SigmaCamp's *Problem of the Month* Contest

SEPTEMBER 2025

IMPORTANT: For the 2025-2026 season, POM is experimenting with two format changes:

- **Video solutions** must be submitted for each problem.
- Each month will include a **project** (worth 30 points) in place of one or two subjects.
- We now have monthly **POM office hours** where you can ask questions about this month's POM problems! See sigmacamp.org/pom/office-hours for details.

Video Submissions

Starting this year, **all solutions must be accompanied by short videos explaining your work.**

- Videos must be at most **2 minutes long** for 5pt/10pt problems, and at most **6 minutes long** for projects.
- **Solutions must be narrated**, but you do not need to show your face. Acceptable formats include:
  - Screensharing slides or a drawing app (e.g., MS Paint) with narration.
  - Recording a whiteboard, paper, or easel with narration (contents may be pre-written).
  - Speaking directly to the camera.
- **Submit videos as links** (Google Drive, Youtube, Dropbox, etc.). Extra requested files may be submitted as a single PDF file per problem.
- For coding problems, submit your code along with a video explaining your submission. Only **Python-3** (`.py`) and **Java** (`.java`) code submissions are accepted.

Please see sigmacamp.org/pom for full details on the 2025 POM format change.

Physics

5 points:

This problem is about pulleys. If you don't know much about pulleys, **DON'T PANIC!** Links to videos and information can be found at the bottom of the problem. This problem is split into four parts that build on each other.

If you only get through some of the parts, you can get partial points for the ones you do submit. You can also get partial points if your reasoning is on the right path. Since September is the first month of POM, we will be very generous with partial credit when grading.

Additional information that may be helpful is provided at the end of the problem.

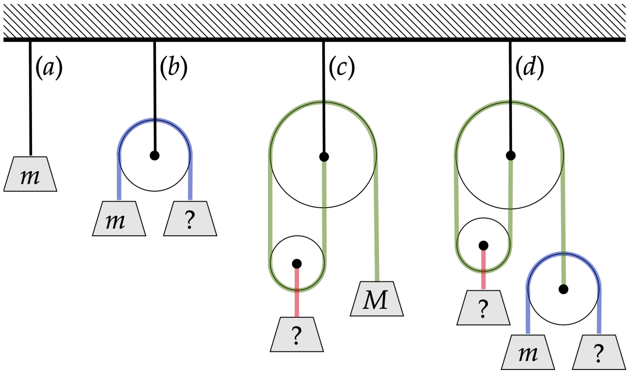


Figure 1: Diagrams for the 5 point Physics problem. All lines, black and coloured, represent strings. Circles represent pulleys, and grey trapezoids represent weights. If a weight is labelled with a letter, that letter represents the weight's mass.

All of the systems in this problem are assumed to be at rest (that is, all masses and pulleys are stationary). The ropes and pulleys are massless.

(a) (0 points) In Figure 1(a), what is the tension in the black string? (Since this is worth 0 points, the answer to this part is at the end of the problem, and you are not require to submit the solution. But think about it before you go look at the answer.)

(b) (1 point) In Figure 1(b), what is the tension in the blue rope? What is the mass of the weight labeled with a question mark? What is the tension in the black rope?

(c) (1 point) In Figure 1(c), what is the tension in the green rope? What is the tension in the red rope? What is the mass of the weight labeled with a question mark?

(d) (3 points) In Figure 1(d), what are the masses of the weights labeled with question marks? Which tensions do you need to compute to find them?

Additional information

- Tension is a force transmitted through a string due to it stretching/being pulled. While physical strings in the real world can be quite complicated (for example, they can stretch, fray, or behave like a spring), in an idealized problem we make a very simple approximation – they have no mass, and they cannot stretch. This simple approximation is often good enough for many real-world applications. This video is a really good introduction to tension and other forces.
- The force due to gravity on an object of mass m on the earth's surface is $F_g = mg$, where $g = 9.81\text{m/s}^2$. However, g is often approximated as 10m/s^2. You may use this approximation in your solutions.

