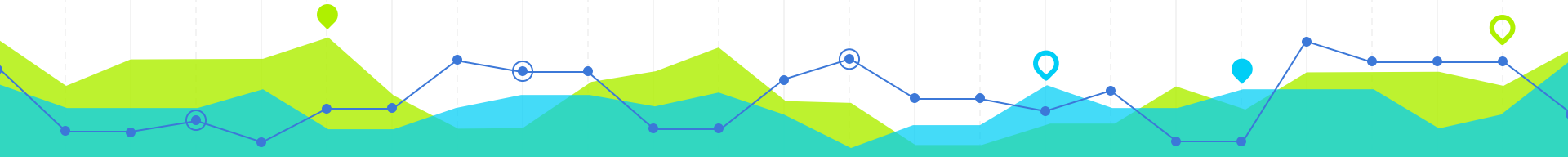
Creating a new Jupyter Notebook for Python 3.

In []:



What is Python?

A fast, powerful, open, object-oriented, readable, all-in-one programming language.

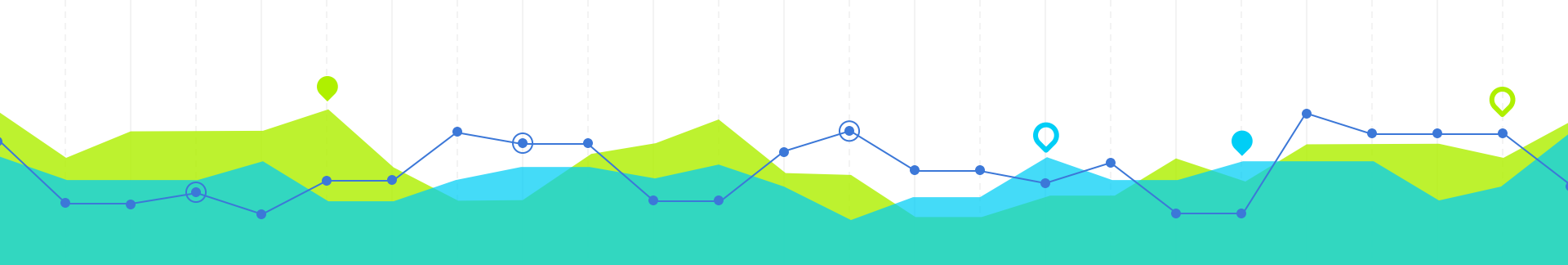




Understanding the Syntax

Indentation, Comments, Operators, Variables,
Types, Control Flow, Functions, File I/O,
Imports

3

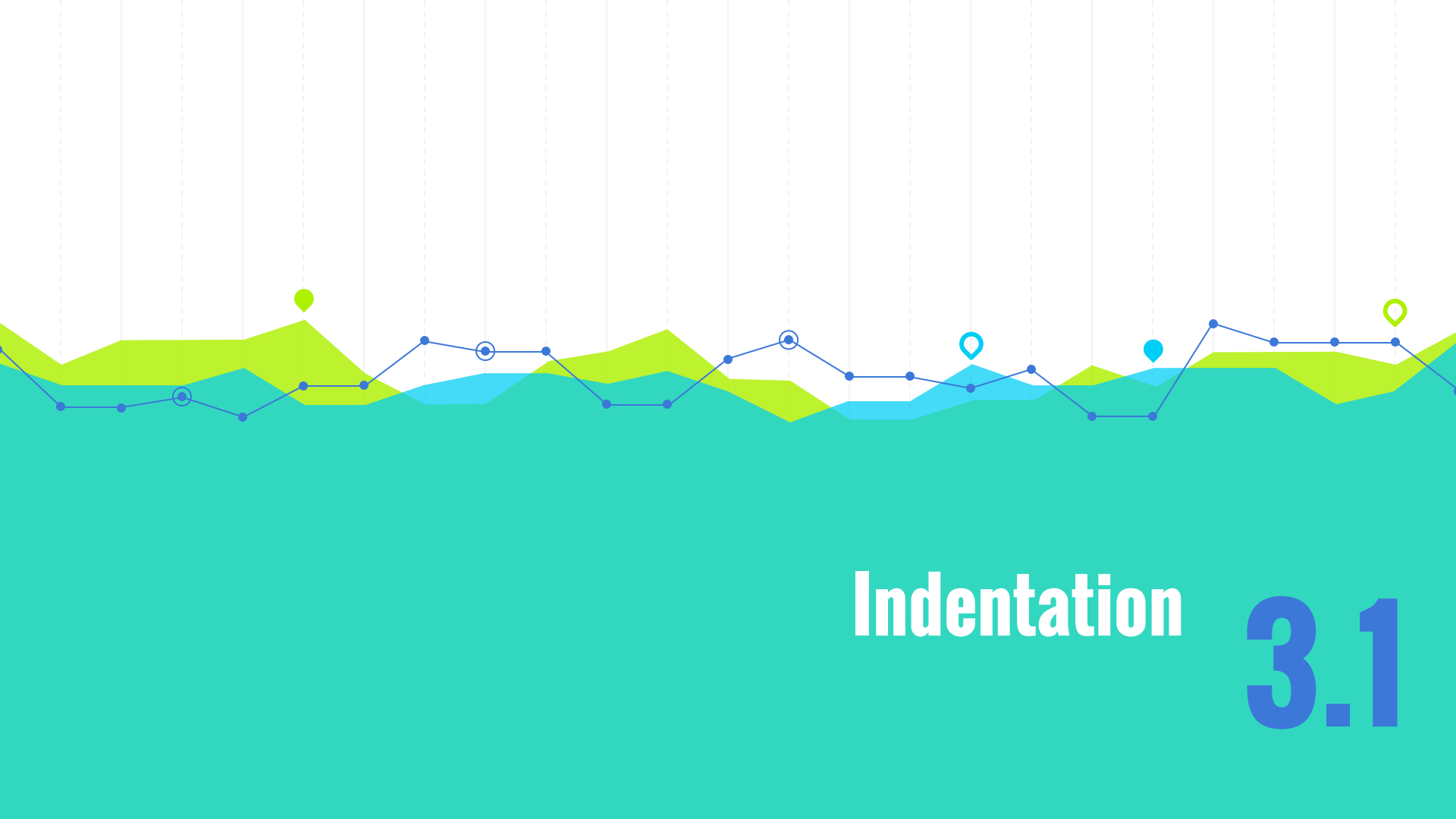


```
#!/usr/bin/env python

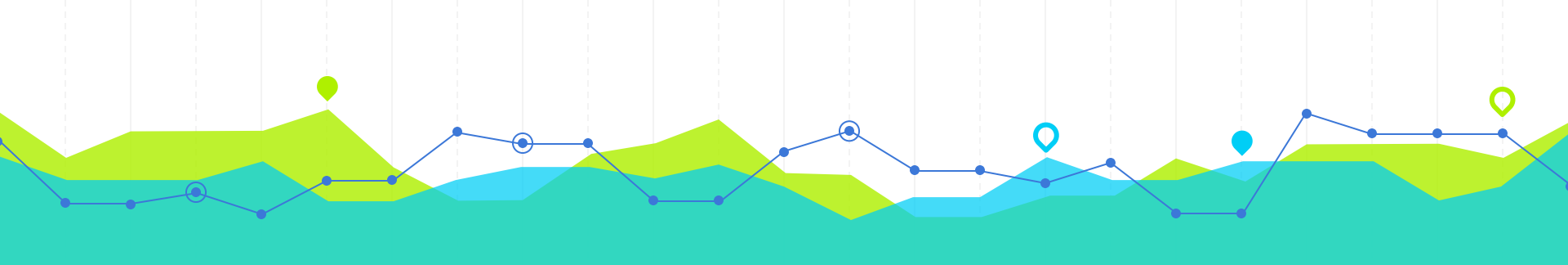
def main():
    print("hello, world!")

if __name__ == "__main__":
    main()
```

