

BytesFunc

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Version: 1.0.0 for 2020-02-19
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Language: Python 3.5 or later

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Introduction

The BytesFunc module provides high speed array processing functions for use with Python 'bytes' and 'bytearray' objects. These functions are patterned after the functions in the standard Python "operator" module together with some additional ones from other sources.

The purpose of these functions is to perform mathematical calculations on "bytes" and "bytearray" objects significantly faster than using native Python.

Function Summary

The compare operators used for 'ball', 'bany', and 'findindex' are examples only, and other compare operations are available. Many functions will accept other parameter combinations of sequences and numeric parameters. See the details for each function for what parameter combinations are valid.

Brief Description

Function	Equivalent to
and_	Perform a bitwise AND across the sequence.
ball	True if all elements of the sequence meet the match criteria.
bany	True if any elements of the sequence meet the match criteria.
bmax	Return the maximum value in the sequence.
bmin	Return the minimum value in the sequence.
bsum	Return the sum of the sequence.
eq	True if all elements of the sequence equal the compare value.
findindex	Returns the index of the first value in an array to meet the specified criteria.
ge	True if all elements of the sequence are greater than or equal to the compare value.

gt	True if all elements of the sequence are greater than the compare value.
invert	Perform a bitwise invert across the sequence.
le	True if all elements of the sequence are less than or equal to the compare value.
lshift	Perform a bitwise left shift across the sequence.
lt	True if all elements of the sequence are less than the compare value.
ne	True if all elements of the sequence are not equal the compare value.
or_	Perform a bitwise OR across the sequence.
rshift	Perform a bitwise right shift across the sequence.
xor	Perform a bitwise XOR across the sequence.

Python Equivalent

Function	Equivalent to
and_	[x & param for x in sequence1]
ball	all([(x > param) for x in array])
bany	any([(x > param) for x in array])
bmax	max(sequence)
bmin	min(sequence)
bsum	sum(sequence)
eq	all([x == param for x in sequence])
findindex	[x for x,y in enumerate(array) if y > param][0]
ge	all([x >= param for x in sequence])
gt	all([x > param for x in sequence])
invert	[~x for x in sequence1]
le	all([x <= param for x in sequence])
lshift	[x << param for x in sequence1]
lt	all([x < param for x in sequence])
ne	all([x != param for x in sequence])
or_	[x param for x in sequence1]
rshift	[x >> param for x in sequence1]
xor	[x ^ param for x in sequence1]

Description

Parameters

Parameter Formats

Parameters come in several forms.

- Sequences. Sequences are either "bytes" or "bytearray" objects. Bytes sequences are immutable and must not be used for output destinations. Bytearray sequences are mutable, and may be used for inputs or outputs.
- Numeric parameters. Numeric input parameters are individual integers and must be in the range of 0 to 255.
- Comparison operators. Comparison operators are unicode strings in the form used by Python for compare operations. These must be quoted strings, and not bare Python symbols. See the section below for a list of these.
- Sequence length control. Sequence length control allows only part of a sequence to be used as an input. See the section below for details.
- Overflow detection disable. Overflow detection control is used for disable integer overflow. See the section below for details.

Example:

```
sequence = bytes([1, 2, 5, 99, 8])
# Find the maximum value and return it. The answer should be 99.
result = bytesfunc.bmax(sequence)
```

Example:

```
sequence1 = bytes([1, 2, 5, 99, 8])
sequence2 = bytearray([0, 0, 0, 0, 0])
# Xor each element in sequence1 with '7', and write the output to
# sequence2. Sequence2 should be bytearray(b'\x06\x05\x02d\x0f').
bytesfunc.xor(sequence1, 7, sequence2)
```

Example:

```
sequence1 = bytes([1, 2, 5, 99, 8, 101])
# Find the first index of sequence1 which is greater than or equal to 99.
# The answer should be 3.
result = bytesfunc.findindex('>=', sequence, 99)
```

Function Documentation Details

and_

Calculate `and_` over the values in a bytes or bytearray object.

