PROBLEM OF THE MONTH

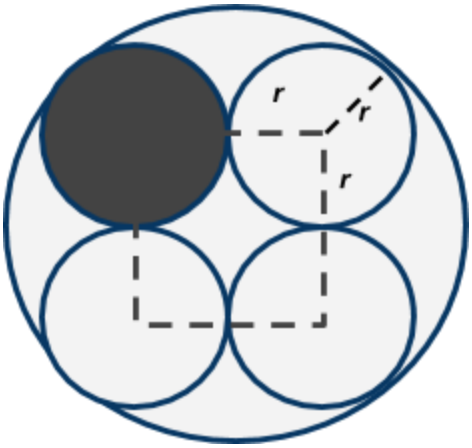
POM

2017-2018

January, 2018

MATHEMATICS

5 points: Four circles of the same size are inscribed in a bigger circle, as shown in the Figure. One of the small circles is shaded black. Find the fraction of the area of the large circle which is shaded.

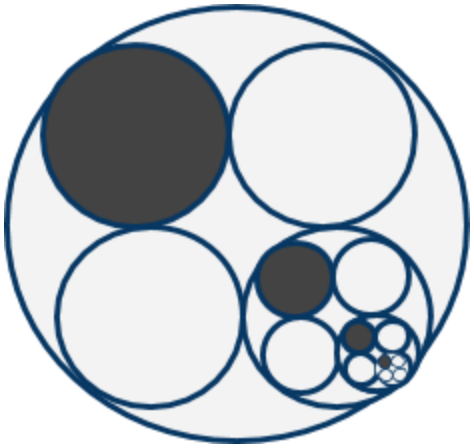


Hint: Let the radius of a small circle be ***r***. Note that centers of the four small circles are sittings in the corners of a square with side 2r (see Figure). Try to find the radius of a big circle in terms of r.

Answer: $\frac{1}{3+2\sqrt{2}}$

Solution: Let the radius of a small circle be ***r***. Note that centers of the four small circles are sittings in the corners of a square with side 2r (see Figure). We can find the diagonal of this square $D = 2\sqrt{2}r$. The radius of the large circle is $R = D/2 + r = \left(\sqrt{2}+1\right)r$. We can now find the ratio of the areas of the small and large circles: $p = (\pi r^2)/\left(\pi R^2\right) = 1/\left(\sqrt{2}+1\right)^2 = \frac{1}{3+2\sqrt{2}}$.

10 points: Four circles of the same size are inscribed in a bigger circle, as shown in the Figure. One of the small circles is shaded black. Four smaller equal circles are now inscribed into another one. Out of them, one is shaded, and another is again replaced by a smaller version of the whole figure… Find the fraction of the area of the large circle which is shaded as a result of this never-ending sequence of inscription and shading.



Hint: Let p be the result of the 5pt problem, and x be the fraction of shaded area in this problem. Than x can be represented as a sum of two contributions: (1) the fully-shaded small circle (which occupies

fraction p of the bigger one), and (2) partially-filled circle, that also occupies fraction p, of which fraction x is shaded. From this consideration, construct an Equation for x, and solve it.

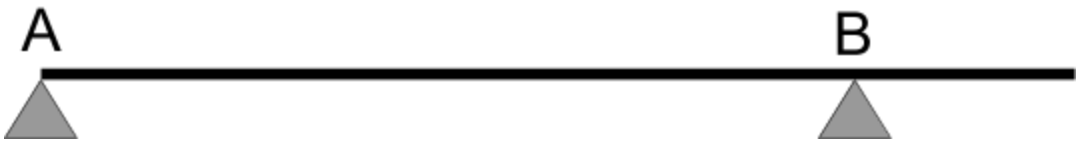
Answer: $\frac{1}{2+2\sqrt{2}}$

Solution: Let p= $\frac{1}{3+2\sqrt{2}}$ be the result of the 5pt problem, and x be the fraction of shaded area in this problem. Than x can be represented as a sum of two contributions: (1) the fully-shaded small circle (which occupies fraction p of the bigger one), and (2) partially-filled circle, that also occupies fraction p, of which fraction x is shaded. In other words, $x = p + px$. By solving this equation for x, we obtain: $x = p/(1-p) = \frac{1}{2+2\sqrt{2}}$.