Example 1: Hello World



Indentation **3.1**



```
#!/usr/bin/env python
```

```
def main():
```

```
    print("hello")
```

```
    print("hello again")
```

```
if __name__ == "__main__":
```

```
    main()
```

Example 2: Indentation



Comments **3.2**

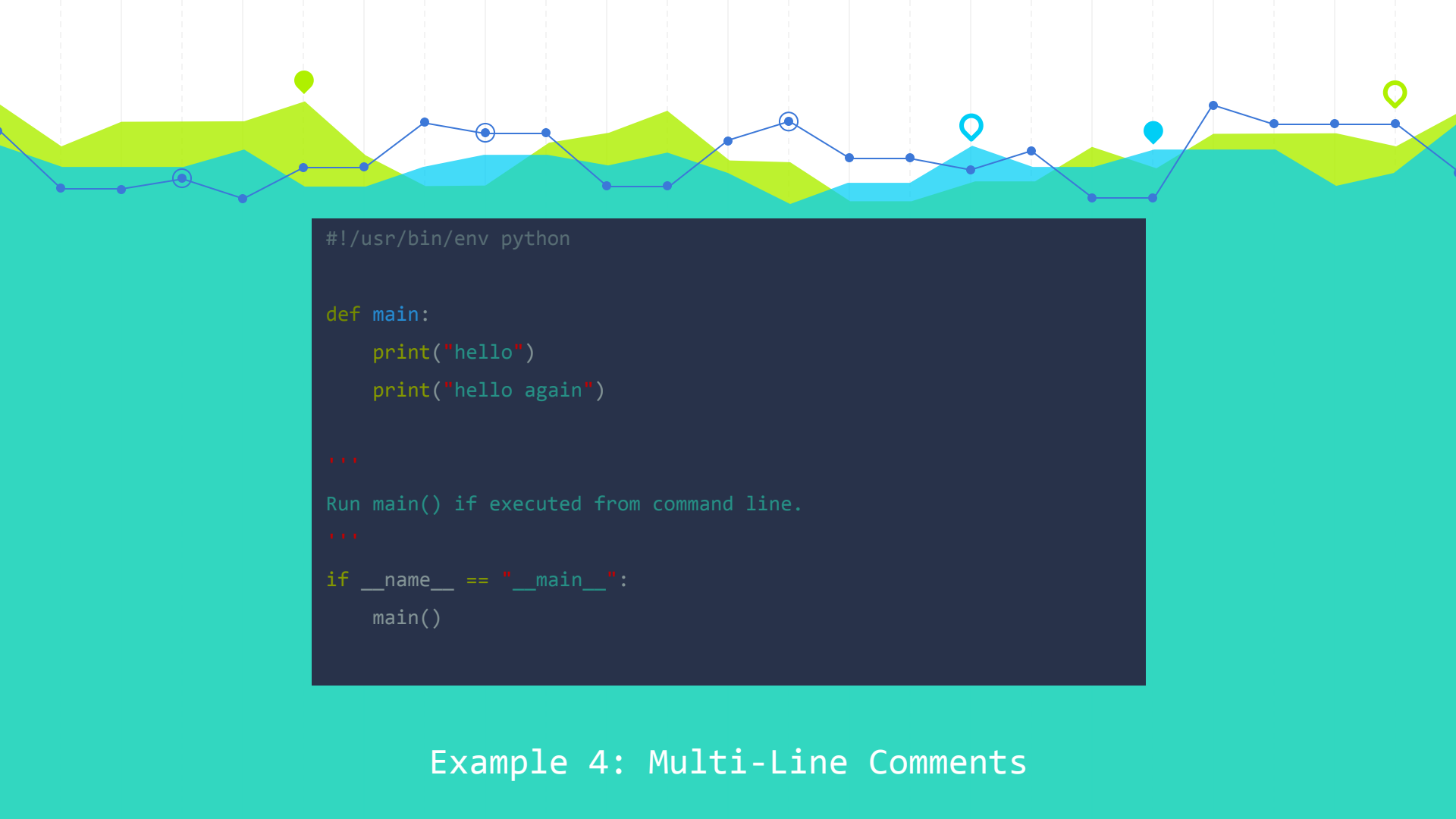


```
#!/usr/bin/env python
```

```
def main:  
    print("hello")  
    print("hello again") # prints hello again
```

```
if __name__ == "__main__":  
    main()
```