- Newton's second law states that the acceleration $\vec{a}$ of an object of mass m is related to the net forces $\vec{F}_{net}$ acting on the object as follows: $\vec{F}_{net} = m\vec{a}$.
- When working on problems with multiple masses, it is often convenient to draw what is called a "free body diagram" for each mass (here's a good video). A free body diagram for an object is a diagram indicating all the forces acting on the object. Such a diagram can be used to find an equation for the net force on the object.
- You might find this block-and-tackle video good for improving your intuition about how pulleys work. This article goes into more depth. It is especially useful for part (c).

The answer to (a) is that mass pulls down with force $F_g = mg$, so to counterbalance it, the tension in the rope must be mg.

Hint:

First, consider any of the ropes. Any point on the rope has the same tension as any other point on that same rope. If this rope is vertical, for example, this means that everything above that rope is being dragged down with force equal to the tension, and everything below is being dragged up with that same force.

Now, consider any of the pulleys. If you draw a box around a pulley, there will be ropes coming out of that box in various directions. If the pulley is not moving anywhere, this means all the tensions in those ropes must cancel each other out.

These two principles are enough to solve the problem.

Solution:

The key idea here is that if an object is not moving, its acceleration $\vec{a} = \vec{0}$. By Newton's second law, $\vec{F}_{\text{net}} = m\vec{a}$, so $\vec{F}_{\text{net}} = 0$ for an object at rest.

(b) Each of the two weights in this problem experiences two forces: gravitational pulling down, and tension pulling up. Thus, the net force on the left weight is $F_{\text{net},l} = T - mg$. In order for the net force on the left weight to be 0, $T = mg$. Similarly, $T = m_{right}g$, where m_{right} is the mass of the right weight. Thus, $m_{right} = m$. In order for the pulley to not move, the total system must be in equilibrium. Here, we apply the same analysis that we did on the individual weights, but taking all of the weights into account. Thus, $\vec{F}_{\text{net}} = 0 = T_{black} - 2mg$, so $T_{black} = 2mg$.

(c) We can solve this problem by moving from the right to the left. Similarly to part (b), the weight with mass M experiences a downward gravitational force, and a tensional force upwards. Because the system is at rest, $F_{\text{net},r} = 0 = T - Mg$. Thus, we can determine the tension in the green rope: $T_{green} = Mg$. Moving to the left, we can then break down the forces on the left pulley: $F_{\text{net},l} = 0 = 2 \cdot T_{green} - m_{left} \cdot g$, where m_{left} is the mass of the left weight. Thus, $m_{left} = 2M$. Finally, we can solve for the tension of the red rope, T_{red}. This is similar to part (a) — the mass pulls down with force $2Mg$, so $T_{red} = 2Mg$.

(d) This problem is a combination of parts (b) and (c). Similarly to part (c), we'll solve this by moving from the right to the left. In general, many physics problems that may look a bit scary at the outset can be made more approachable by breaking them into parts and dealing with one thing at a time. From our solution to part (b), we can analyze the blue pulley, and determine that $m_{right} = m$ by determining the tension in the blue rope. We now know that the mass of the right pulley is equal to $2m$, and thus its weight is $2mg$. We can then determine the tension in the green rope by analyzing the forces on the right: $F_{\text{net},r} = 0 = T_{green} - 2mg$. When we move to the left, we'll once again break down the forces on the left pulley: $F_{\text{net},l} = 0 = 2 \cdot T_{green} - m_{left} \cdot g$. Thus, $m_{left} = 4m$. We've determined the masses of both weights, and we needed to determine the tensions in the blue, green, and red ropes.