Equivalent to:	[x & param for x in sequence1]
or	[param & x for x in sequence1]
or	[x & y for x,y in zip(sequence1, sequence2)]

Call formats:

```
and_(sequence1, param)
and_(sequence1, param, outpsequence)
and_(param, sequence1)
and_(param, sequence1, outpsequence)
and_(sequence1, sequence2)
and_(sequence1, sequence2, outpsequence)
```

```
and_(sequence1, param, maxlen=y)
and_(sequence1, param, nosimd=False)
```

- sequence1 - The first input data bytes or bytearray sequence to be examined. If no output sequence is provided the results will overwrite the input data.
- param - A non-sequence numeric parameter.
- sequence2 - A second input data sequence. Each element in this sequence is applied to the corresponding element in the first sequence.
- outpsequence - The output sequence. This parameter is optional.
- maxlen - Limit the length of the sequence used. This must be a valid positive integer. If a zero or negative length, or a value which is greater than the actual length of the sequence is specified, this parameter is ignored.
- nosimd - If True, SIMD acceleration is disabled. This parameter is

ball

Calculate ball over the values a bytes or bytearray object.

Equivalent to:	<code>all([(x > param) for x in array])</code>
----------------	---

Call formats:

```
result = ball(opstr, sequence, param)
result = ball(opstr, sequence, param, maxlen=y)
result = ball(opstr, sequence, param, nosimd=False)
```

- **opstr - The arithmetic comparison operation as a string.**

These are: '==', '>', '>=', '<', '<=', '!='.

- sequence - An input bytes or bytearray to be examined.
- param - A non-array numeric parameter.
- maxlen - Limit the length of the sequence used. This must be a valid positive integer. If a zero or negative length, or a value which is greater than the actual length of the sequence is specified, this parameter is ignored.
- nosimd - If True, SIMD acceleration is disabled if present. The default is False (SIMD acceleration is enabled if present).
- result - A boolean value corresponding to the result of all the comparison operations. If any comparison operations result in true, the return value will be true. If all of them result in false, the return value will be false.

bany

Calculate bany over the values a bytes or bytearray object.

Equivalent to:	<code>any([(x > param) for x in array])</code>
----------------	---

Call formats:

```
result = bany(opstr, sequence, param)
result = bany(opstr, sequence, param, maxlen=y)
result = bany(opstr, sequence, param, nosimd=False)
```

- **opstr** - The arithmetic comparison operation as a string.

These are: '==', '>', '>=', '<', '<=', '!='.

- **sequence** - An input bytes or bytearray to be examined.
- **param** - A non-array numeric parameter.
- **maxlen** - Limit the length of the sequence used. This must be a valid positive integer. If a zero or negative length, or a value which is greater than the actual length of the sequence is specified, this parameter is ignored.
- **nosimd** - If True, SIMD acceleration is disabled if present. The default is False (SIMD acceleration is enabled if present).
- **result** - A boolean value corresponding to the result of all the comparison operations. If all comparison operations result in true, the return value will be true. If any of them result in false, the return value will be false.

bmax

Calculate bmax over the values in an array.

Equivalent to:	max(sequence)
----------------	---------------

Call formats:

```
result = bmax(sequence)
result = bmax(sequence, maxlen=y)
result = bmax(sequence, nosimd=False)
```

- **sequence** - The input bytes or bytearray to be examined.
- **maxlen** - Limit the length of the sequence used. This must be a valid positive integer. If a zero or negative length, or a value which is greater than the actual length of the sequence is specified, this parameter is ignored.
- **nosimd** - If True, SIMD acceleration is disabled if present. The default is False (SIMD acceleration is enabled if present).
- **result** = The maximum of all the values in the sequence.

bmin

Calculate bmin over the values in an array.

Equivalent to:	min(sequence)
----------------	---------------

Call formats:

```
result = bmin(sequence)
result = bmin(sequence, maxlen=y)
result = bmin(sequence, nosimd=False)
```

- **sequence** - The input bytes or bytearray to be examined.
- **maxlen** - Limit the length of the sequence used. This must be a valid positive integer. If a zero or negative length, or a value which is greater than the actual length of the sequence is specified, this parameter is ignored.
- **nosimd** - If True, SIMD acceleration is disabled if present. The default is False (SIMD acceleration is enabled if present).

