6.3. difflib — Helpers for computing deltas

Source code: Lib/difflib.py

This module provides classes and functions for comparing sequences. It can be used for example, for comparing files, and can produce difference information in various formats, including HTML and context and unified diffs. For comparing directories and files, see also, the filecmp module.

class difflib. SequenceMatcher

This is a flexible class for comparing pairs of sequences of any type, so long as the sequence elements are hashable. The basic algorithm predates, and is a little fancier than, an algorithm published in the late 1980's by Ratcliff and Obershelp under the hyperbolic name "gestalt pattern matching." The idea is to find the longest contiguous matching subsequence that contains no "junk" elements; these "junk" elements are ones that are uninteresting in some sense, such as blank lines or whitespace. (Handling junk is an extension to the Ratcliff and Obershelp algorithm.) The same idea is then applied recursively to the pieces of the sequences to the left and to the right of the matching subsequence. This does not yield minimal edit sequences, but does tend to yield matches that "look right" to people.

Timing: The basic Ratcliff-Obershelp algorithm is cubic time in the worst case and quadratic time in the expected case. SequenceMatcher is quadratic time for the worst case and has expected-case behavior dependent in a complicated way on how many elements the sequences have in common; best case time is linear.

Automatic junk heuristic: SequenceMatcher supports a heuristic that automatically treats certain sequence items as junk. The heuristic counts how many times each individual item appears in the sequence. If an item's duplicates (after the first one) account for more than 1% of the sequence and the sequence is at least 200 items long, this item is marked as "popular" and is treated as junk for the purpose of sequence matching. This heuristic can be turned off by setting the autojunk argument to False when creating the SequenceMatcher.

New in version 3.2: The autojunk parameter.

class difflib. Differ

This is a class for comparing sequences of lines of text, and producing humanreadable differences or deltas. Differ uses SequenceMatcher both to compare sequences of lines, and to compare sequences of characters within similar (near-matching) lines.

Each line of a Differ delta begins with a two-letter code:

Code	Meaning
'- '	line unique to sequence 1
'+ '	line unique to sequence 2
1 1	line common to both sequences
'?'	line not present in either input sequence

Lines beginning with '?' attempt to guide the eye to intraline differences, and were not present in either input sequence. These lines can be confusing if the sequences contain tab characters.

class difflib. HtmlDiff

This class can be used to create an HTML table (or a complete HTML file containing the table) showing a side by side, line by line comparison of text with inter-line and intra-line change highlights. The table can be generated in either full or contextual difference mode.

The constructor for this class is:

__init__(tabsize=8, wrapcolumn=None, linejunk=None, charjunk=IS_CHARACTER_JUNK)

Initializes instance of HtmlDiff.

tabsize is an optional keyword argument to specify tab stop spacing and defaults to 8.

wrapcolumn is an optional keyword to specify column number where lines are broken and wrapped, defaults to None where lines are not wrapped.

linejunk and *charjunk* are optional keyword arguments passed into ndiff() (used by HtmlDiff to generate the side by side HTML differences). See ndiff() documentation for argument default values and descriptions.

The following methods are public:

make_file(fromlines, tolines, fromdesc=", todesc=", context=False, num-lines=5, *, charset='utf-8')

Compares *fromlines* and *tolines* (lists of strings) and returns a string which is a complete HTML file containing a table showing line by line differences with inter-line and intra-line changes highlighted.

fromdesc and todesc are optional keyword arguments to specify from/to file column header strings (both default to an empty string).

context and numlines are both optional keyword arguments. Set context to True when contextual differences are to be shown, else the default is False to show the full files. numlines defaults to 5. When context is True numlines controls the number of context lines which surround the difference highlights. When context is False numlines controls the number of lines which are shown before a difference highlight when using the "next" hyperlinks (setting to zero would cause the "next" hyperlinks to place the next difference highlight at the top of the browser without any leading context).