Example 3: In-Line Comments



```
#!/usr/bin/env python
```

```
def main:  
    print("hello")  
    print("hello again")
```

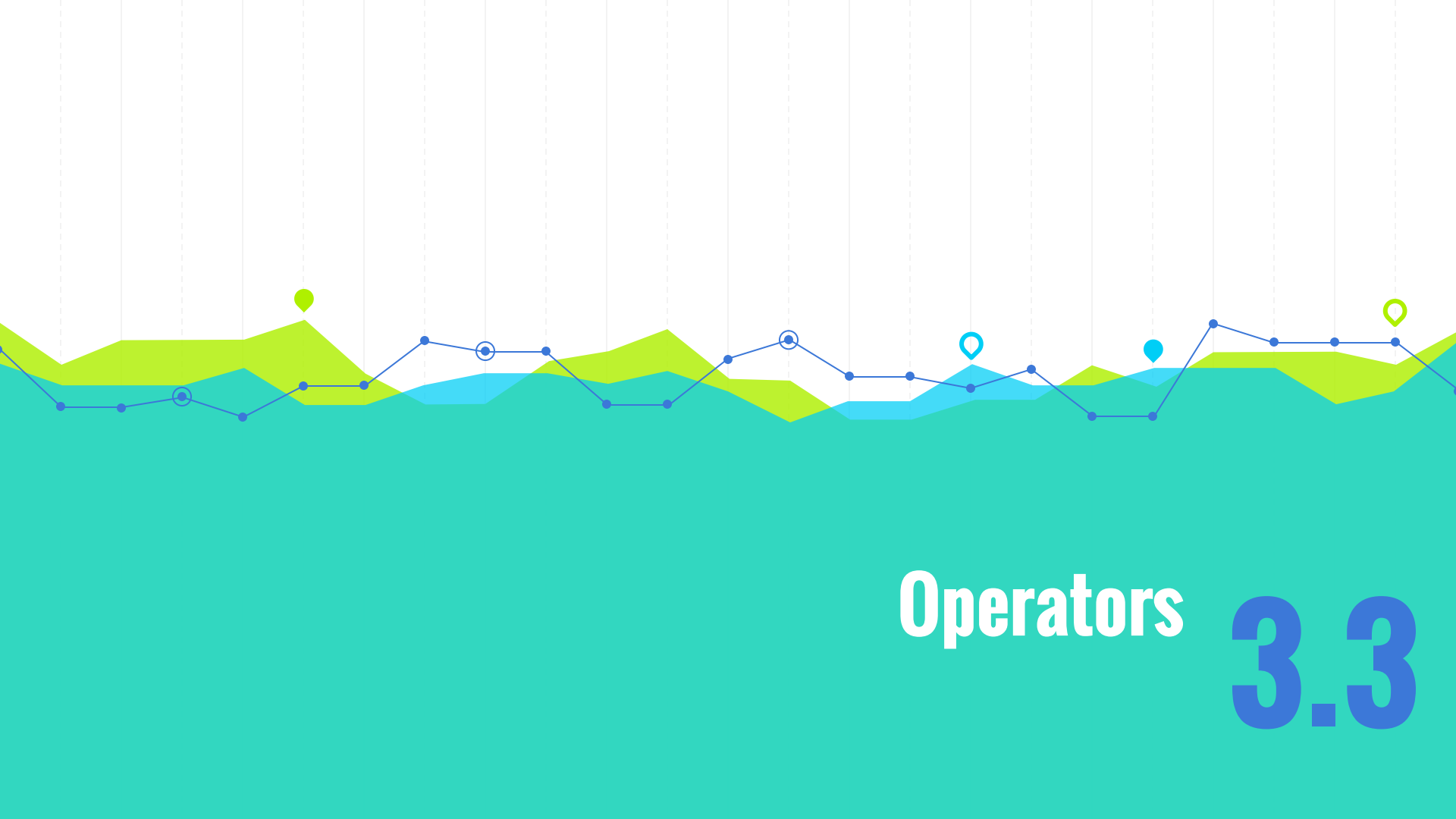
```
...
```

```
Run main() if executed from command line.
```


```
...
```

```
if __name__ == "__main__":  
    main()
```