- result = The minimum of all the values in the sequence.

bsum

Calculate the arithmetic sum of an bytes or bytearray sequence.

Equivalent to:	sum(sequence)
----------------	---------------

Call formats:

```
result = bsum(sequence)
result = bsum(sequence, maxlen=y)
result = bsum(sequence, matherrors=False)
```

- sequence - An input bytes or bytearray to be examined.
- maxlen - Limit the length of the sequence used. This must be a valid positive integer. If a zero or negative length, or a value which is greater than the actual length of the sequence is specified, this parameter is ignored.
- matherrors - If True, checks for numerical errors including integer overflow are ignored.
- result - The sum of the sequence.

eq

Calculate eq over the values in a bytes or bytearray object.

Equivalent to:	all([x == param for x in sequence])
or	all([param == x for x in sequence])
or	all([x == y for x,y in zip(sequence1, sequence2)])

Call formats:

```
result = eq(sequence1, param)
result = eq(param, sequence1)
result = eq(sequence1, sequence2)
result = eq(sequence1, param, maxlen=y)
result = eq(sequence1, param, nosimd=False)
```

- sequence1 - An input bytes or bytearray to be examined.
- sequence2 - An input bytes or bytearray to be examined.
- param - A integer numeric input parameter in the range 0 - 255.
- The first and second parameters are compared to each other. If one parameter is a sequence and the other is an integer, the integer is compared to each element in the sequence. If both parameters are sequences, each element of one sequence is compared to the corresponding element of the other sequence.
- maxlen - Limit the length of the sequence used. This must be a valid positive integer. If a zero or negative length, or a value which is greater than the actual length of the sequence is specified, this parameter is ignored.
- nosimd - If True, SIMD acceleration is disabled if present. The default is False (SIMD acceleration is enabled if present).

- **result** - A boolean value corresponding to the result of all the comparison operations. If all comparison operations result in true, the return value will be true. If any of them result in false, the return value will be false.

findindex

Calculate findindex over the values a bytes or bytearray object.

Equivalent to:	[x for x,y in enumerate(array) if y > param][0]
----------------	---

Call formats:

```
result = findindex(opstr, sequence, param)
result = findindex(opstr, sequence, param, maxlen=y)
result = findindex(opstr, sequence, param, nosimd=False)
```

- **opstr** - The arithmetic comparison operation as a string.

These are: '==', '>', '>=', '<', '<=', '!='.

- **sequence** - An input bytes or bytearray to be examined.
- **param** - A non-array numeric parameter.
- **maxlen** - Limit the length of the sequence used. This must be a valid positive integer. If a zero or negative length, or a value which is greater than the actual length of the sequence is specified, this parameter is ignored.
- **nosimd** - If True, SIMD acceleration is disabled if present. The default is False (SIMD acceleration is enabled if present).
- **result** - The resulting index. This will be negative if no match was found.

ge

Calculate ge over the values in a bytes or bytearray object.

Equivalent to:	all([x >= param for x in sequence])
or	all([param >= x for x in sequence])
or	all([x >= y for x,y in zip(sequence1, sequence2)])

Call formats:

```
result = ge(sequence1, param)
result = ge(param, sequence1)
result = ge(sequence1, sequence2)
result = ge(sequence1, param, maxlen=y)
result = ge(sequence1, param, nosimd=False)
```

- **sequence1** - An input bytes or bytearray to be examined.
- **sequence2** - An input bytes or bytearray to be examined.
- **param** - A integer numeric input parameter in the range 0 - 255.
- The first and second parameters are compared to each other. If one parameter is a sequence and the other is an integer, the integer is compared to each element in the sequence. If both parameters are sequences, each element of one sequence is compared to the corresponding element of the other sequence.

- **maxlen** - Limit the length of the sequence used. This must be a valid positive integer. If a zero or negative length, or a value which is greater than the actual length of the sequence is specified, this parameter is ignored.
- **nosimd** - If True, SIMD acceleration is disabled if present. The default is False (SIMD acceleration is enabled if present).
- **result** - A boolean value corresponding to the result of all the comparison operations. If all comparison operations result in true, the return value will be true. If any of them result in false, the return value will be false.

gt

Calculate gt over the values in a bytes or bytearray object.