Changed in version 3.5: charset keyword-only argument was added. The default charset of HTML document changed from 'ISO-8859-1' to 'utf-8'.

make_table(fromlines, tolines, fromdesc=", todesc=", context=False, num-lines=5)

Compares *fromlines* and *tolines* (lists of strings) and returns a string which is a complete HTML table showing line by line differences with inter-line and intra-line changes highlighted.

The arguments for this method are the same as those for the make_file() method.

Tools/scripts/diff.py is a command-line front-end to this class and contains a good example of its use.

difflib. context_diff(a, b, fromfile=", tofile=", fromfiledate=", tofiledate=", n=3, lineterm='\n')

Compare a and b (lists of strings); return a delta (a generator generating the delta lines) in context diff format.

Context diffs are a compact way of showing just the lines that have changed plus a few lines of context. The changes are shown in a before/after style. The number of context lines is set by *n* which defaults to three.

By default, the diff control lines (those with *** or ---) are created with a trailing newline. This is helpful so that inputs created from io.IOBase.readlines() result in diffs that are suitable for use with io.IOBase.writelines() since both the inputs and outputs have trailing newlines.

For inputs that do not have trailing newlines, set the *lineterm* argument to "" so that the output will be uniformly newline free.

The context diff format normally has a header for filenames and modification times. Any or all of these may be specified using strings for *fromfile*, *tofile*, *fromfiledate*, and *tofiledate*. The modification times are normally expressed in the ISO 8601 format. If not specified, the strings default to blanks.

```
>>>
>>> s1 = ['bacon\n', 'eggs\n', 'ham\n', 'guido\n']
>>> s2 = ['python\n', 'eggy\n', 'hamster\n', 'guido\n']
>>> sys.stdout.writelines(context_diff(s1, s2, fromfile='before.py
*** before.py
--- after.pv
******
*** 1,4 ****
! bacon
! eggs
! ham
 guido
--- 1,4 ----
! python
! eggy
! hamster
 guido
```

See A command-line interface to difflib for a more detailed example.

```
difflib.get close matches(word, possibilities, n=3, cutoff=0.6)
```

Return a list of the best "good enough" matches. *word* is a sequence for which close matches are desired (typically a string), and *possibilities* is a list of sequences against which to match *word* (typically a list of strings).

Optional argument n (default 3) is the maximum number of close matches to return; n must be greater than 0.

Optional argument *cutoff* (default 0.6) is a float in the range [0, 1]. Possibilities that don't score at least that similar to *word* are ignored.

The best (no more than n) matches among the possibilities are returned in a list, sorted by similarity score, most similar first.

```
>>> get_close_matches('appel', ['ape', 'apple', 'peach', 'pupp)
['apple', 'ape']
>>> import keyword
>>> get_close_matches('wheel', keyword.kwlist)
['while']
>>> get_close_matches('pineapple', keyword.kwlist)
[]
>>> get_close_matches('accept', keyword.kwlist)
['except']
```

```
difflib. ndiff(a, b, linejunk=None, charjunk=IS CHARACTER JUNK)
```

Compare *a* and *b* (lists of strings); return a Differ-style delta (a generator generating the delta lines).

Optional keyword parameters *linejunk* and *charjunk* are filtering functions (or None):

linejunk: A function that accepts a single string argument, and returns true if the string is junk, or false if not. The default is None. There is also a module-level function IS_LINE_JUNK(), which filters out lines without visible characters, except for at most one pound character ('#') — however the underlying SequenceMatcher class does a dynamic analysis of which lines are so frequent as to constitute noise, and this usually works better than using this function.

charjunk: A function that accepts a character (a string of length 1), and returns if the character is junk, or false if not. The default is module-level function IS_CHARACTER_JUNK(), which filters out whitespace characters (a blank or tab; it's a bad idea to include newline in this!).

Tools/scripts/ndiff.py is a command-line front-end to this function.

```
>>> diff = ndiff('one\ntwo\nthree\n'.splitlines(keepends=True),
>>> print(''.join(diff), end="")
- one
? ^
+ ore
? ^
- two
- three
? -
+ tree
+ emu
```

difflib. restore(sequence, which)

Return one of the two sequences that generated a delta.