Example 4: Multi-Line Comments



Operators 3.3

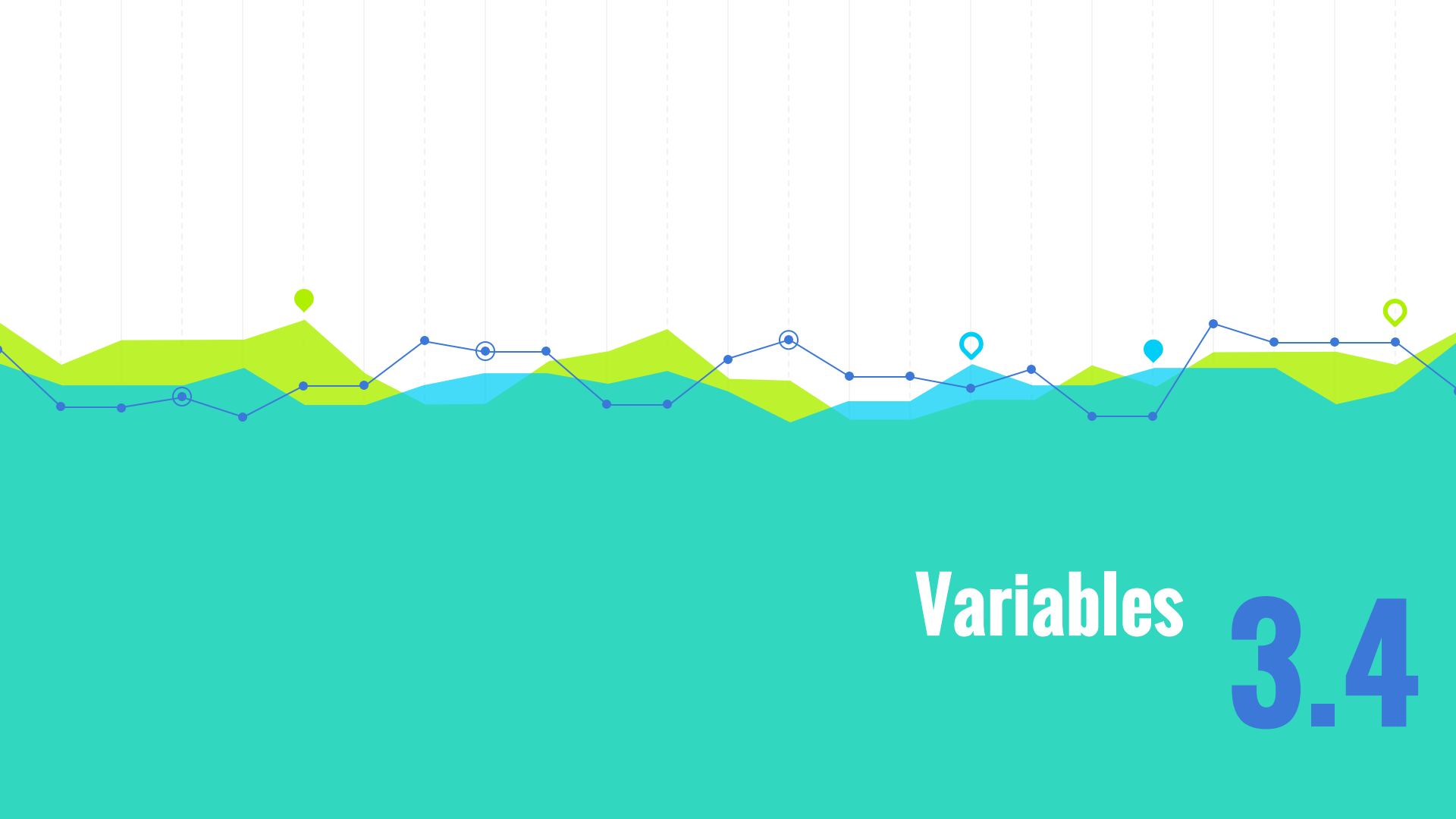


```
#!/usr/bin/env python
```

```
def main:
    print(5 + 5)      # Addition
    print(27 / 3)     # Floating-Point Division
    print(5 * 5)      # Multiplication
    print(5**5)       # Exponentiation
    print(100 // 3)   # Integer Division
    print(5 % 4)      # Remainder (modulo)
    print(13.5 - 14.5) # Subtraction
    print(True + 1)   # ???

if __name__ == "__main__":
    main()
```

Example 5: Operators



Variables 3.4



```
#!/usr/bin/env python
```

```
def main:
```

```
    x = 5
```

```
    y = 6
```

```
    z = 7
```

```
    print(x - y)
```

```
    print(y - x)
```

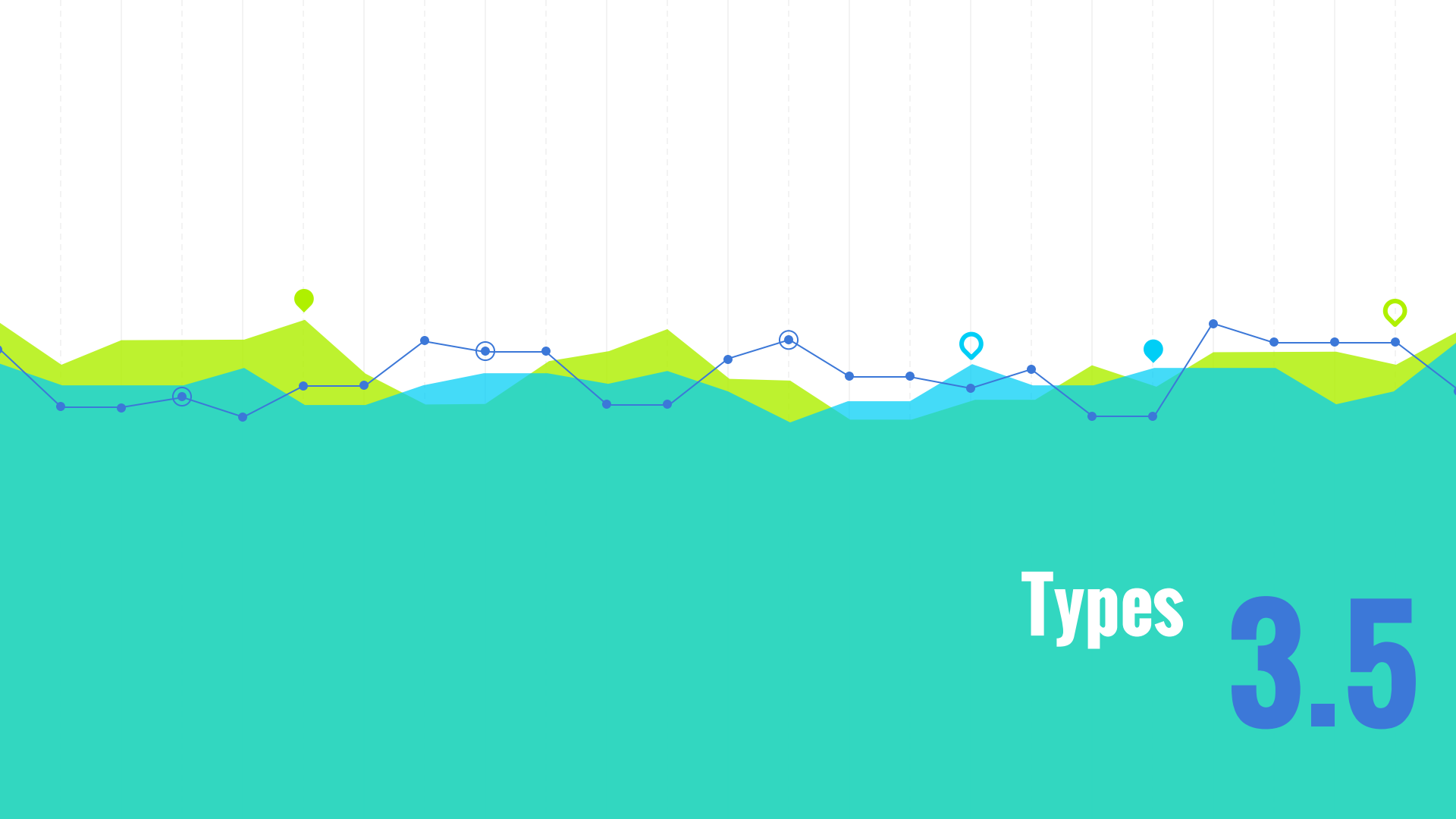
```
    print(x + y + z)
```

```
    print(x == y)
```

```
if __name__ == "__main__":
```

```
    main()
```

