Project 1

September 15, 2015

In [1]:
```
%matplotlib inline
```

In [2]:
```
import matplotlib.pyplot as plt
```

0.0.1 Download the Campy genome

Here we use Biopython to download the campy genome and save as file campy.fa

In [3]:
```
from Bio import Entrez, SeqIO
```

In [9]:
```
Entrez.email = "hcorrada@gmail.com"
handle = Entrez.efetch(db="nucleotide", id="AL111168.1", rettype="gb", retmode="text")
record = SeqIO.read(handle, "genbank")
handle.close()

SeqIO.write(record, "campy.fa", "fasta")
```

Out[9]:
```
1
```

0.0.2 Calculate skew for campylobacter

This function computes skew

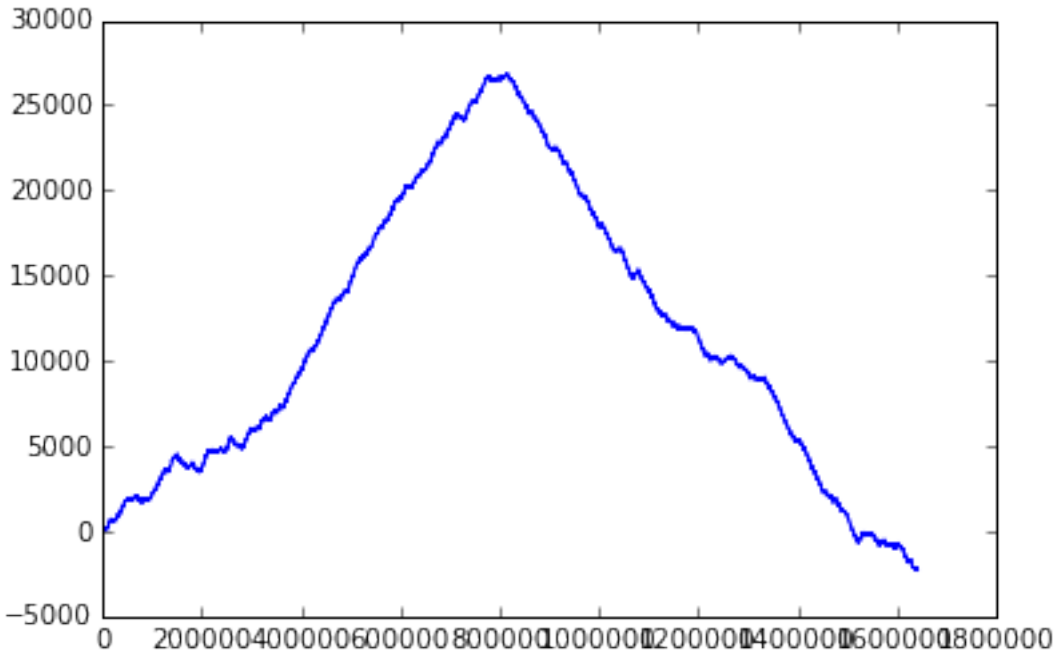
In [4]:
```
def get_skew_vec(genome):
    res = [0]
    skew = 0
    for i in xrange(len(genome)):
        c = genome[i]

        if c == 'C':
            skew = skew - 1
        elif c == 'G':
            skew = skew + 1
        res.append(skew)
    return res
```

Now compute the skew for campy and plot it.

In [5]:
```
record = SeqIO.read("campy.fa", "fasta")
skew_vec = get_skew_vec(record)
plt.plot(skew_vec)
```

Out[5]:
```
[<matplotlib.lines.Line2D at 0x1054ea490>]
```



It looks like the minimum skew is at the end of the file, which suggests that oriC is around the beginning of the file. So let's take the last 250bp followed by the first 250bp as the candidate oriC region.

```
In [6]: candidate_region = record[-250:] + record[:250]
        len(candidate_region)
```

```
Out[6]: 500
```