PHYSICS

This month Physics problems are on the mechanical equilibrium and simple machines. You might find the following links useful.
http://hyperphysics.phy-astr.gsu.edu/hbase/Mechanics/lever.html
http://hyperphysics.phy-astr.gsu.edu/hbase/Mechanics/simmac.html#c1
http://hyperphysics.phy-astr.gsu.edu/hbase/torq.html#equi
http://hyperphysics.phy-astr.gsu.edu/hbase/fequ.html#equ
http://hyperphysics.phy-astr.gsu.edu/hbase/toreq.html

5 points: Two people are carrying a plank of the length L, supporting it at points A and B as schematically shown in the Figure. What should be the distance between points A and B for the person A to carry exactly one third of the weight of the plank. The plank is uniform and horizontal.

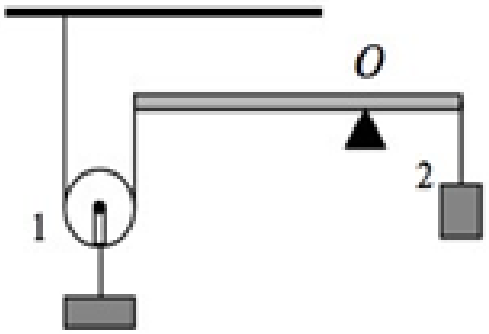


Hint: Apply the law of the lever. The plank's gravity force is applied to its center of mass.

Answer: $x = \frac{3}{4}L$

Solution: The person B carries two thirds of the weight of the plank W. Applying the law of the lever with pivot at point A we have $W\frac{L}{2} = \frac{2}{3}Wx$ and find $x = \frac{3}{4}L$.

10 points: Two masses $m_1 = 2$ kg and m_2=3 kg are suspended motionlessly with the help of a pulley, ropes and a plank as presented on the diagram. At what distance from the left end of the plank should you place a pivot point O to keep the system in equilibrium if the length of the plank is 0.6 m and the mass of the plank is $M = 5$ kg. The masses of the pulley and ropes are negligible.



Hint: Apply the law of the lever. The plank's gravity force is applied to its center of mass. The tension of the rope at pulley is half of the weight of m_1.

Answer: $x = \frac{11}{18}L \approx 37$ cm

Solution: The tension of the rope at the pulley is found from $2T = m_1 g$. The net normal force applied to the plank at point O is, therefore, $(\frac{m_1}{2} + m_2 + M)g$. The law of the lever with pivot at the left end of the plank gives $(\frac{m_1}{2} + m_2 + M)gx = Mg\frac{L}{2} + m_2 gL$. Solving for x we obtain $x = \frac{M/2+m_2}{m_1/2+m_2+M}L = \frac{5/2+3}{1+3+5}L = \frac{11}{18}L \approx 37$ cm.

CHEMISTRY

5 points:

An elastic balloon made of a semipermeable membrane (a membrane that is permeable for water molecules, but not for inorganic ions and larger molecules or ions) was filled with 5.9% aqueous solution of sodium chloride and sealed. Then the balloon was placed into a beaker filled with 11.7% solution of potassium sulfate. Both solutions are at equilibrium, which means the balloon is not shrinking or expanding. The solution in the beaker was diluted with an equal volume of 7.4% aqueous calcium chloride. How will the balloon's volume change?

Hint:

Two solutions separated by a semipermeable membrane are at equilibrium when the concentration of particles (i.e. the number of individual particles per 1 liter) in both solutions are equal.

Solution:

Two solutions separated by a semipermeable membrane are at equilibrium when the concentration of particles (i.e. the number of individual particles per 1 liter) at both sides of the membrane. That means NaCl and K_2SO_4 are at equilibrium when the amount of all particles except water per 1 L is the same. To make sure it is the case, let's do some calculations.
When NaCl and K2SO4 dissolve in water, they dissociate according to the equations:

$NaCl \rightarrow Na^+ + Cl^+$

and

$K_2SO_4 \rightarrow 2K^+ + SO_4^{2-}$

Note, that dissociation of sodium chloride produces two moles of particles per one mole of the salt, whereas three moles of particles (two moles of potassium ions and one mole of sulfate ions) form after dissociation of potassium sulfate.

If we calculate molar concentrations of both solutions, we will see that NaCl concentration is 1 M (5.9 gram per 100 mL is 1 mole per liter), and K_2SO_4 is 0.66 M (11.7 gram per 100 mL is 117 gram per 1L, which is 117/(40+40+32+16×4) = 117/176=0.66M. Since 1×2 = 0.66×3, we conclude the concentrations of particles inside and outside of the balloon are the same, so the solutions *are* at equilibrium.