Example 6: Variables



Types 3.5

```
#!/usr/bin/env python
```

```
def main:
```

```
    dna_sequence = 'ACTGACTGACTGTATATATATATATA'
```

```
    dna_complement = 'TGACTGACTGACATATATATATATAT'
```

```
    rna_sequence = 'ACUGACUGACUGUAUAUAUAUAUAUA'
```

```
    amino_acid = 'MetLeuSerTyrTyrGluSerIleMetLeuSerTyrTyrGluSerIle'
```

```
    x = 'A'
```

```
    x = x + 'C'
```

```
    print(x)
```

```
    print(x[0])
```

```
    print(x[1])
```

```
if __name__ == "__main__":
```

```
    main()
```

Example 7: Strings


```
#!/usr/bin/env python
```

```
def main:
    cancer_genes = ['ABI1', 'ABL1', 'ABL2', 'ACKR3', 'ACSL3', 'ACSL6', 'AVCR1', 'AFF1']

    first_gene = cancer_genes[0]
    print("The first gene is: " + first_gene)

    last_gene = cancer_genes[len(cancer_genes) - 1]
    print("The last gene is: " + last_gene)

    cancer_genes.insert(2, 'BRCA1')
    print("Cancer genes: " + str(cancer_genes))

    cancer_genes.append('BRCA1')
    print("Cancer genes: " + str(cancer_genes))

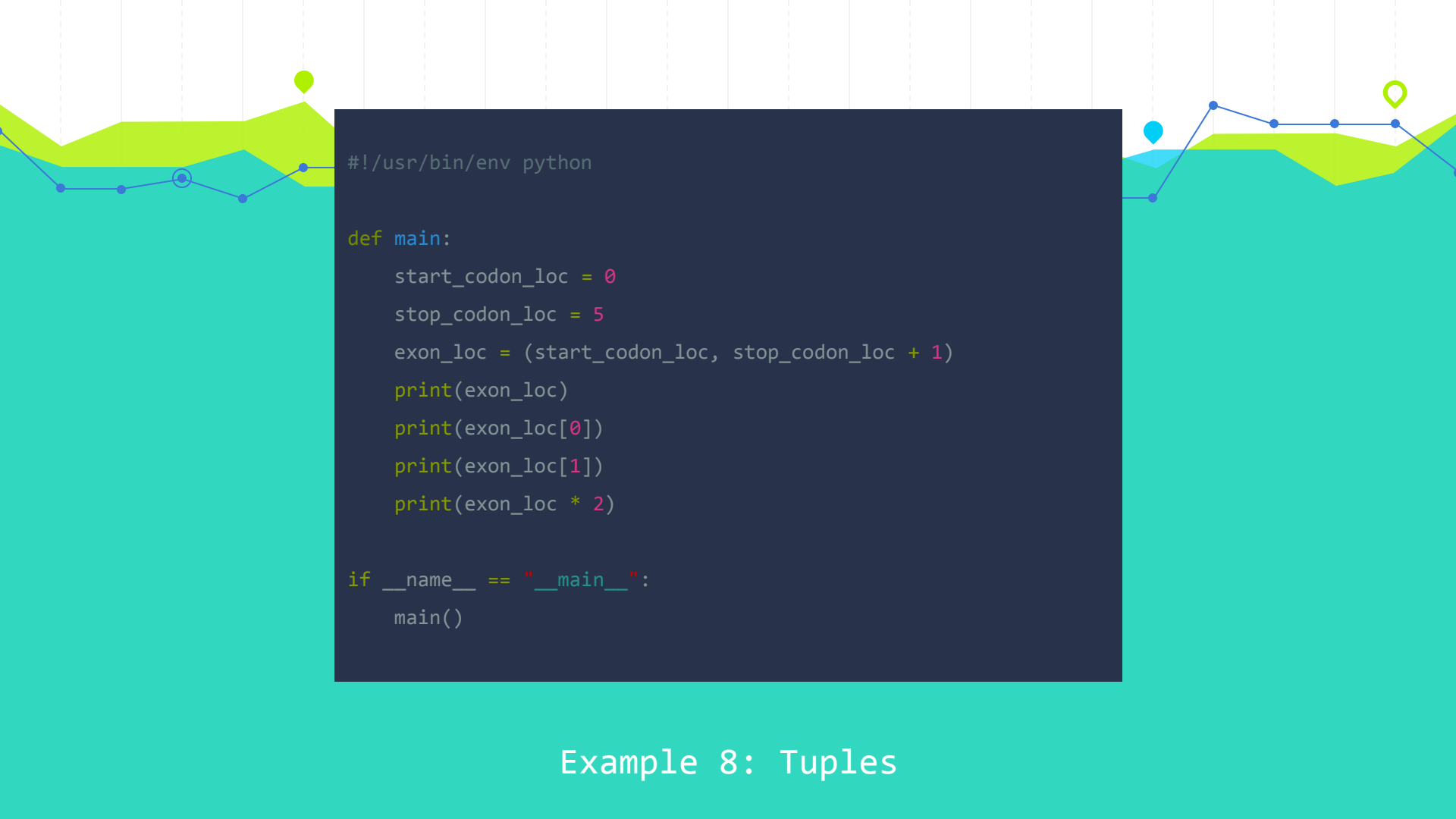
    cancer_genes.remove('ABI1')
    print("Cancer genes: " + str(cancer_genes))

    print("The number of BRCA1 genes is: " + str(cancer_genes.count('BRCA1')))
    print("The index of BRCA1 is: " + str(cancer_genes.index('BRCA1')))

    cancer_genes.reverse()
    print("Cancer genes: " + str(cancer_genes))

if __name__ == "__main__":
    main()
```