10 points:

(a) (2 points) Consider the system of blocks and pulleys drawn in in Fig. 2(a). All blocks are frictionless. Pulleys and ropes have no mass. In the absence of all external forces besides gravity, find the accel-

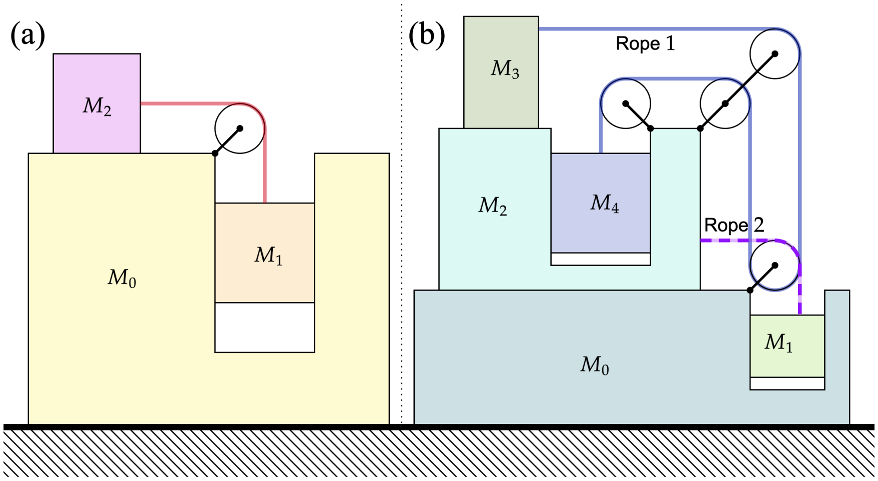


Figure 2: Diagram for the 10 point Physics problem.

eration of M_0 in terms of M_1 and M_2. This is a standard problem – using external resources in your solution is allowed, but you must cite them.

(b) (8 points) Consider the block and pulley system shown in Fig. 2 (b). Find the initial acceleration of M_0 in terms of M_1, M_2, M_3, and M_4. Make the following simplifying assumptions:

- There is no friction between blocks, between M_0 and the ground, or between the rope and the blocks.
- There is no slipping between either rope and the pulley. In particular, note that both ropes are wrapped around the *same* pulley.
- The sizes of the drilled holes are such that M_1 and M_4 can only move vertically, not swing horizontally.

Hint:

Part (a) is a very standard textbook problem – some googling may give a pedagogical solution, for example here. You are welcome to use these sources, but you must cite them. Problem (b) may be solved by the same methods as (a).

Solution:

(a) We solve this problem by noting that the force applied to the system is due to the gravitational potential energy of M_1. One can see, by staring at the diagram, that once the system starts M_1 will fall. As it falls, its gravitational potential energy will decrease and be transferred into kinetic energy. This kinetic energy will be distributed among M_1, M_2, and M_0.

We also note that the system must satisfy two constraints. First, M_1 and M_2 are tied by an unstretchable string, so if we know how far M_1 moved, we know how far M_2 moved. Second, there are no net forces on the whole system in the horizontal direction, so its center of mass stays constant. If we know how far M_1 and M_2 move, we also know how far M_0 moves. We can therefore solve for the positions of M_2 and M_1 in terms of M_0.

Let x_0, x_1, and x_2 respectively represent how far M_0, M_1, and M_2 have moved along the x direction from their starting point. Suppose M_1 drops by a distance h. This means that M_2 has moved by a distance h relative to M_0. M_1 and M_0 have no relative horizontal velocity. We therefore can write

$$\begin{aligned}
&x_1 = x_0, \\
&x_2 - x_0 = h, \\
&(M_0 + M_1)x_0 + M_2 x_2 = 0, \\
&\implies (M_0 + M_1)x_0 + M_2(x_0 + h) = 0, \\
&\implies x_0 = -\frac{M_2 h}{M_0 + M_1 + M_2}, \quad x_2 = \frac{(M_1 + M_0)h}{M_0 + M_1 + M_2}.
\end{aligned} \tag{1}$$