Equivalent to:	<code>all([x > param for x in sequence])</code>
or	<code>all([param > x for x in sequence])</code>
or	<code>all([x > y for x,y in zip(sequence1, sequence2)])</code>

Call formats:

```
result = gt(sequence1, param)
result = gt(param, sequence1)
result = gt(sequence1, sequence2)
result = gt(sequence1, param, maxlen=y)
result = gt(sequence1, param, nosimd=False)
```

- **sequence1** - An input bytes or bytearray to be examined.
- **sequence2** - An input bytes or bytearray to be examined.
- **param** - A integer numeric input parameter in the range 0 - 255.
- The first and second parameters are compared to each other. If one parameter is a sequence and the other is an integer, the integer is compared to each element in the sequence. If both parameters are sequences, each element of one sequence is compared to the corresponding element of the other sequence.
- **maxlen** - Limit the length of the sequence used. This must be a valid positive integer. If a zero or negative length, or a value which is greater than the actual length of the sequence is specified, this parameter is ignored.
- **nosimd** - If True, SIMD acceleration is disabled if present. The default is False (SIMD acceleration is enabled if present).
- **result** - A boolean value corresponding to the result of all the comparison operations. If all comparison operations result in true, the return value will be true. If any of them result in false, the return value will be false.

invert

Calculate invert over the values in a bytes or bytearray object.

Equivalent to:	<code>[~x for x in sequence1]</code>
----------------	--------------------------------------

Call formats:

```
invert(sequence1)
invert(sequence1, outpseq)
```

```
invert(sequence1, maxlen=y)
invert(sequence1, nosimd=False)
```

- sequence1 - The input bytes or bytearray to be examined. If no output bytearray is provided the results will overwrite the input data, in which case it must be a bytearray.
- outpseq - The output bytearray. This parameter is optional.
- maxlen - Limit the length of the sequence used. This must be a valid positive integer. If a zero or negative length, or a value which is greater than the actual length of the sequence is specified, this parameter is ignored.
- nosimd - If True, SIMD acceleration is disabled. This parameter is optional. The default is FALSE.

le

Calculate le over the values in a bytes or bytearray object.

Equivalent to:	all([x <= param for x in sequence])
or	all([param <= x for x in sequence])
or	all([x <= y for x,y in zip(sequence1, sequence2)])

Call formats:

```
result = le(sequence1, param)
result = le(param, sequence1)
result = le(sequence1, sequence2)
result = le(sequence1, param, maxlen=y)
result = le(sequence1, param, nosimd=False)
```

- sequence1 - An input bytes or bytearray to be examined.
- sequence2 - An input bytes or bytearray to be examined.
- param - A integer numeric input parameter in the range 0 - 255.
- The first and second parameters are compared to each other. If one parameter is a sequence and the other is an integer, the integer is compared to each element in the sequence. If both parameters are sequences, each element of one sequence is compared to the corresponding element of the other sequence.
- maxlen - Limit the length of the sequence used. This must be a valid positive integer. If a zero or negative length, or a value which is greater than the actual length of the sequence is specified, this parameter is ignored.
- nosimd - If True, SIMD acceleration is disabled if present. The default is False (SIMD acceleration is enabled if present).
- result - A boolean value corresponding to the result of all the comparison operations. If all comparison operations result in true, the return value will be true. If any of them result in false, the return value will be false.

lshift

Calculate lshift over the values in a bytes or bytearray object.

Equivalent to:	[x << param for x in sequence1]
or	[param << x for x in sequence1]

or	[x << y for x,y in zip(sequence1, sequence2)]
----	---

Call formats:

```
lshift(sequence1, param)
lshift(sequence1, param, outpsequence)
lshift(param, sequence1)
lshift(param, sequence1, outpsequence)
lshift(sequence1, sequence2)
lshift(sequence1, sequence2, outpsequence)
lshift(sequence1, param, maxlen=y)
lshift(sequence1, param, nosimd=False)
```

- sequence1 - The first input data bytes or bytearray sequence to be examined. If no output sequence is provided the results will overwrite the input data.
- param - A non-sequence numeric parameter.
- sequence2 - A second input data sequence. Each element in this sequence is applied to the corresponding element in the first sequence.
- outpsequence - The output sequence. This parameter is optional.
- maxlen - Limit the length of the sequence used. This must be a valid positive integer. If a zero or negative length, or a value which is greater than the actual length of the sequence is specified, this parameter is ignored.
- nosimd - If True, SIMD acceleration is disabled. This parameter is

lt

Calculate lt over the values in a bytes or bytearray object.