Example 8: Lists



```
#!/usr/bin/env python
```

```
def main:
```

```
    start_codon_loc = 0
```

```
    stop_codon_loc = 5
```

```
    exon_loc = (start_codon_loc, stop_codon_loc + 1)
```

```
    print(exon_loc)
```

```
    print(exon_loc[0])
```


```
    print(exon_loc[1])
```

```
    print(exon_loc * 2)
```

```
if __name__ == "__main__":
```

```
    main()
```

Example 8: Tuples



```
#!/usr/bin/env python
```

```
def main:
```

```
    dna_to_rna = {'A':'A', 'C':'C', 'G':'G'}
```

```
    dna_to_rna['T'] = 'U'
```

```
    print(dna_to_rna['A'])
```

```
    print(list(dna_to_rna.keys()))
```

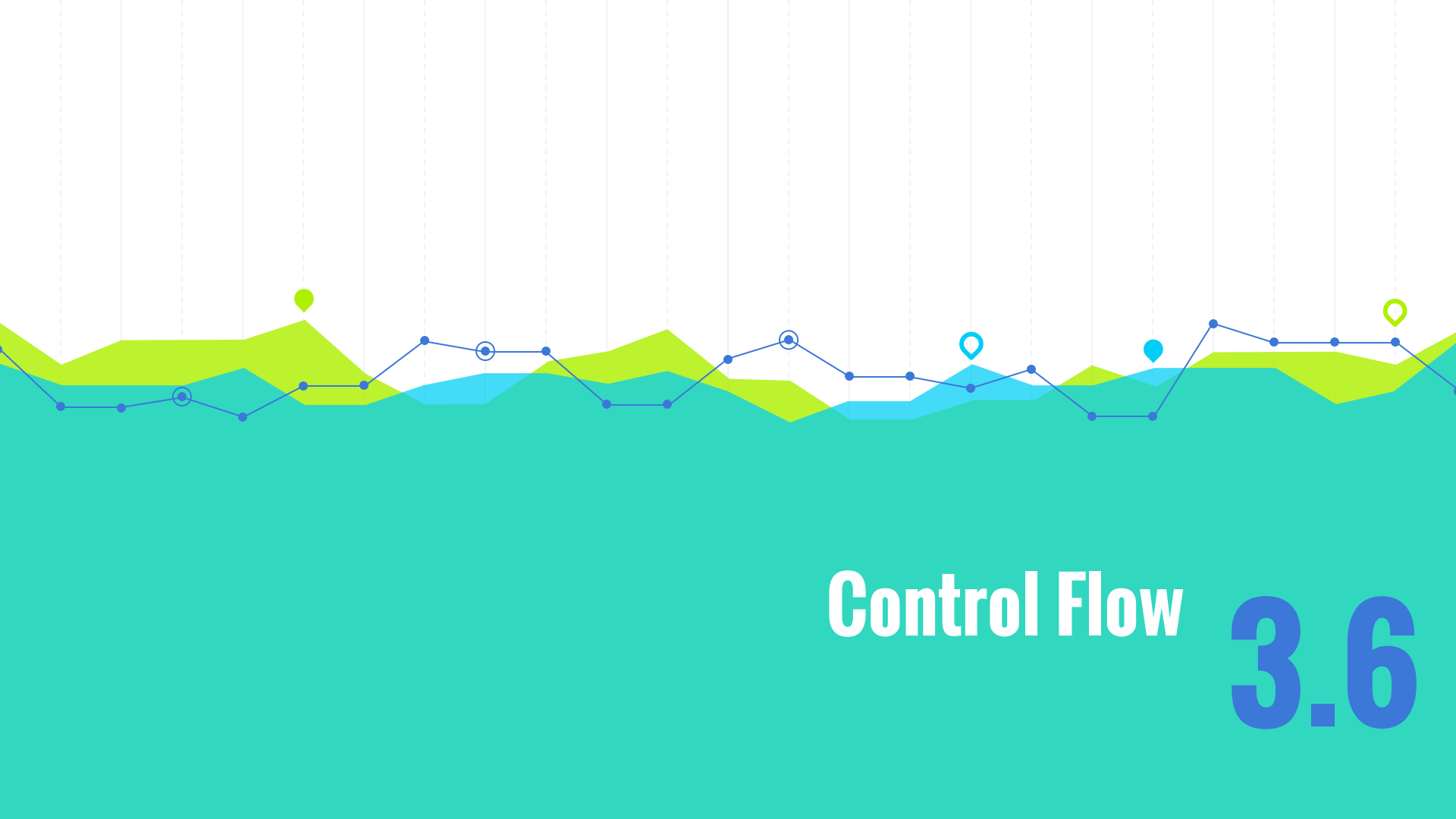
```
    print('Y' in dna_to_rna)
```

```
    print(list(dna_to_rna.values()))
```

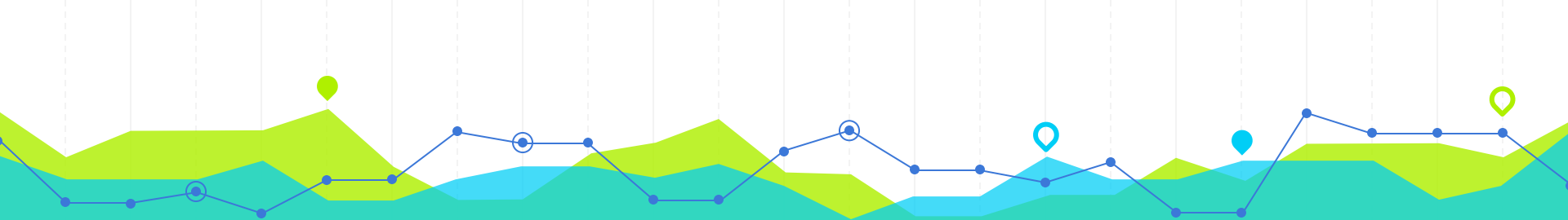
```
if __name__ == "__main__":
```

```
    main()
```

