

```
<HTML>
<HEAD><TITLE>CGI 101</TITLE></HEAD>
<BODY>
<H1>A first user interaction form</H1>
<hr>
```

HTML

```
<FORM method=POST action="test.cgi">
```

```
<P><B>Enter your name</B>
```

```
<P><input type=text name=user>
```

```
<P><B>Comments:</B>
```

```
<P><input type=textarea name=comment>
```

```
<P><INPUT type=submit>
```

```
</FORM>
```

```
</BODY>
```

```
</HTML>
```

```
#!/usr/local/bin/python
```

```
import sys  
sys.stderr = sys.stdout  
import cgi  
import cgitb  
cgitb.enable()
```

```
form = cgi.FieldStorage()
```

```
print "Content-type: text/html\n"  
print "<html><body><STRONG><font color=red></font></STRONG>"
```

```
html = """  
<TITLE>Grretings.cgi</Title>  
<H1>Greetings</H1>  
<HR>  
<P>%s</P>  
<HR>"""
```

```
if not form.has_key('user'):
    print html % 'Who are you'

else:
    print html % ('Hello Mr. %s.' % form['user'].value)

if not form.has_key('comment'):
    print 'Sorry, you did not provide any comment'
else:
    print "%s, your input: <P>'%s' <P>is valuable<HR>" %
        (form['user'].value, form['comment'].value)
```

```
import time
now = time.localtime()
now_time = time.asctime(now)
file = open('comment.txt', 'a')
→ file.write(now_time)
file.write('\n')
→ file.write(form['user'].value)
file.write(':\n\t')
→ file.write(form['comment'].value)
file.write('\n')
file.close()

print "</body></html>"
```

Fri Apr 5 18:13:06 2002

singh:

It is still good

Fri Apr 5 18:13:43 2002

scott:

one more time

Wed Apr 10 16:00:38 2002

chris:

hello

Fri May 3 09:44:56 2002

Josh:

I like this course

```
import Bioperl  
use Bio::DB::GenBank
```

```
$gb = new Bio::DB::GenBank();
```

```
$seq1 = $gb->get_Seq_by_id('MUSIGHBA1');
```

this returns a Seq object :

```
$seq2 = $gb->get_Seq_by_acc('AF303112');
```

```
$seqio = $gb->get_Stream_by_batch(  
[ qw(J00522 AF303112 2981014)]);
```

This is the best we could

At such a short notice

First time around and

Once a week, For

biologists w/o prior experience

The End