Equivalent to:	all([x < param for x in sequence])
or	all([param < x for x in sequence])
or	all([x < y for x,y in zip(sequence1, sequence2)])

Call formats:

```
result = lt(sequence1, param)
result = lt(param, sequence1)
result = lt(sequence1, sequence2)
result = lt(sequence1, param, maxlen=y)
result = lt(sequence1, param, nosimd=False)
```

- sequence1 - An input bytes or bytearray to be examined.
- sequence2 - An input bytes or bytearray to be examined.
- param - A integer numeric input parameter in the range 0 - 255.
- The first and second parameters are compared to each other. If one parameter is a sequence and the other is an integer, the integer is compared to each element in the sequence. If both parameters are sequences, each element of one sequence is compared to the corresponding element of the other sequence.
- maxlen - Limit the length of the sequence used. This must be a valid positive integer. If a zero or negative length, or a value which is greater than the actual length of the sequence is specified, this parameter is ignored.

- **nosimd** - If True, SIMD acceleration is disabled if present. The default is False (SIMD acceleration is enabled if present).
- **result** - A boolean value corresponding to the result of all the comparison operations. If all comparison operations result in true, the return value will be true. If any of them result in false, the return value will be false.

ne

Calculate ne over the values in a bytes or bytearray object.

Equivalent to:	<code>all([x != param for x in sequence])</code>
or	<code>all([param != x for x in sequence])</code>
or	<code>all([x != y for x,y in zip(sequence1, sequence2)])</code>

Call formats:

```
result = ne(sequence1, param)
result = ne(param, sequence1)
result = ne(sequence1, sequence2)
result = ne(sequence1, param, maxlen=y)
result = ne(sequence1, param, nosimd=False)
```

- **sequence1** - An input bytes or bytearray to be examined.
- **sequence2** - An input bytes or bytearray to be examined.
- **param** - A integer numeric input parameter in the range 0 - 255.
- The first and second parameters are compared to each other. If one parameter is a sequence and the other is an integer, the integer is compared to each element in the sequence. If both parameters are sequences, each element of one sequence is compared to the corresponding element of the other sequence.
- **maxlen** - Limit the length of the sequence used. This must be a valid positive integer. If a zero or negative length, or a value which is greater than the actual length of the sequence is specified, this parameter is ignored.
- **nosimd** - If True, SIMD acceleration is disabled if present. The default is False (SIMD acceleration is enabled if present).
- **result** - A boolean value corresponding to the result of all the comparison operations. If all comparison operations result in true, the return value will be true. If any of them result in false, the return value will be false.

or_

Calculate or_ over the values in a bytes or bytearray object.

Equivalent to:	<code>[x param for x in sequence1]</code>
or	<code>[param x for x in sequence1]</code>
or	<code>[x y for x,y in zip(sequence1, sequence2)]</code>

Call formats:

```
or_(sequence1, param)
or_(sequence1, param, outpsequence)
or_(param, sequence1)
```

```

or_(param, sequence1, outpsequence)
or_(sequence1, sequence2)
or_(sequence1, sequence2, outpsequence)
or_(sequence1, param, maxlen=y)
or_(sequence1, param, nosimd=False)

```

- sequence1 - The first input data bytes or bytearray sequence to be examined. If no output sequence is provided the results will overwrite the input data.
- param - A non-sequence numeric parameter.
- sequence2 - A second input data sequence. Each element in this sequence is applied to the corresponding element in the first sequence.
- outpsequence - The output sequence. This parameter is optional.
- maxlen - Limit the length of the sequence used. This must be a valid positive integer. If a zero or negative length, or a value which is greater than the actual length of the sequence is specified, this parameter is ignored.
- nosimd - If True, SIMD acceleration is disabled. This parameter is

rshift

Calculate rshift over the values in a bytes or bytearray object.

