#!/usr/bin/python

import cgi

import cgitb

from subprocess import call

import pdb

print 'Content-Type: text/html\n'

print '<META HTTP-EQUIV=\"CACHE-CONTROL\" CONTENT=\"NO-CACHE\">'

print '''<HTML>

<BODY>'''

cgitb.enable()

form = cgi.FieldStorage()

if not form:

    print 'Please input name of gene to plot:<br>'

    print '<form name \"myform\" action = "plotting.py" method="post">'

    print '<input type="text" name="gene" size="8">'

    print '</form>'

else:

    call(['rm','/var/www/tmpimages/\*.png'])

    genecoordinates=[]

    genename = form.getfirst("gene","").upper()

    f = open('/usr/lib/cgi-bin/normalized\_tsneout.tsv')

    for line in f:

        columns = line.rstrip().split()

        if columns[0].upper()==genename:

            genecoordinates.append([float(columns[2]),float(columns[3])])

    filenamecounter=0

    if not genecoordinates:

        print 'Could not find any genes with that name in the probelist!<br>'

    for coordinates in genecoordinates:

        xrange = (str(coordinates[0]-2),str(coordinates[0]+2))

        yrange = (str(coordinates[1]-2),str(coordinates[1]+2))

        call(["gnuplot","-e",''.join([

        'set xrange [{}:{}];'.format(xrange[0],xrange[1]),

        'set yrange [{}:{}];'.format(yrange[0],yrange[1]),

        'set term pngcairo size 1280,1024;',

        "set output '{}';".format('/var/www/tmpimages/'+str(filenamecounter)+'.png'),

        "plot '/usr/lib/cgi-bin/normalized\_tsneout.tsv' ",

        'using 3:4:1 with labels;'])])

        filenamecounter+=1

        for i in range(filenamecounter):

            print '<img src="[http://genjflab.tcd.ie/tmpimages/{}.png](https://go.tcd.ie/owa/redir.aspx?C=6OJNnIgxO0-bGaqRUbkvb_ac4BVVj9FIx0_Z_ejwpfcqYcivdfg8vu9EHBGYFWPOGeXq-a2Bkt4.&URL=http%3a%2f%2fgenjflab.tcd.ie%2ftmpimages%2f%7b%7d.png)">'.format(str(i))

print '''</BODY></HTML>'''