0.0.3 Find frequent words

This code finds frequent words with mismatches and reverse complement

```
In [8]: from collections import defaultdict

        # use this hash table to get complementary nucleotides
        complement = dict(A="T", C="G", G="C", T="A")

        # compute the reverse complement of a given string
        # input:
        #  text: a string
        # output:
        #  the reverse complement of text
        def revcomp(text):
            # turn the string into a list
            out = list(text)

            # reverse the list (in place)
            out.reverse()

            # get complement at each position of list
            for i in xrange(len(out)):
```

```
        out[i] = complement[out[i]]

    # turn back into string and return
    return ''.join(out)

# generate the d neighborhood of a DNA string
nucleotides = list('ACGT')

def get_neighbors(pattern, d):
    if d == 0:
        return [(pattern,0)]
    if len(pattern) == 1:
        return [(nuc, 1 if nuc != pattern else 0) for nuc in nucleotides]

    neighborhood = set()
    suffix_neighbors = get_neighbors(pattern[1:], d)
    for (text, cur_d) in suffix_neighbors:
        if cur_d < d:
            for nuc in nucleotides:
                distance = cur_d + 1 if nuc != pattern[0] else cur_d
                neighborhood.add((nuc + text, distance))
        else:
            neighborhood.add((pattern[0] + text, d))
    return neighborhood

# compute most frequent words allowing d mismatches, including reverse complements
# input:
#   text: input string
#   k: k-mer length
#   d: maximum number of mismatches
def freq_words_mismatch_revcomp(text, k, d):
    kmer_counts = defaultdict(int)

    n = len(text)
    for i in xrange(n-k+1):
        kmer = text[slice(i,i+k)]
        neighbors = get_neighbors(kmer, d)
        for neighbor, _ in neighbors:
            kmer_counts[neighbor] += 1
        kmer = revcomp(kmer)
        neighbors = get_neighbors(kmer, d)
        for neighbor, _ in neighbors:
            kmer_counts[neighbor] += 1

    max_count = 0
    frequent_words = list()
    for kmer, count in kmer_counts.items():
        if count == max_count:
            frequent_words.append(kmer)
        if count > max_count:
            frequent_words = [kmer]
            max_count = count
    return frequent_words, max_count
```

Ok, now run this code for k=3,4,5,6,7,8 and 9, counting the number of frequent words and their number of occurences

```
In [10]: kvec = range(3,10)
         res = list()
         for k in kvec:
             print "running k=", k
             freq_words, count = freq_words_mismatch_revcomp(candidate_region, k, 2)
             res.append((k, len(freq_words), count))
```

```
running k= 3
running k= 4
running k= 5
running k= 6
running k= 7
running k= 8
running k= 9
```

Let's make a pretty table to include in our report

```
In [13]: # based on http://calebmadrigal.com/display-list-as-table-in-ipython-notebook/
         class ResTable(list):
             def _repr_html_(self):
                 html = ["<table>"]
                 html.append("<th>k</th><th>num kmers</th><th>num occurrences</th>")
                 for row in self:
                     html.append("<tr>")
                     for col in row:
                         html.append("<td>{0}</td>".format(col))
                     html.append("</tr>")
                 html.append("</table>")
                 return ''.join(html)
         ResTable(res)
```

```
Out[13]: [(3, 1, 704),
          (4, 1, 389),
          (5, 1, 247),
          (6, 1, 146),
          (7, 1, 79),
          (8, 1, 47),
          (9, 1, 29)]
```

Looks like there is a single kmer that occurs most frequently. Let's see that kmer for k=7,8,9.

```
In [14]: words_7, _ = freq_words_mismatch_revcomp(candidate_region, 7, 2)
         words_8, _ = freq_words_mismatch_revcomp(candidate_region, 8, 2)
         words_9, _ = freq_words_mismatch_revcomp(candidate_region, 9, 2)
         print "k=7", words_7
         print "k=8", words_8
         print "k=9", words_9
```

```
k=7 ['TTTTTTT']
k=8 ['TTTTTTTT']
k=9 ['TTTTTTTTT']
```

Well, that's not very interesting. At this point, I would run with bigger k.

```
In [ ]:
```