Equivalent to:	[x >> param for x in sequence1]
or	[param >> x for x in sequence1]
or	[x >> y for x,y in zip(sequence1, sequence2)]

Call formats:

```

rshift(sequence1, param)
rshift(sequence1, param, outpsequence)
rshift(param, sequence1)
rshift(param, sequence1, outpsequence)
rshift(sequence1, sequence2)
rshift(sequence1, sequence2, outpsequence)
rshift(sequence1, param, maxlen=y)
rshift(sequence1, param, nosimd=False)

```

- sequence1 - The first input data bytes or bytearray sequence to be examined. If no output sequence is provided the results will overwrite the input data.
- param - A non-sequence numeric parameter.
- sequence2 - A second input data sequence. Each element in this sequence is applied to the corresponding element in the first sequence.
- outpsequence - The output sequence. This parameter is optional.
- maxlen - Limit the length of the sequence used. This must be a valid positive integer. If a zero or negative length, or a value which is greater than the actual length of the sequence is specified, this parameter is ignored.
- nosimd - If True, SIMD acceleration is disabled. This parameter is

xor

Calculate xor over the values in a bytes or bytearray object.

Equivalent to:	[x ^ param for x in sequence1]
or	[param ^ x for x in sequence1]
or	[x ^ y for x,y in zip(sequence1, sequence2)]

Call formats:

```
xor(sequence1, param)
xor(sequence1, param, outpsequence)
xor(param, sequence1)
xor(param, sequence1, outpsequence)
xor(sequence1, sequence2)
xor(sequence1, sequence2, outpsequence)
xor(sequence1, param, maxlen=y)
xor(sequence1, param, nosimd=False)
```

- sequence1 - The first input data bytes or bytearray sequence to be examined. If no output sequence is provided the results will overwrite the input data.
- param - A non-sequence numeric parameter.
- sequence2 - A second input data sequence. Each element in this sequence is applied to the corresponding element in the first sequence.
- outpsequence - The output sequence. This parameter is optional.
- maxlen - Limit the length of the sequence used. This must be a valid positive integer. If a zero or negative length, or a value which is greater than the actual length of the sequence is specified, this parameter is ignored.
- nosimd - If True, SIMD acceleration is disabled. This parameter is

Parameter Details

Comparison Operators

Some functions use comparison operators. These are unicode strings containing the Python compare operators and include following:

Operator	Description
'<'	Less than.
'<='	Less than or equal to.
'>'	Greater than.
'>='	Greater than or equal to.
'=='	Equal to.
'!='	Not equal to.

All comparison operators must contain only the above characters and may not include any leading or trailing spaces or other characters.

Numeric Parameters

"Bytes" and "bytearray" objects are sequences of 8 bit bytes with each element being in the range of 0 to 255. When a function accepts a non-sequence numeric parameter, this must also be in the range of 0 to 255.

Using Less than the Entire Sequence

If the size of the sequence is larger than the desired length of the calculation, it may be limited to the first part of the sequence by using the 'maxlen' parameter. In the following example only the first 3 elements will be operated on, with the following ones left unchanged.:

```
x = bytes([20,21,22,23,24,25])
result = bytesfunc.bmax(x, maxlen=3)
```

Suppressing or Ignoring Math Errors

Some functions can be made to ignore some mathematical errors (e.g. integer overflow) by setting the 'matherrors' keyword parameter to True.:

```
x = bytes([20,21,22,23,24,250,250])
result = bytesfunc.sum(x, matherrors=True)
```

Ignoring errors may be desirable if the side effect (e.g. the result of an integer overflow) is the intended effect, or for reasons of a minor performance improvement in some cases. Benchmark your calculation before deciding if this is worth while.

Differences with Native Python

In some cases 'BytesFunc' will not produce exactly the same result as Python. There are several reasons for this, the primary one being that BytesFunc operates on different underlying data types. Specifically, BytesFunc uses the platform's native integer types while Python integers are of arbitrary size and can never overflow (Python simply expands the word size indefinitely), while BytesFunc integers will overflow the same as they would with programs written in C.