Given a *sequence* produced by Differ.compare() or ndiff(), extract lines originating from file 1 or 2 (parameter *which*), stripping off line prefixes.

Example:

```
two
three
>>> print(''.join(restore(diff, 2)), end="")
ore
tree
emu
```

```
difflib. unified_diff(a, b, fromfile=", tofile=", fromfiledate=", tofiledate=", n=3, lineterm='\n')
```

Compare a and b (lists of strings); return a delta (a generator generating the delta lines) in unified diff format.

Unified diffs are a compact way of showing just the lines that have changed plus a few lines of context. The changes are shown in an inline style (instead of separate before/after blocks). The number of context lines is set by *n* which defaults to three.

By default, the diff control lines (those with ---, +++, or @@) are created with a trailing newline. This is helpful so that inputs created from io.IOBase.readlines() result in diffs that are suitable for use with io.IOBase.writelines() since both the inputs and outputs have trailing newlines.

For inputs that do not have trailing newlines, set the *lineterm* argument to "" so that the output will be uniformly newline free.

The context diff format normally has a header for filenames and modification times. Any or all of these may be specified using strings for *fromfile*, *tofile*, *fromfiledate*, and *tofiledate*. The modification times are normally expressed in the ISO 8601 format. If not specified, the strings default to blanks.

```
>>> s1 = ['bacon\n', 'eggs\n', 'ham\n', 'guido\n']
>>> s2 = ['python\n', 'eggy\n', 'hamster\n', 'guido\n']
>>> sys.stdout.writelines(unified_diff(s1, s2, fromfile='before.py
--- before.py
+++ after.py
@@ -1,4 +1,4 @@
-bacon
-eggs
-ham
+python
+eggy
+hamster
guido
```

See A command-line interface to difflib for a more detailed example.

difflib. diff_bytes(dfunc, a, b, fromfile=b", tofile=b", fromfiledate=b", tofiledate=b", n=3, lineterm=b'\n')

Compare a and b (lists of bytes objects) using dfunc; yield a sequence of delta lines (also bytes) in the format returned by dfunc. dfunc must be a callable, typically either unified diff() or context diff().

Allows you to compare data with unknown or inconsistent encoding. All inputs except n must be bytes objects, not str. Works by losslessly converting all inputs (except n) to str, and calling dfunc(a, b, fromfile, tofile, fromfiledate, tofiledate, n, lineterm). The output of *dfunc* is then converted back to bytes, so the delta lines that you receive have the same unknown/inconsistent encodings as a and b.

New in version 3.5.

difflib. IS_LINE_JUNK(line)

Return true for ignorable lines. The line *line* is ignorable if *line* is blank or contains a single '#', otherwise it is not ignorable. Used as a default for parameter *linejunk* in ndiff() in older versions.

difflib. IS_CHARACTER_JUNK(ch)

Return true for ignorable characters. The character *ch* is ignorable if *ch* is a space or tab, otherwise it is not ignorable. Used as a default for parameter *charjunk* in ndiff().

See also:

Pattern Matching: The Gestalt Approach

Discussion of a similar algorithm by John W. Ratcliff and D. E. Metzener. This was published in Dr. Dobb's Journal in July, 1988.

6.3.1. SequenceMatcher Objects

The SequenceMatcher class has this constructor:

class difflib. **SequenceMatcher** (isjunk=None, a=", b=", autojunk=True)

Optional argument *isjunk* must be None (the default) or a one-argument function that takes a sequence element and returns true if and only if the element is "junk" and should be ignored. Passing None for *isjunk* is equivalent to passing lambda x: 0; in other words, no elements are ignored. For example, pass:

lambda $x: x in " \t"$

if you're comparing lines as sequences of characters, and don't want to synch up on blanks or hard tabs.

The optional arguments *a* and *b* are sequences to be compared; both default to empty strings. The elements of both sequences must be hashable.

The optional argument *autojunk* can be used to disable the automatic junk heuristic.

New in version 3.2: The autojunk parameter.

