

Multiprocessing in Python

Making Embarassingly Parallel Tasks Embarassingly Fast

Vítek Novotný witiko@mail.muni.cz

Faculty of Informatics, Masaryk University

May 12, 2021

Introduction

Introduction

In Python, you can achieve several kinds of parallelism:

Single Instruction, Single Data (SISD) Plain Python. Ok for logic, slow for computation. Single Instruction, Multiple Data (SIMD) Vector instructions for CPUs. Use numpy.

Single Program, Multiple Data (SPMD) Many processes of one program work in parallel.

Shared Memory One machine. Use multiprocessing.

Distributed Memory Many machines. Use GNU Parallel.

In this tutorial, I will show you how you can transform SISD code into SIMD and SPMD in your second term project with examples. This will *significantly speed up your code*. ; -)



SISD to SIMD I

Say you have the following code for computing the cosine similarity of vectors X and Y:

>>> **from math import** sqrt $\sum X_i \cdot Y_i$ >>> X = [1.0, 0.0, 0.0, 1.0, 0.0, 1.0] * 100>>> Y = [0.0, 1.0, 1.0, 1.0, 0.0, 1.0] * 100 $\sqrt{\sum_{i=1}^{n} X_i^2} \cdot \sqrt{\sum_{i=1}^{n} Y_i^2}$ >>> similarity, norm X, norm Y = 0.0, 0.0, 0.0>>> **for** x. y **in** zip(X, Y): \ldots similarity += x * y... norm $X += x^{**2}$... norm Y += v^{**2} >>> norm = sqrt(norm X) * sqrt(norm Y) >>> similarity /= norm if norm > 0.0 else 1.0 >>> **print**(similarity) 0.5773502691896258 \$ python -m timeit -s 'from ex1 import similarity' 'similarity()' 10000 loops, best of 3: 69.7 usec per loop V. Novotný • Multiprocessing in Python • May 12, 2021 3/8

SISD to SIMD II

Modern processors support *vector instructions*, which can process many elements at once. By using the numpy library, we can perform the same operation much more efficiently:

```
>>> import numpy as np
```

```
>>> X = np.array([1.0, 0.0, 0.0, 1.0, 0.0, 1.0] * 100)
```

>>> Y = np.array([0.0, 1.0, 1.0, 1.0, 0.0, 1.0] * 100)

- >>> norm = np.sqrt(np.sum(X)) * np.sqrt(np.sum(Y))
- >>> similarity /= norm if norm > 0.0 else 1.0
- >>> print(similarity)

0.5773502691896258

\$ python -m timeit -s 'from ex2 import similarity' 'similarity()'
100000 loops, best of 3: 11.8 usec per loop

We have received a $7 \times$ speed-up. If we compute similarity between many vectors, the speed-up is even bigger, since numpy uses optimized BLAS matrix operations.

SIMD to SPMD I

Say you have the following code for preprocessing the TREC collection documents:

- >>> from pv211_utils.trec.loader import load_documents
- >>> from gensim.utils import simple_preprocess
- >>> **from tqdm import** tqdm

>>>

- >>> documents = load_documents(Document)
- >>> tokenized_documents = []
- >>> for document in tqdm(documents.values()):
- ... tokenized_document = simple_preprocess(document.body)
 ... tokenized_documents.append(tokenized_document)

```
2%|| | 8689/527890 [00:12<11:24, 758.54it/s]
```

This is pretty to read, but also *pretty inefficient*, since we are using only a single CPU! : (

SIMD to SPMD II

On your notebook, you have up to 8 CPUs. On the aura.fi.muni.cz server, you have 64 CPUs. You can split documents into *chunks* and have CPUs process them in parallel:

- >>> from pv211_utils.trec.loader import load_documents
- >>> from gensim.utils import simple_preprocess
- >>> **from tqdm import** tqdm
- >>> from multiprocessing import Pool

```
>>>
```

>>> documents = load_documents(Document)

```
>>> with Pool(None) as pool: # None means we use all CPUs!
```

```
... document_bodies = (document.body for document in documents.values())
```

```
... document_bodies = tqdm(document_bodies, total=len(documents))
```

On 64 CPUs, we have received a $7 \times$ speed-up. You can see that the scaling is not linear and there is overhead, since Python has to *pickle* and send Document objects to the individual CPUs and then pickle and retrieve the results. This is the price of Python's *GIL*. We get $50 \times$ speed-up by exchanging bigger chunks: pool.map(..., chunksize=10000).

SIMD to SPMD III

The previous design pattern is not unique to Python. You can parallelize any *any program* that processes one file one at a time. Suppose you have a script called tokenize.py, which takes an input text file and produces a tokenized output text file:

\$ for INPUT in input/*.txt

> **do**

- > OUTPUT=output/"\${INPUT#input/}"
- > python tokenize.py "\$INPUT" "\$OUTPUT"

> done

You can use the GNU Parallel tool to run the script on all your CPUs in parallel:

\$ parallel python tokenize.py {} output/{/} ::: input/*.txt
If your disk can catch up, we will receive a full 64× speed-up on 64 CPUs! ^_^
We can go even further and run our script on many different machines:

\$ parallel --sshlogin user@machine1 --sshlogin user@machine2 ... Unix admins beware!

Conclusion

Conclusion

Python is a nice language for writing logic, but slow for computation. In order not to wither while waiting for results, you should obey the following rules:

- For vector and matrix computation, replace for loops with numpy.
- For processing many independent elements with single-CPU transformations, replace for loops with multiprocessing (or GNU Parallel).

I wish you the best of luck with your projects!



MUNI FACULTY OF INFORMATICS