NGS analysis for gene regulation and epigenomics

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Python crash course for genomics

Variables and functions

- Straight forward syntax, no type declaration
- Indentation used to specify nesting
- Indices start at 0 (unlike R)

```
def print_numbers(n):
    """This functions prints numbers from 0 to n-1"""
    for i in range(n):
        print(i)

>>> x = 3
>>> print_numbers(x)
0
1
2
```

Text formatting

Embed variables in strings using f-strings:

```
def make_ucsc_range(chrom, start, end):
    """Given a chromosome, start and end coordinates,
    return a string in format chr:start-end
    """
    ucsc_range = f"{chrom}:{start}-{end}"
    return ucsc_range
>>> make_ucsc_range('chr1', 3000, 15000)
'chr1:3000-15000'
```

Basic data structures

Some useful native data structures:

Lists can contain any types of values:

```
>>> my_list = [1, "a", "a"]
>>> for i in my_list: print(i)
1
"a"
"a"
>>> my_list[0]
1
>> my_list[:2]
[1, "a"]
```

Basic data structures

Sets contain unique unordered values and can perform set operations:

```
>>> fruit_set = {'apple', 'grape', 'orange'}
>>> color_set = {'red', 'orange'}
>>> "zebra" in fruit_set
False
>>> fruit_set & color_set
{'orange'}
>>> fruit_set | color_set
{'apple', 'grape', 'orange', 'red'}
```

Basic data structures

Dictionaries allow to map keys to values:

```
>>> legs_dict = {'dog': 4, 'duck': 2}
>>> legs_dict['dog']
4
>>> for animal, legs in legs_dict.items():
>>> print(f"{animal}s have {legs} legs")
dogs have 4 legs
ducks have 2 legs
```

Arrays

Operations are not vectorized by default in python (unlike R):

```
>>> [1, 2, 3] * 2
[1, 2, 3, 1, 2, 3]
```

The numpy package provides multidimensional arrays and vectorized operations:

Dataframes

- The pandas package provides an equivalent to R's dataframes.
- DataFrames are arrays with named dimensions which can hold different datatypes.

```
>>> import pandas as pd
>>> my_df = pd.DataFrame({
>>> 'animal': ['duck', 'dog', 'snail', 'ant'],
>>> 'legs': [2, 4, 0, 6]})
>>> my_df
   animal legs
0 duck 2
1 dog 4
2 snail 0
3 ant 6
```

Dataframes

- The pandas package provides an equivalent to R's dataframes.
- DataFrames are arrays with named dimensions which can hold different datatypes.

Selecting in dataframes

Dataframes can be subsetted using two methods:

- · iloc, which is uses indices
- · loc, which uses masks

```
>>> my_df.iloc[[1, 3], :]
   animal legs
1   dog   4
3   ant   6
>>> my_df.iloc[2:, 0]
2   snail
3   ant
Name: animal, dtype: object
```

Selecting in dataframes

Dataframes can be subsetted using two methods:

- · iloc, which is uses indices
- · loc, which uses masks

```
>>> my_df.loc[my_df.legs < 4, :]
   animal legs
0 duck 2
2 snail 0</pre>
```

Data structures summary

Native structures:

- No vectorized operations
- · Lists: any datatype [x, ...]
- Sets: any datatype, unique values $\{x, ...\}$
- · Dictionaries: Key-value map, unique keys, any datatype {x: y, ...}

Data structures summary

Numpy arrays Docs:

- Single datatype np.array([1, 2, 3])
- Vectorized operations arr.sum()
- N-dimensional np.array([[1, 2, 3], [10, 20, 30]])

Pandas dataframes Docs:

- · 1 data-type per column
- columns selected either with df['col'] or df.col
- subset using df.loc (conditions) or df.iloc (indices)

In practice

 Genomic tracks are often stored in bed files, which can be read into a dataframe:

```
>>> genes = pd.read csv('genes.bed', sep='\t', names=['chrom', 'start', 'end'])
>>> genes.head()
Out[34]:
 chrom start
                 end
 chr1
         4658
                5004
1 chr1 18063 18704
2 chr1 64549
             65197
  chr1 69468
              69735
 chr1 73476
              73845
 chr1 78433 79316
```

- · Hi-C matrices can be represented using 2D numpy arrays of floats
- The cooler package provides pd.DataFrame and np.array objects