What happens when we add 7.4% $CaCl_2$ to the beaker? Molar mass of $CaCl_2$ is 40 + 35.5+35.5=111, which means the concentration is 0.66 M. Taking into account that dissociation of calcium chloride occurs according to the equation:

$CaCl_2 \rightarrow Ca^+ + 2Cl^-$

one mole of $CaCl_2$ produces three moles of ions, so the concentration of all ions is 2 M (exactly as in the potassium sulfate solution). In other words, when we mix two solutions, each of which contain 2 M concentration of all ions, the total concentration of ions is not supposed to change.

However, there is one thing here that we have to take into account. By mixing the solutions of calcium chloride and potassium sulfate we create a mixture of ions that cannot coexist in solutions at high concentrations: calcium and sulfate ions form a low soluble salt, calcium sulfate, which will precipitate from the solution, so the only salt that will remain in the solution will be potassium chloride, and its concentration will be 0.66 × 2 = 1.32M. To compensate the difference in concentration, water will start to diffuse into the balloon, so **the balloon will start to expand**.

10 points:

Mercury and its salts are very toxic substances. The maximum allowed concentration of mercury salts in drinking water is 2 ppb (2 ng/L). Unfortunately, in some areas, drinking water may be contaminated by mercury, for example, due to the proximity of mercury deposits. Imagine you came to a small town where the only well that serves as source of drinking water contains inorganic mercury salts at concentration of 30 ppb, which is considerably higher than the maximum allowed concentration. There is an unlimited amount of the following reagents in this town:

> *Sodium sulfide, potassium iodide, sodium sulfate, lithium bromide, calcium chloride, ammonium nitrate.*

Which chemicals from this list would you advise to add to the drinking water to neutralize a toxic effect of mercury (at least, as a temporary solution), and in what concentration should these chemicals be used?

Hint:

To remove some mercury compound from a solution, one has to convert it into something insoluble.

Solution:

Mercury sulfide is among the most insoluble minerals. Its solubility product (i.e. the maximal achievable value of the product of concentrations of mercury and sulfide ions) is ca 10^{-53}. That means if we maintain the concentration of S^{2-} at the nanomolar level (10^{-9} M), the concentration of mercury ions will not exceed 10^{-44} M (or $10^{-53}/10^{-9}$), which is pretty acceptable.

BIOLOGY

5 points:

The 4th season of the *Black Mirror* TV show starts with the story of some virtual world where digital clones of real humans had been placed. To make these clones, the main hero obtained biological samples from them (for example, by picking up traces of their saliva). Then, he placed these samples into some machine that performed some "scanning" (the details of this procedure are not explained in the film), and, after the scanning is complete, a digital clone of this individual appears in the virtual world. These clones completely retained the personality of their real world prototypes. To them, the process of transfer looked like if they have been suddenly transferred from the real world into the virtual world.

Can such a technology be developed (at least in a remote future), and what are major technical challenges for its implementation? If the answer is negative (it is impossible in principle), explain why?

Hint:

To answer this question, we need to remember which kind of information is stored in *every* cell of our body and which information is tissue or organ specific.

Answer:

Our brain memorises information by changing conductivity of axons, long fibers that connect neurons to each other. Each fact you remember is just an ensemble of connections between different neuron layers. That means the information our brain is keping and our genetic information are totally different things: whereas every cell nucleus contains all essential information that is sufficient to reproduce an almost complete genetic copy of our body (the major difference between this copy and us will be the absence of acquired immunity), there is impossible to reproduce our memory based on a small biological sample obtained from our body. This is a fundamental limitation, because our memory is stored by our brain as a whole organ, which changes (activates or deactivates new interneuronal connections) every time we memorize new facts. These changes have no effect on other parts of our bodies, and accordingly, this information cannot be collected by analyzing other tissues of our bodies.

10 points:

As a rule, when some animal or bird species is characterized by a significant sexual dimorphism, males look more "beautiful", bright, and aesthetically attractive than females. Accordingly, during the mating period, a male demonstrates some specific behaviour to attract female's attention, whereas a female take no special efforts to attract attention of males, and just selects the male who look more attractive than others.

In contrast, humans demonstrate totally opposite behaviour: usually, a woman tries to look aesthetically attractive, and woman's role traditionally consists in accepting or rejecting a man, whereas the initiative comes from the men's side.

