

Converting GenBank (or other formats) to ~~test(a)~~ ~~in~~ ~~and~~ ~~3~~ ~~ra~~ ~~0~~ ~~0~~

Now that we understand how things will be working internally, let's write the code that drives the conversion process. First, we open up a handle to read from the GenBank file, and a handle to write to the output Fasta file. Assuming you've somehow defined `input_file`, which is an existing file of GenBank records, and `output_file`, the name of the output file, this is just standard python:

```
input_handle = open(input_file)
```

```
from Bio import GenBank
```

```
iterator = GenBank.Iterator(input_handle, GenBank.RecordParser())
```