SequenceMatcher objects get three data attributes: bjunk is the set of elements of b for which isjunk is True; bpopular is the set of non-junk elements considered popular by the heuristic (if it is not disabled); b2j is a dict mapping the remaining elements of b to a list of positions where they occur. All three are reset whenever b is reset with set seqs() or set seq2().

New in version 3.2: The bjunk and bpopular attributes.

SequenceMatcher objects have the following methods:

set_seqs(a, b)

Set the two sequences to be compared.

SequenceMatcher computes and caches detailed information about the second sequence, so if you want to compare one sequence against many sequences, use set_seq2() to set the commonly used sequence once and call set_seq1 () repeatedly, once for each of the other sequences.

set_seq1(a)

Set the first sequence to be compared. The second sequence to be compared is not changed.

set_seq2(b)

Set the second sequence to be compared. The first sequence to be compared is not changed.

find_longest_match(alo, ahi, blo, bhi)

Find longest matching block in a[alo:ahi] and b[blo:bhi].

If isjunk was omitted or None, $find_longest_match()$ returns (i, j, k) such that a[i:i+k] is equal to b[j:j+k], where alo <= i <= i+k <= ahi and blo <= j <= j+k <= bhi. For all (i', j', k') meeting those conditions, the additional conditions k >= k', i <= i', and if i == i', j <= j' are also met. In other words, of all maximal matching blocks, return one that

starts earliest in *a*, and of all those maximal matching blocks that start earliest in *a*, return the one that starts earliest in *b*.

```
>>> s = SequenceMatcher(None, " abcd", "abcd abcd")
>>> s.find_longest_match(0, 5, 0, 9)
Match(a=0, b=4, size=5)
```

If *isjunk* was provided, first the longest matching block is determined as above, but with the additional restriction that no junk element appears in the block. Then that block is extended as far as possible by matching (only) junk elements on both sides. So the resulting block never matches on junk except as identical junk happens to be adjacent to an interesting match.

Here's the same example as before, but considering blanks to be junk. That prevents 'abcd' from matching the 'abcd' at the tail end of the second sequence directly. Instead only the 'abcd' can match, and matches the leftmost 'abcd' in the second sequence:

```
>>> s = SequenceMatcher(lambda x: x==" ", " abcd", "abcd ab2d")
>>> s.find_longest_match(0, 5, 0, 9)
Match(a=1, b=0, size=4)
```

If no blocks match, this returns (alo, blo, 0).

This method returns a named tuple Match(a, b, size).

get matching blocks()

Return list of triples describing matching subsequences. Each triple is of the form (i, j, n), and means that a[i:i+n] == b[j:j+n]. The triples are monotonically increasing in i and j.

The last triple is a dummy, and has the value (len(a), len(b), 0). It is the only triple with n == 0. If (i, j, n) and (i', j', n') are adjacent triples in the list, and the second is not the last triple in the list, then i+n != i' or j+n != j'; in other words, adjacent triples always describe non-adjacent equal blocks.

```
>>> s = SequenceMatcher(None, "abxcd", "abcd")
>>> s.get_matching_blocks()
[Match(a=0, b=0, size=2), Match(a=3, b=2, size=2), Match(a=5, k)
```

get_opcodes()

Return list of 5-tuples describing how to turn a into b. Each tuple is of the form (tag, i1, i2, j1, j2). The first tuple has i1 == j1 == 0, and re-

maining tuples have i1 equal to the i2 from the preceding tuple, and, likewise, j1 equal to the previous j2.

The *tag* values are strings, with these meanings:

Value	Meaning
'replace'	a[i1:i2] should be replaced by b[j1:j2].
'delete'	a[i1:i2] should be deleted. Note that $j1 == j2$ in this case.
'insert'	<pre>b[j1:j2] should be inserted at a[i1:i1]. Note that i1 == i2 in this case.</pre>
'equal'	a[i1:i2] == b[j1:j2] (the sub-sequences are equal).