Is that difference a result of some social stereotypes, or it has some evolutionary origin? Explain your answer.

Hint:

To answer this question, you have to take a look at the role of the males *after* mating, and how families are organized in species where males are “beautiful” and in the species where females are “beautiful”.

Answer:

In the species where males attract females, the former do not participate in rising offsprings. As a rule, male’s task is just to mate with the maximal number of females to maximize transfer of good quality genes to the next generation. Accordingly, females are very fertile, the birth rate is high, so the mortality can be high too, so no extraordinary efforts are needed to take care about the offsprings, and females can do that without male’s help.

In contrast, in human population, every child is important, because a woman is less fertile than an average animal female. The reason is that a big brain size requires baby’s head to be relatively large, which makes child delivery a painful and dangerous process (much more dangerous than in other species). Second, the amount of information children have to accumulate during maturation is much bigger than that in other species, which means children need a support and protection during a very long period, and an average woman cannot provide it alone (of course, all said above relates to pre-historical times, the times when *Homo sapience* as a biological species formed; in modern societies, the situation may be different).

All said above implies that for humans the male’s role is not limited with transferring his genes to a child. Moreover, the strategy that makes an emphasys at mating with the maximal number of women may be not fruitful, but harmful because it minimizes the man’s role in protecting and raising of each individual child.

Accordingly, for a woman, an ideal partner is not the partner with the most attractive phenotype, but the partner that will be taking care of their common children. How can a woman find such a partner? By being attractive for a maximally long period of time: if the man will stay with her and take care of her, he will take care of their children too.

In summary, the evolutionary role of each individual consists in maximising the efficiency of transfer of its genes to offsprings (only those offsprings counts that will survive until their maturity). Different species achieve this using different strategies:

I. In animal species with sexual dimorphism:
   - a female selects a male with the best possible set of genes (using male’s phenotype as an indicator), which will increase the chances of survival of the offsprings.
   - a male tries to mate with the maximal number of females; for a male, “to be a good father” means literally “to be a father”: a male with attractive phenotype (which serves as

an indicator of good genes) mates with many females, whereas less attractive males leave no offsprings, thereby eliminating their genes from the population.

II. In humans:
- a woman tries to find a man who will provide maximal support for her and her children for as long time as possible; to achieve that, a woman needs to be maximally attractive for a man during the time children are being raised. Accordingly, the man who selects this concrete woman is more likely to stay with her for a longer period of time, and he will take care of her children.
- for a man, “to be a good father” means not only to transfer his genes to children, but to participate in raising children; a man who provides little or no support for his children decreases the chances of survival of his genes.

Is this difference in behaviour of humans and animals determined genetically of socially? This question is a subject of debates, especially among feminists, who consider a desire of a woman to look attractive (they call it “sexual objectification”) as a result of centuries of pressure by patriarchal society. However, some recent research made in countries with long traditions of gender equality (which means patriarchal social stereotypes do not affect woman’s behaviour in these societies) demonstrate that this aspect of human behaviour may be genetically determined, and social stereotypes play a secondary role.

COMPUTER SCIENCE

- You can write and compile your code here: http://www.tutorialspoint.com/codingground.htm
- Your program should be written in Java or Python
- No GUI should be used in your program: eg., easygui in Python. All problems in POM require only text input and output. GUI usage complicates solution validation, for which we are also using *codingground* site. Solutions with GUI will have points deducted or won't receive any points at all.
- Please make sure that the code compiles and runs on http://www.tutorialspoint.com/codingground.htm before submitting it.
- Any input data specified in the problem should be supplied as user input, not hard-coded into the text of the program.
- Submit the problem in a plain text file, such as .txt, .dat, etc. **No .pdf, .doc, .docx, etc!**

5 points:

Given an 1-D array of integers, your program needs to find which two cells of non-equal value have the greatest number of cells separating them. Your program should enter the array on input. Please indicate the farthest cells in the output of your program in some way.