The total kinetic energy of the system can be expressed in terms of the rate of change of h, which we can call v_h. Let v_0, v_1, and v_2 represent the rates of change of x_0, x_1, and x_2:

$$\begin{aligned}
KE &= \frac{1}{2}\left(M_1 v_1^2 + M_2 v_2^2 + M_0 v_0^2\right) + \frac{1}{2} M_1 v_h^2 \\
&= \frac{1}{2}\left[M_1 + (M_1 + M_0)\left(\frac{M_2}{M_0 + M_1 + M_2}\right)^2 + M_2\left(\frac{M_1 + M_0}{M_0 + M_1 + M_2}\right)^2\right] v_h^2 \\
&= \frac{1}{2}\left[M_1 + \frac{M_2(M_1 + M_0)}{M_2 + M_1 + M_0}\right] v_h^2
\end{aligned} \tag{2}$$

The prefactor of v_h^2 in the above expression may be recognized as an effective mass. Using $F = ma$ and the gravitational force, we find the acceleration a_h is

$$a_h = \frac{M_1}{M_1 + \frac{M_2(M_1+M_0)}{M_2+M_1+M_0}} g. \tag{3}$$

The acceleration of x_0, which we are after, is then

$$a_0 = -\frac{M_1}{M_1 + \frac{M_2(M_1+M_0)}{M_2+M_1+M_0}} \frac{M_2}{M_0 + M_1 + M_2} = -\frac{M_1 M_2}{M_1(M_0 + M_1 + M_2) + M_2(M_1 + M_0)}. \tag{4}$$

(b) Part (b) proceeds identically in strategy, with some more complicated algebra. For convenience, call $M_{tot} = M_0 + M_1 + M_2 + M_3 + M_4$. Now, the fact that rope 1 and rope 2 are wrapped around the same pulley ensures that if M_1 drops by height h, M_4 *also* drops by height h. In the horizontal direction, we have five mass positions x_0 through x_4. The constraints between them are:

$$\begin{aligned}
&x_1 = x_0, \\
&x_2 = x_4, \\
&M_0 x_0 + M_1 x_1 + M_2 x_2 + M_3 x_3 + M_4 x_4 = 0, \\
&x_2 - x_0 = h, \\
&x_3 - x_2 = h, \\
&\implies (M_0 + M_1)x_0 + (M_2 + M_4)(x_0 + h) + M_3(x_0 + 2h) = 0, \\
&\implies x_0 = -\frac{M_2 + M_4 + 2M_3}{M_{tot}} h, \quad x_2 = \frac{M_0 + M_1 - M_3}{M_{tot}} h, \quad x_3 = \frac{M_2 + M_4 + 2(M_0 + M_1)}{M_{tot}} h.
\end{aligned} \tag{5}$$

The kinetic energy is:

$$\begin{aligned}KE = \frac{1}{2}\Bigg[M_1 + M_4 + (M_1 + M_0)\left(\frac{(M_2 + M_4 + 2M_3)}{M_{tot}}\right)^2 + (M_2 + M_4)\left(\frac{(M_0 + M_1 - M_3)}{M_{tot}}\right)^2 + \\ + M_3\left(\frac{M_2 + M_4 + 2(M_0 + M_1)}{M_{tot}}\right)^2\Bigg] v_h^2 = \\ \frac{1}{2}\left[\frac{M_1^2 + 2M_1M_2 + 5M_1M_3 + M_2M_3 + (3M_1 + M_2 + 2M_3)M_4 + M_0(M_1 + M_2 + 4M_3 + 2M_4)}{M_{tot}}\right] v_h^2.\end{aligned} \tag{6}$$

