

Converting GenBank (or other formats) to FASTA and Brat

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())
```