For example:

```
>>>
>>> a = "qabxcd"
>>> b = "abycdf"
>>> s = SequenceMatcher(None, a, b)
>>> for tag, i1, i2, j1, j2 in s.get_opcodes():
        print('{:7} a[{}:{}] --> b[{}:{}] {!r:>8} --> {!r}'.f
            tag, i1, i2, j1, j2, a[i1:i2], b[j1:j2]))
. . .
                                 'q' --> ''
delete
          a[0:1] --> b[0:0]
         a[1:3] --> b[0:2]
                                'ab' --> 'ab'
equal
                                 'x' --> 'y'
          a[3:4] --> b[2:3]
replace
                                'cd' --> 'cd'
equal
          a[4:6] --> b[3:5]
                                     --> 'f'
insert
          a[6:6] --> b[5:6]
```

get_grouped_opcodes(n=3)

Return a generator of groups with up to *n* lines of context.

Starting with the groups returned by get_opcodes(), this method splits out smaller change clusters and eliminates intervening ranges which have no changes.

The groups are returned in the same format as get_opcodes().

ratio()

Return a measure of the sequences' similarity as a float in the range [0, 1].

Where T is the total number of elements in both sequences, and M is the number of matches, this is 2.0*M / T. Note that this is 1.0 if the sequences are identical, and 0.0 if they have nothing in common.

This is expensive to compute if get_matching_blocks() or get_opcodes () hasn't already been called, in which case you may want to try quick_ratio() or real_quick_ratio() first to get an upper bound.

```
quick_ratio()
```

Return an upper bound on ratio() relatively quickly.

```
real_quick_ratio()
```

Return an upper bound on ratio() very quickly.

The three methods that return the ratio of matching to total characters can give different results due to differing levels of approximation, although quick_ratio() and real_quick_ratio() are always at least as large as ratio():

```
>>> s = SequenceMatcher(None, "abcd", "bcde")
>>> s.ratio()
0.75
>>> s.quick_ratio()
0.75
>>> s.real_quick_ratio()
1.0
```

6.3.2. SequenceMatcher Examples

This example compares two strings, considering blanks to be "junk":

ratio() returns a float in [0, 1], measuring the similarity of the sequences. As a rule of thumb, a ratio() value over 0.6 means the sequences are close matches:

```
>>> print(round(s.ratio(), 3))
0.866
```

If you're only interested in where the sequences match, get_matching_blocks() is handy:

```
>>> for block in s.get_matching_blocks():
... print("a[%d] and b[%d] match for %d elements" % block)
a[0] and b[0] match for 8 elements
a[8] and b[17] match for 21 elements
a[29] and b[38] match for 0 elements
```

Note that the last tuple returned by $get_matching_blocks()$ is always a dummy, (len(a), len(b), 0), and this is the only case in which the last tuple element (number of elements matched) is 0.

If you want to know how to change the first sequence into the second, use get_opcodes():

```
>>> for opcode in s.get_opcodes():
... print("%6s a[%d:%d] b[%d:%d]" % opcode)
  equal a[0:8] b[0:8]
insert a[8:8] b[8:17]
  equal a[8:29] b[17:38]
```

See also:

- The get_close_matches() function in this module which shows how simple code building on SequenceMatcher can be used to do useful work.
- Simple version control recipe for a small application built with SequenceMatcher.

6.3.3. Differ Objects

Note that Differ-generated deltas make no claim to be **minimal** diffs. To the contrary, minimal diffs are often counter-intuitive, because they synch up anywhere possible, sometimes accidental matches 100 pages apart. Restricting synch points to contiguous matches preserves some notion of locality, at the occasional cost of producing a longer diff.

The Differ class has this constructor:

```
class difflib. Differ(linejunk=None, charjunk=None)
```

Optional keyword parameters *linejunk* and *charjunk* are for filter functions (or None):

linejunk: A function that accepts a single string argument, and returns true if the string is junk. The default is None, meaning that no line is considered junk.

charjunk: A function that accepts a single character argument (a string of length 1), and returns true if the character is junk. The default is None, meaning that no character is considered junk.

These junk-filtering functions speed up matching to find differences and do not cause any differing lines or characters to be ignored. Read the description of the find longest match() method's *isjunk* parameter for an explanation.