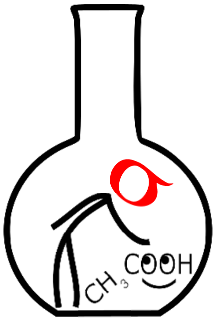
The force downward is now $F_g = (M_1 + M_4)g$, so the acceleration of M_1 and M_4 downwards is

$$a_h = \frac{(M_1 + M_4)M_{tot}g}{M_1^2 + 2M_1M_2 + 5M_1M_3 + M_2M_3 + (3M_1 + M_2 + 2M_3)M_4 + M_0(M_1 + M_2 + 4M_3 + 2M_4)}. \tag{7}$$

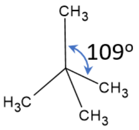
We can therefore deduce that the acceleration of x_0 is

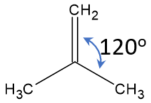
$$a_0 = -\frac{(M_1 + M_4)(M_2 + M_4 + 2M_3)g}{M_1^2 + 2M_1M_2 + 5M_1M_3 + M_2M_3 + (3M_1 + M_2 + 2M_3)M_4 + M_0(M_1 + M_2 + 4M_3 + 2M_4)}. \tag{8}$$

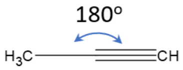
Chemistry

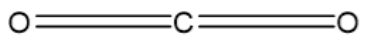


In the second half of the 19th century, chemists realized that molecules are not random heaps of atoms: their atoms are arranged according to rules, and each molecule has a definite three-dimensional shape. They later showed that a molecule's geometry can be inferred from the types and numbers of bonds between its atoms. For example, a carbon atom with four single bonds has tetrahedral geometry with bond angles of about 109.5°. A carbon involved in a double bond is trigonal planar with angles near 120°. A carbon in a triple bond is linear, giving 180° bond angles; the same linear geometry occurs when a carbon forms two double bonds to two different atoms (as in CO2).

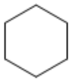








When an organic molecule contains only single bonds, it tends to adopt conformations with bond angles close to 109.5°. Single bonds usually allow rotation, which lets the molecule relieve strain. Cyclohexane, for instance, would have 120° angles if it were a flat hexagon, but it never adopts that planar form because it would be too strained. Instead, the ring puckers into the chair conformation, in which the C–C bonds are staggered (wedged bonds point toward the viewer and dashed bonds away from the plane of the page, see figure below).

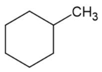


What if the optimal angles cannot be achieved, even after bond rotation? That occurs, for example, in small rings such as cyclopropane and cyclobutane (three- and four-membered rings). In such cases the molecule experiences ring strain—especially angle and torsional strain—because the bonds cannot adopt their preferred geometries. These molecules can exist, but they are higher in energy than expected. Strain can arise not only in very small (and sometimes very large) rings, but whenever a molecule cannot adopt a conformation with near-optimal bond angles and torsional relationships. Significant strain raises a compound's energy, making it more reactive and increasing its heat of combustion. If the strain is extreme, the molecule becomes too reactive to isolate and is considered unstable.

To help with the following problems, you may build models of these molecules using toothpicks and clay beads and examine how their valence-bond angles are distorted. To simplify modelling, you may represent methyl group as balls (just make sure their radius is realistic: not too big and not too small). When building the models, remember that H–C and C–C bond lengths differ. **To facilitate grading, please attach the pictures of the models you made for both problems, along with brief explanations in one PDF file.**

5 points:

The hydrocarbons 1-5 shown below have the same empirical formula, C_7H_{14}.



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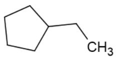

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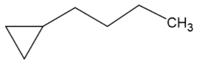

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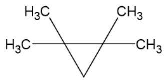

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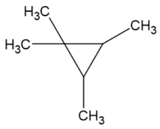

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Consequently, their combustion produces the same amounts of CO_2 and H_2O, so the balanced combustion equation is identical for all five. However, their heat released during combustion is different. Rank compounds 1-5 from highest to lowest heat release during combustion. As mentioned above, you may build models of the molecules to help you, and attach images.