Think of BytesFunc as exposing C style semantics in a form convenient to use in Python. Some convenience which Python provides (e.g. no limit to the size of integers) is traded off for large performance increases.

SIMD Support

General

SIMD (Single Instruction Multiple Data) is a set of CPU features which allow multiple operations to take place in parallel. Some, but not all, functions may make use of these instructions to speed up execution.

Disabling SIMD

Those functions which do support SIMD features will automatically make use of them by default unless this feature is disabled. There is normally no reason to disable SIMD, but should there be hardware related problems the function can be forced to fall back to conventional execution mode.

If the optional parameter "nosimd" is set to true ("nosimd=True"), SIMD execution will be disabled. The default is "False".

To repeat, there is normally no reason to wish to disable SIMD.

Platform Support

SIMD instructions are presently supported only on 64 bit x86 (i.e. AMD64) and ARMv7 using the GCC compiler. Other compilers or platforms will still run the same functions and should produce the same results, but they will not benefit from SIMD acceleration.

However, non-SIMD functions will still be much faster standard Python code. See the performance benchmarks to see what the relative speed differences are.

Raspberry Pi 3 versus 4

The Raspberry Pi uses an ARM CPU. The Raspberry Pi 3 has an ARMv7 CPU, which supports NEON SIMD with 64 bit vectors. The Raspberry Pi 4 has an ARMv8 CPU, which supports NEON SIMD with 128 bit vectors.

This means that the SIMD instructions for the RPi 3 are different from those of the RPi 4 (64 bit versus 128 bit). Due to hardware availability for testing, SIMD support for ARMv8 is not currently available in this library.

However, the straight 'C' code should still compile and run, and still provide performance many times faster than when using native Python.

SIMD Function Support

The following table shows which functions are supported by SIMD on which CPU architectures.

Function	x86	ARMv7
and_	X	X
ball	X	X
bany	X	X
bmax	X	X
bmin	X	X
bsum		
eq	X	X
findindex	X	X
ge	X	X
gt	X	X
invert	X	X
le	X	X
lshift		X
lt	X	X
ne	X	X
or_	X	X
rshift		X
xor	X	X

SIMD Support Attributes

There is an attribute which can be tested to detect if BytesFunc is compiled with SIMD support and if the current hardware supports the required SIMD level.

`bytesfunc.simdsupport.hassimd`

The attribute "hassimd" will be True if the module supports SIMD.

example:

```
import bytesfunc
bytesfunc.simdsupport.hassimd
==> True
```

Performance

Variables affecting Performance

The purpose of the BytesFunc module is to execute common operations faster than native Python. The relative speed will depend upon a number of factors:

- The function.
- Function options. Turning checking off will result in faster performance.
- The data in the sequence and the parameters.
- The size of the sequence.
- The platform, including CPU type (e.g. x86 or ARM), operating system, and compiler.

The speeds listed below should be used as rough guidelines only. More exact results will require application specific testing. The numbers shown are the execution time of each function relative to native Python. For example, a value of '50' means that the corresponding BytesFunc operation ran 50 times faster than the closest native Python equivalent.

Both relative performance (the speed-up as compared to Python) and absolute performance (the actual execution speed of Python and BytesFunc) will vary significantly depending upon the compiler (which is OS platform dependent) and whether compiled to 32 or 64 bit. If your precise actual benchmark performance results matter, be sure to conduct your testing using the actual OS and compiler your final program will be deployed on. The values listed below were measured on x86-64 Linux compiled with GCC.

Note: Some more complex BytesFunc functions do not work exactly the same way as the native Python equivalents. This means that the benchmark results should be taken as general guidelines rather than precise comparisons.

Typical Performance Readings

In this set of tests, all error checking was turned on and SIMD acceleration was enabled where this did not conflict with the preceding (the defaults in each case).

The Bytesfunc versus Python factor of 100.0 means the bytesfunc version ran 100 times faster than in native Python on that platform. Benchmarks for different hardware and platforms cannot be compared via this benchmark in terms of absolute performance as these are relative, not absolute numbers.