Example 9: Dictionaries




Control Flow 3.6



```
#!/usr/bin/env python
```

```
def main():  
    if(True):  
        print("hello")  
        print("hello again")  
    else:  
        print("goodbye")  
  
if __name__ == "__main__":  
    main()
```

Example 10: If / Else



```
#!/usr/bin/env python
```

```
def main:
```

```
    dna_sequence = 'ACTGACGTCTATATA'
```

```
    for base in dna_sequence:
```

```
        print(base)
```

```
    print("\n")
```

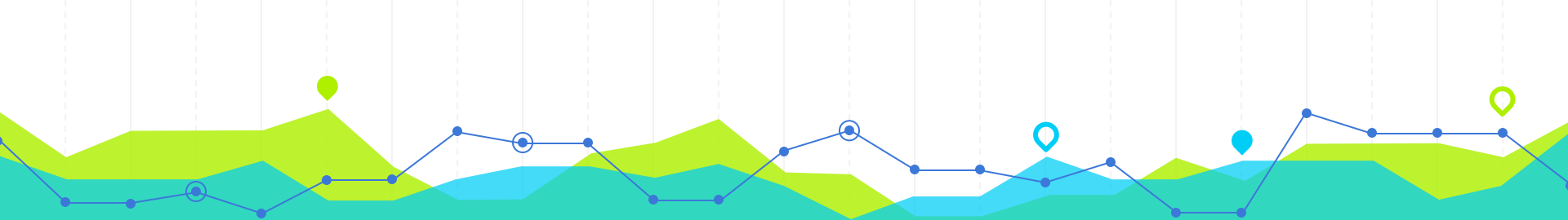
```
    for i in range(len(dna_sequence)):
```

```
        print(dna_sequence[i])
```

```
if __name__ == "__main__":
```

```
    main()
```

Example 11: For



```
#!/usr/bin/env python
```

```
def main:
```

```
    dna_sequence = 'AAAAAACTGA'
```

```
    i = 0
```

```
    while(dna_sequence[i] == 'A' and i < len(dna_sequence)):
```

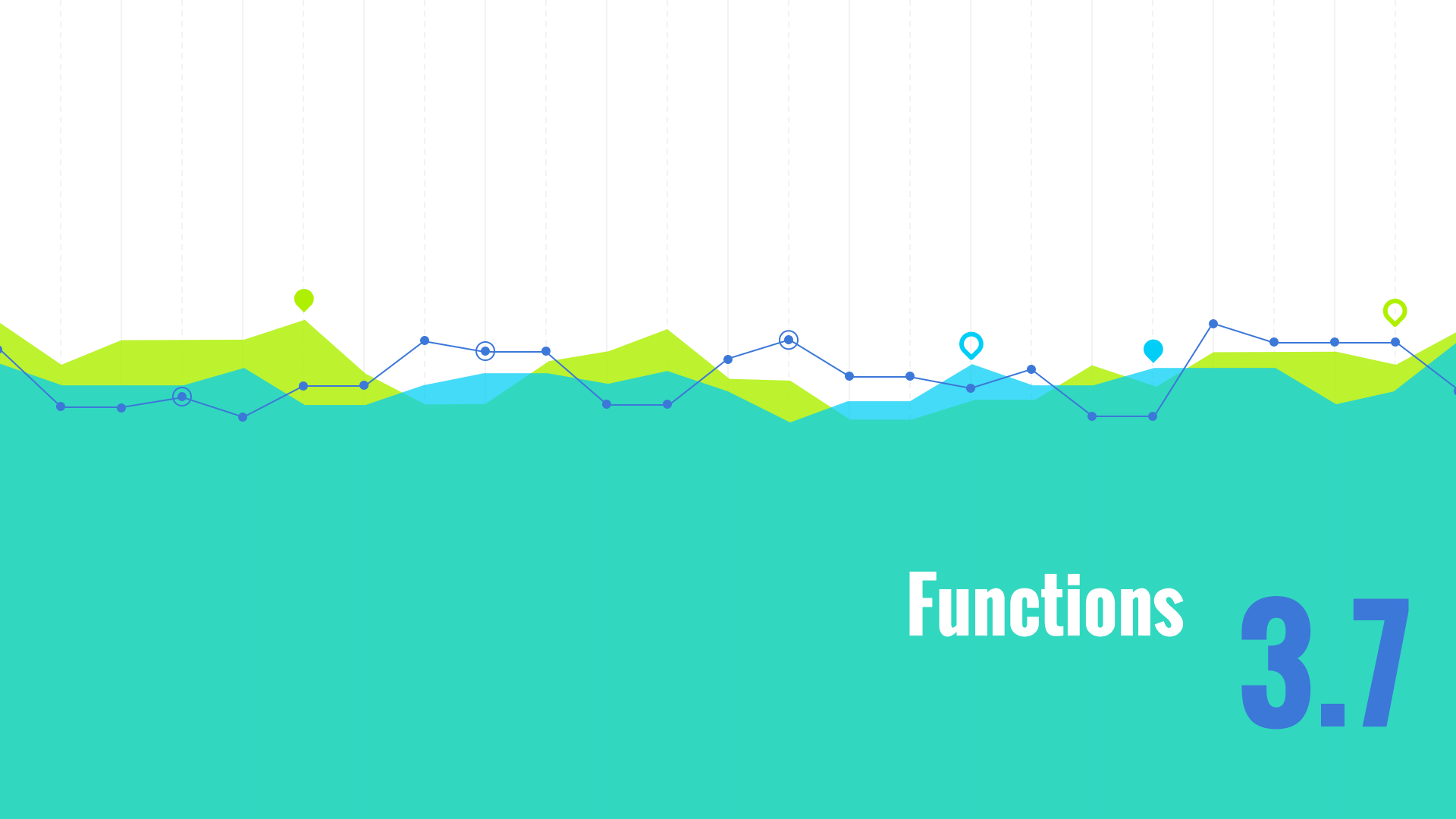
```
        print(dna_sequence[i])
```

```
        i = i + 1
```

```
if __name__ == "__main__":
```

```
    main()
```