Hint:

As you can see, all these molecules contain only two types of bonds—carbon–carbon and carbon–hydrogen—and each molecule has the same number of each. Their combustion products are also identical, and the numbers of H_2O and CO_2 molecules formed are the same. In any reaction, however, the energy released equals the difference between the energies of the reactants and the products.

A compound's energy is often approximated as the sum of its bond energies. By that logic, these compounds should produce the the same heat during combustion. Yet they do not, because their geometries differ: in some molecules, the bond angles are suboptimal, introducing strain. Clearly, when strained molecules burn, the energy of that strain is released, thereby increasing heat of combustion. If you identify which bond angles are suboptimal and the extent of the geometric distortion, you can arrive at the correct explanation.

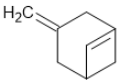
Solution:

The energy released by each compound will vary depending on its stability, or more specifically, its degree of strain. A highly strained molecule takes more energy to form, and also releases more energy when it is destroyed. So we are looking to rank the molecules from most strained (highest heat) to least strained (lowest heat.)

The first source of strain to consider is angle strain. When carbon is bonded to 4 groups, those groups tend to arrange themselves as far apart as possible, forming 109.5 degree angles (the angle between vertices and the center of a regular tetrahedron.) If carbon atoms are forced to have smaller bond angles, this causes strain. For compound 1, a flat hexagon has 120-degree angles at each of its vertices; but the compound can bend in 3D to form a "chair" configuration, where each carbon atom has an exactly 109.5 degree angle between it and its neighbors. For compound 2, a pentagonal ring has 108 degree angles between its atoms, which is close to ideal, generating only a small amount of strain. For compounds 3-5, a triangular ring has 60 degree bond angles and no ability to bend out of plane, generating a very high amount of strain.

10 points:

The image shows several organic molecules drawn in standard notation (carbon atoms are implied at the vertices, and hydrogens on carbon are omitted, except in methyl groups).



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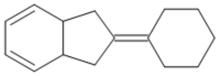

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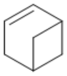

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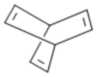

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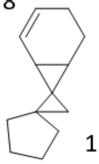

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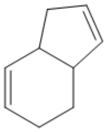

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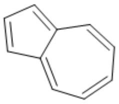

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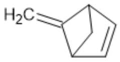

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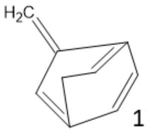

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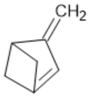

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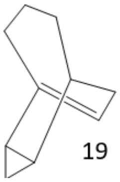

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Given that compounds 2–4 exist at room temperature, whereas 1 and 5 do not, identify which other compounds in the set are stable and can be prepared in pure form. As mentioned above, you may build models of the molecules to help you visualize these molecules and identify possible steric strain, and attach images.

Hint:

Consider the geometry of carbon atoms involved in double bonds. Ideally, they are perfectly planar: the carbon atom, its double-bonded partner, and the two other atoms attached to it all lie in the same plane. Any deviation from planarity—even by a single atom—comes with a significant energetic penalty.

Solution:

Featured Solution

by Julia Gilman

https://www.youtube.com/watch?v=JNnm52YZj84

Official solution below.

Compounds 2, 3, 4, 6, 7, 9, 12, 13, 14, 15, 16 can be prepared. Compounds 1, 5, 8, 10, 11, 17, 18, 19 are not stable.

In order for a carbon's orbitals to properly align and form a double bond, the bond must be planar. This means that the two bonded carbons, as well as all of the other atoms bonded to them, must lie on the same plane.

Many of the compounds in this problem are bridged rings, meaning that they are two rings that are connected, not by a single bond but by a chain of several bonds; think of it like two rings "joined at the hip." Necessarily, that means that at least one of the rings, or the bridge between the rings, needs to jut out of plane in order to keep the orbitals from becoming too tightly compressed (see 5pt for a discussion of this). Therefore, the two carbons connecting the rings to the bridge cannot be planar, and so cannot form any double bonds. This is known as Bredt's rule.