An SIMD versus non-SIMD factor of 10.0 means the SIMD version was 10 times faster than the non-SIMD version. An SIMD versus non-SIMD factor of 0.0 means the function did not support SIMD on the tested platform.

x86-64 Benchmarks

The following tests were conducted on an x86-64 CPU.

Relative Performance - Python Time / Bytesfunc Time.

function	Bytesfunc vs Python	SIMD vs non-SIMD
bmax	79.6	4.2
bmin	79.5	4.2
bsum	7.4	0.0
ball	619.4	15.2
bany	477.0	11.8
findindex	680.7	10.9
eq	668.1	12.2
ge	671.2	11.3
gt	794.8	8.7
le	630.9	11.1
lt	492.2	7.5
ne	801.0	11.9
and_	1511.2	8.7
or_	1119.4	9.9
xor	1001.7	10.1
lshift	131.1	0.0
rshift	97.6	0.0
invert	987.6	8.7

Stat	Value
Average:	602.8
Maximum:	1511.2
Minimum:	7.4
Array size:	100000

ARMv7 Benchmarks

The following tests were conducted on an ARMv7 CPU on a Raspberry Pi 3.

Relative Performance - Python Time / Bytesfunc Time.

function	Bytefunc vs Python	SIMD vs non-SIMD
bmax	222.6	4.4
bmin	225.5	4.4
bsum	10.3	0.0

ball	343.1	2.6
bany	391.4	2.9
findindex	523.8	3.6
eq	344.2	2.6
ge	358.7	2.6
gt	358.8	2.6
le	359.8	2.6
lt	359.9	2.6
ne	390.6	2.9
and_	1040.1	3.8
or_	1072.1	3.8
xor	1066.3	3.8
lshift	1289.6	4.5
rshift	933.1	4.4
invert	846.2	3.8

Stat	Value
Average:	563.1
Maximum:	1289.6
Minimum:	10.3
Array size:	100000

Platform Effects

The platform, including CPU, OS, compiler, and compiler version can affect performance, and this influence can change significantly for different functions.

If your application requires exact performance data, then benchmark your application in the specific platform (hardware, OS, and compiler) that you will be using.

Platform support

List of tested Operation Systems, Compilers, and CPU Architectures

BytesFunc is written in 'C' and uses the standard C libraries to implement the underlying math functions. BytesFunc has been tested on the following platforms.

OS	Bits	Compiler	Python Version Tested
Ubuntu 18.04 LTS	64 bit	GCC	3.6
Ubuntu 19.10	64 bit	GCC	3.7
Ubuntu 20.04 beta	64 bit	GCC	3.8

Debian 10	32 bit	GCC	3.7
Debian 10	64 bit	GCC	3.7
OpenSuse 15	64 bit	GCC	3.6
Centos 8	64 bit	GCC	3.6
FreeBSD 12	64 bit	LLVM	3.7
OpenBSD 6.5	64 bit	LLVM	3.6
MS Windows 10	64 bit	MS Visual Studio C 2015	3.8
Raspbian (RPi 3)	32 bit	GCC	3.7

The Raspbian (RPi 3) tests were conducted on a Raspberry Pi 3 ARMV7 CPU. All others were conducted using VMs running on x86 hardware.

Platform Oddities

As most operators are implemented using native behaviour, details of some operations may depend on the CPU architecture.

Lshift and rshift will exhibit a behaviour that depends on the CPU type whether it is 32 or 64 bit, and array size.

For 32 bit x86 systems, if the array word size is 32 bits or less, the shift is masked to 5 bits. That is, shift amounts greater than 32 will "roll over", repeating smaller shifts.

On 64 bit systems, this behaviour will vary depending on whether SIMD is used or not. Arrays which are not even multiples of SIMD register sizes may exhibit different behaviour at different array indexes (depending on whether SIMD or non-SIMD instructions were used for those parts of the array).

ARM does not display this roll-over behaviour, and so may give different results than x86. However, negative shift values may result in the shift operation being conducted in the opposite direction (e.g. right shift instead of left shift).

The conclusion is that bit shift operations which use a shift amount which is not in the range of 0 to "maximum number" may produce undefined results. So valid bit shift amounts should be 0 to 7.