Example 12: While



Functions 3.7


```
#!/usr/bin/env python

def transcribe(dna):
    rna = ''
    for base in dna:
        if (base == 'T'):
            rna = rna + 'U'
        else: rna = rna + base
    return rna

def main():
    dna_sequence = 'ACTGATCAGATGCA'
    rna = transcribe(dna_sequence)
    print(rna)

if __name__ == "__main__":
    main()
```

Example 13: Functions



File I/O 3.8

```
#!/usr/bin/env python

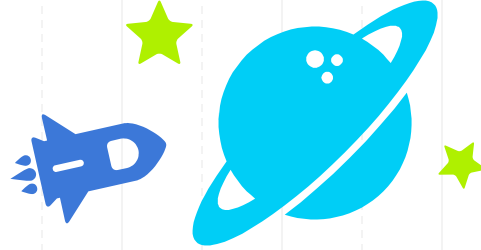
def transcribe(dna):
    rna = ''
    for base in dna:
        if (base == 'T'):
            rna = rna + 'U'
        else: rna = rna + base
    return rna

def main():
    f = open('dna_sample.txt', 'r') # Read the dna sample file.
    dna_sample = f.read()
    print(dna_sample)
    print("\n")
    rna_sample = transcribe(dna_sample)
    print(rna_sample)

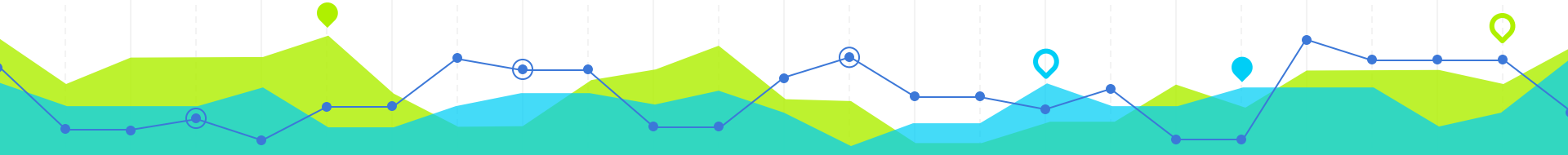
    w = open('rna_sample.txt', 'w')
    w.write(rna_sample)

if __name__ == '__main__':
    main()
```

Example 14: File I/O



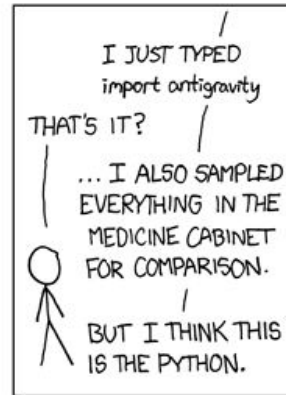
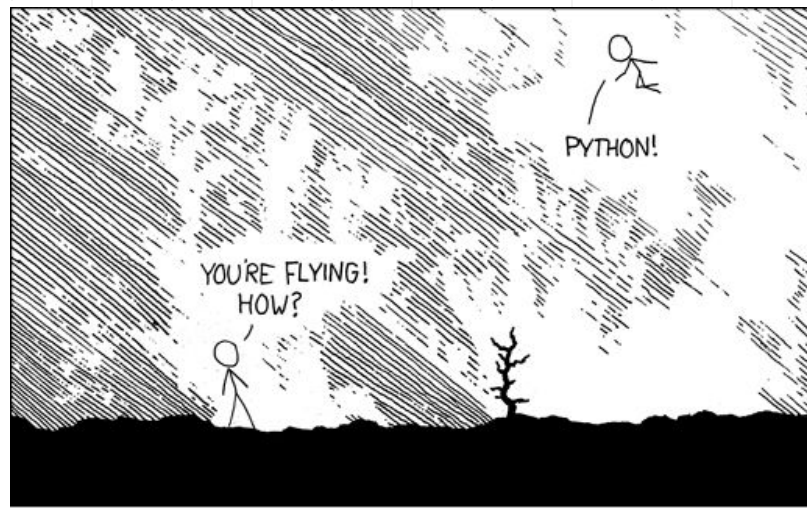
Simple, yet Powerful



Next Time: Applying Python to Bioinformatics

4





THANKS!

Any questions?

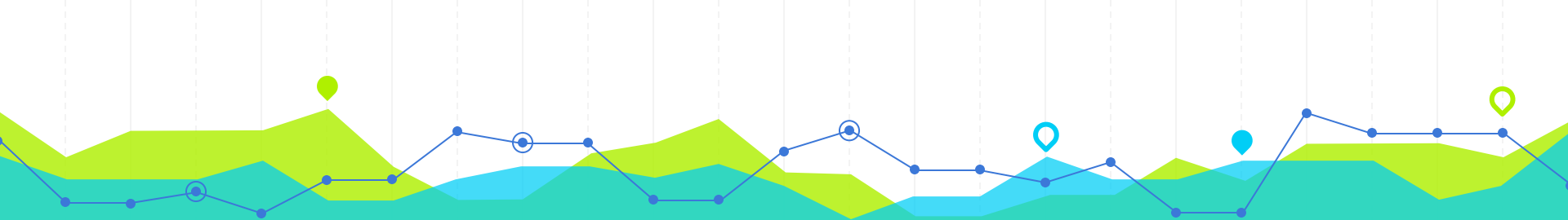
You can find me at
trentonbeckendorff@utexas.edu





Citations

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2. Presentation slide template by SlidesCarnival
3. Python comic by XKCD



Indentation:

- use 4 spaces per indentation level
- 'hanging indentations' should be distinguishable

Tabs or Spaces?

- spaces > tabs
- Python 3: no mixing of tabs and spaces

Line Length:

- maximum of 79 characters
- limit docstrings / comments to 72 characters

Blank Lines:

- use in functions (sparingly) to separate logical sections
- 2 blank lines b/t functions

Source File Encoding:

- UTF-8

Imports:

- use separate line for each import
- always at the top of the file
 - standard library imports
 - third party imports
 - local imports

Quotes:

- double or single

Whitespace:

- avoid extraneous whitespace
- always surround operators

Comments:

- should be complete sentences
- should be updated when modifying code
- inline comments: use sparingly

PEP8 Style Guide: *Key Concepts*