Example:
Input:
1, 1, 2, 2, 0, 1
Output:
(1,1,2,2,0),1

Solution:

Java:

```
/*
the longest chain cannot be inside; it must terminate at either end
so if both ends have the same symbols then we move toward the middle from
both ends until either end does not match the other end anymore
*/

import java.io.BufferedReader;
import java.io.InputStreamReader;
import java.util.ArrayList;
import java.util.Arrays;

public class LongestNonEqual5 {
  public static void main(String[] args) throws Exception {
    System.out.println("enter a line with symbols separated by comma: ");
    BufferedReader br = new BufferedReader(new InputStreamReader(System.in));
```

```
    String line = br.readLine().trim();
    ArrayList<String> a = new ArrayList<>(Arrays.asList(line.split("\\s*,\\s*")));
    System.out.println(a);
    int i = 0; // left index
    int j = a.size() - 1; // right index
    if(a.get(i).equals(a.get(j))) {
      while(i <= j) {
        i++;
        j--;
        if(i > j)
          break;
        if(!a.get(i).equals(a.get(a.size()-1))) {
          j = a.size() - 1;
          break;
        }
        if(!a.get(0).equals(a.get(j))) {
          i = 0;
          break;
        }
      }
    }
    if(i > j)
          System.out.println("there is no solution - all values are equal");
    else {
      a.add(i, "(");
      a.add(j+2, ")");
      System.out.println(a);
    }
    System.out.println("end.");
  }
}
/* =>
[1, 1, 2, 2, 0, 1]
[(, 1, 1, 2, 2, 0, ), 1]
*/
```

Python:

```
"""
the longest chain cannot be inside; it must terminate at either end
so if both ends have the same symbols then we move toward the middle from
both ends until either end does not match the other end anymore
"""
import numpy as np

a = list(map(str.strip, input("enter a line with symbols separated by comma: ").split(',')))
print(a)
i = 0 # left index
j = len(a) - 1 # right index
if a[i] == a[j]:
  while i <= j:
    i += 1
    j -= 1
    if i > j:
      #j = i
      break
    if a[i] != a[len(a)-1]:
```

```
      j = len(a) - 1
      break
    if a[0] != a[j]:
      i = 0
      break
if i > j:
  print("there is no solution - all values are equal")
else:
  a.insert(i, '(')
  a.insert(j+2, ')')
  print(a)
print("end.")
```

10 points:

Same as the above, but with an additional condition that the values of the determined "outside" cells cannot repeat between them.

For example, if we take the same input as in the 5 pts problem:
1, 1, 2, 2, 0, 1
the same solution will not stand as then value 1 will repeat within the sub-array between the outside cells. Correct solution in this case is
1,(1,2,2,0),1

To make the problem even more interesting (and to make your program more efficient), try to avoid nested loops in your program (that is a loop within a loop).

Solution:

Java:

```
/*
we scan the entire array keeping track of the longest chain for
each pair of symbols which does not have the end-point symbols inside
*/

import java.io.BufferedReader;
import java.io.InputStreamReader;
import java.util.*;

interface PairParam {} // marker interface

class DiffBookEnds implements PairParam {
  int maxStart;
  int maxEnd;
  boolean seen;
}
```

```
class SameBookEnds implements PairParam {
  int curStart;

  SameBookEnds(int curStart) {
    this.curStart = curStart;
  }
}

public class LongestNonEqual10 {
  public static void main(String[] args) throws Exception {
    System.out.println("enter a line with symbols separated by comma: ");
    BufferedReader br = new BufferedReader(new InputStreamReader(System.in));
    String line = br.readLine().trim();
    ArrayList<String> a = new ArrayList<>(Arrays.asList(line.split("\\s*,\\s*")));
    System.out.println(a);

    // symbol         -> symbol (different) -> (max_start, max_end, seen)
    //                           (same)      -> cur_start
    // sequence start    sequence end
    Map<String, Map<String, PairParam>> distances = new HashMap<>();
    Set<String> symbols = new HashSet<>();
    int maxMaxStart = 0;
    int maxMaxEnd = -1;
    int i = 0;
    for(; i<a.size(); i++) {
      String endSymbol = a.get(i);
      if(!distances.containsKey(endSymbol)) { // 1st time we see this symbol
        symbols.add(endSymbol);
        Map<String, PairParam> val = new HashMap<>();
        val.put(endSymbol, new SameBookEnds(i));
        distances.put(endSymbol, val);
      }

      Map<String, PairParam> val = distances.get(endSymbol);
      SameBookEnds curStart = (SameBookEnds)val.get(endSymbol);
      curStart.curStart = i;
      val.put(endSymbol, curStart);
      distances.put(endSymbol, val);

      // reset seen to 0
      for(String startSymbol : symbols) {
        if(!startSymbol.equals(endSymbol) && distances.get(endSymbol).containsKey(startSymbol))
{ // different symbol
          Map<String, PairParam> x = distances.get(endSymbol);
          DiffBookEnds x2 = (DiffBookEnds)x.get(startSymbol);
          x2.seen = false;
          x.put(startSymbol, x2);
          distances.put(endSymbol, x);
        }
      }

      for(String startSymbol : symbols) {
        if(!startSymbol.equals(endSymbol)) { // different symbol
                                                                    int       curStartInd       =
((SameBookEnds)distances.get(startSymbol).get(startSymbol)).curStart;
          if(!distances.get(startSymbol).containsKey(endSymbol)) {
```

```
            Map<String, PairParam> x = distances.get(startSymbol);
            DiffBookEnds x2 = new DiffBookEnds();
            x2.maxStart = curStartInd;
            x2.maxEnd = i;
            x2.seen = true;
            x.put(endSymbol, x2);
            distances.put(startSymbol, x);
            if(i-curStartInd > maxMaxEnd-maxMaxStart) { // update global max
              maxMaxStart = curStartInd;
              maxMaxEnd = i;
            }
          }
          else {
            Map<String, PairParam> x = distances.get(startSymbol);
            DiffBookEnds x2 = (DiffBookEnds)x.get(endSymbol);
            if(!x2.seen && i-curStartInd > x2.maxEnd-x2.maxStart) { // new max
              x2.maxStart = curStartInd;
              x2.maxEnd = i;
              x2.seen = true;
              x.put(endSymbol, x2);
              distances.put(startSymbol, x);
              if(i-curStartInd > maxMaxEnd-maxMaxStart) { // update global max
                maxMaxStart = curStartInd;
                maxMaxEnd = i;
              }
            }
            else {
              x2.seen = true;  // mark seen
              x.put(endSymbol, x2);
              distances.put(startSymbol, x);
            }
          }
        }
      }
    }
    //print_distances(distances);
    a.add(maxMaxStart, "(");
    a.add(maxMaxEnd+2, ")");
    System.out.println(a);
    System.out.println("end.");
  }
}
/* =>
[1, 1, 2, 2, 0, 1]
[1, (, 1, 2, 2, 0, ), 1]
*/
```

Python:

```
"""
we scan the entire array keeping track of the longest chain for
each pair of symbols which does not have the end-point symbols inside
"""
import numpy as np

a = list(map(str.strip, input("enter a line with symbols separated by comma: ").split(',')))
print(a)
```

```
def print_distances(d):
  for key1 in sorted(d.keys()):
    for key2 in sorted(d[key1]):
      print("[%s,%s]=%s, " % (key1, key2, d[key1][key2]), end='')
    print("")
  print("")

distances = {} # symbol      -> symbol (different) -> (max_start, max_end, seen)
#                                      (same)      -> cur_start
#              sequence start   sequence end
symbols = set()
(max_max_start, max_max_end) = (0, -1)
for i in range(len(a)):
  end_symbol = a[i]
  if end_symbol not in distances: # 1st time we see this symbol
    symbols.add(end_symbol)
    distances[end_symbol] = {end_symbol : i}

  distances[end_symbol][end_symbol] = i # cur_start
  # reset seen to 0
  for start_symbol in symbols:
    if start_symbol != end_symbol and start_symbol in distances[end_symbol]: # different symbol
      max_start, max_end, seen = distances[end_symbol][start_symbol]
      distances[end_symbol][start_symbol] = (max_start, max_end, 0)
  for start_symbol in symbols:
    if start_symbol != end_symbol: # different symbol
      cur_start_ind = distances[start_symbol][start_symbol]
      if end_symbol not in distances[start_symbol]:
        distances[start_symbol][end_symbol] = (cur_start_ind, i, 1)
        if i-cur_start_ind > max_max_end-max_max_start: # update global max
          max_max_start = cur_start_ind
          max_max_end = i
      else:
        max_start, max_end, seen = distances[start_symbol][end_symbol]
        if not seen and i-cur_start_ind > max_end-max_start:
          distances[start_symbol][end_symbol] = (cur_start_ind, i, 1) # new max
          if i-cur_start_ind > max_max_end-max_max_start: # update global max
            max_max_start = cur_start_ind
            max_max_end = i
        else:
          distances[start_symbol][end_symbol] = (max_start, max_end, 1) # mark seen
# print_distances(distances)
a.insert(max_max_start, '(')
a.insert(max_max_end+2, ')')
print(a)
print("end.")
```