Differ objects are used (deltas generated) via a single method:

```
compare(a, b)
```

Compare two sequences of lines, and generate the delta (a sequence of lines).

Each sequence must contain individual single-line strings ending with new-lines. Such sequences can be obtained from the readlines() method of file-like objects. The delta generated also consists of newline-terminated strings, ready to be printed as-is via the writelines() method of a file-like object.

6.3.4. Differ Example

This example compares two texts. First we set up the texts, sequences of individual single-line strings ending with newlines (such sequences can also be obtained from the readlines() method of file-like objects):

```
>>> text1 = ''' 1. Beautiful is better than ugly.
... 2. Explicit is better than implicit.
... 3. Simple is better than complex.
... 4. Complex is better than complicated.
... '''.splitlines(keepends=True)
>>> len(text1)
4
>>> text1[0][-1]
'\n'
>>> text2 = ''' 1. Beautiful is better than ugly.
... 3. Simple is better than complex.
... 4. Complicated is better than complex.
... 5. Flat is better than nested.
... '''.splitlines(keepends=True)
```

Next we instantiate a Differ object:

```
>>> d = Differ()
```

Note that when instantiating a Differ object we may pass functions to filter out line and character "junk." See the Differ() constructor for details.

Finally, we compare the two:

```
>>> result = list(d.compare(text1, text2))
```

result is a list of strings, so let's pretty-print it:

```
>>>
>>> from pprint import pprint
>>> pprint(result)
     1. Beautiful is better than ugly.\n',
      2. Explicit is better than implicit.\n',
      3. Simple is better than complex.\n',
           Simple is better than complex.\n',
 ٠,
       ++\n',
     4. Complex is better than complicated.\n',
                                      ---- ^\n',
 ۲,
 '+
     4. Complicated is better than complex.\n',
 Ϋ́
              ++++ ^
                                           ^\n',
     5. Flat is better than nested.\n']
```

As a single multi-line string it looks like this:

```
>>>
>>> import sys
>>> sys.stdout.writelines(result)
    1. Beautiful is better than ugly.
    2. Explicit is better than implicit.
    3. Simple is better than complex.
         Simple is better than complex.
+
    3.
?
     ++
   4. Complex is better than complicated.
?
   4. Complicated is better than complex.
+
?
            ++++ ^
    5. Flat is better than nested.
+
```

6.3.5. A command-line interface to difflib

This example shows how to use difflib to create a diff-like utility. It is also contained in the Python source distribution, as Tools/scripts/diff.py.

```
return t.astimezone().isoformat()
def main():
   parser = argparse.ArgumentParser()
   parser.add argument('-c', action='store true', default=False,
                        help='Produce a context format diff (default)
   parser.add argument('-u', action='store true', default=False,
                        help='Produce a unified format diff')
   parser.add_argument('-m', action='store true', default=False.
                        help='Produce HTML side by side diff '
                             '(can use -c and -l in conjunction)')
   parser.add_argument('-n', action='store_true', default=False,
                        help='Produce a ndiff format diff')
   parser.add_argument('-1', '--lines', type=int, default=3,
                        help='Set number of context lines (default 3)
    parser.add argument('fromfile')
    parser.add argument('tofile')
   options = parser.parse args()
   n = options.lines
   fromfile = options.fromfile
   tofile = options.tofile
   fromdate = file mtime(fromfile)
   todate = file mtime(tofile)
   with open(fromfile) as ff:
        fromlines = ff.readlines()
   with open(tofile) as tf:
        tolines = tf.readlines()
   if options.u:
        diff = difflib.unified diff(fromlines, tolines, fromfile, tof)
   elif options.n:
        diff = difflib.ndiff(fromlines, tolines)
    elif options.m:
        diff = difflib.HtmlDiff().make_file(fromlines,tolines,fromfile
   else:
        diff = difflib.context diff(fromlines, tolines, fromfile, tof)
    sys.stdout.writelines(diff)
if __name__ == '__main__':
   main()
```