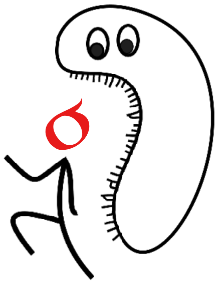
Any molecule that violates Bredt's rule, i.e. has

1. two rings,
2. a bridge between those two rings that consists of > 1 bond, and
3. a double bond attached to any carbon that connects the bridge to the bridge to the rings

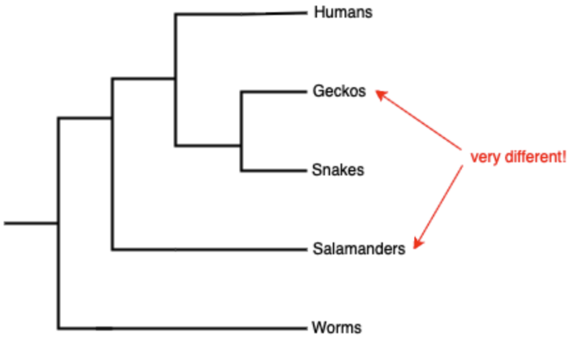
is called an anti-Bredt compound and will not be stable. This rules out all of the compounds listed as unstable above.

It turns out that all of the other compounds can indeed be prepared. Some of these may be surprising, so we can take a look at a few weird ones. Compounds 9 and 16

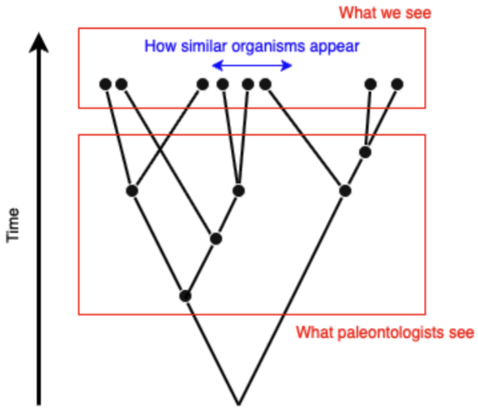
Biology



Some species can look similar morphologically, but be very different in terms of their biological function and evolutionary history, and vice versa. For example, salamanders and geckos are actually very distant types of organisms, even more so than geckos and humans. Snakes are even more distant from worms. Clearly, morphological adaptations don't tell the full story about what makes species different.



An even more drastic example of this effect can be found in the microscopic world. Microbes that are vastly different in terms of how they function as organisms can be very hard to tell apart by sight. Even genetic analysis can prove complicated because of effects like *horizontal gene transfer* and *endosymbiosis*.



Whether it's animals or bacteria, just looking at an organism isn't enough to tell you about its history and biology.

Below are some optional interactive resources that may help you think through this problem or explore it further. You are not required to use them, they are provided as additional references if you'd like more context or guidance:

Tree of Life Web Project

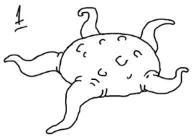
One Zoom Tree of Life Explorer

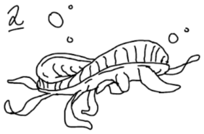
5 points:

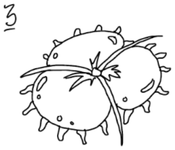
The Sigmanauts discovered a distant planet teeming with life, and two teams of biologists began studying its inhabitants. The first team concentrated on the anatomy and morphology of the local creatures. Based on their observations, they proposed that all species could be divided into six major groups according to outward appearance and lifestyle:

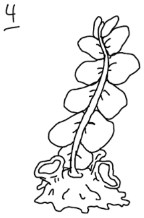
1. Animals with five legs.
2. Freely swimming, disk-shaped creatures with seven fins.
3. Animals displaying threefold symmetry.
4. Sedentary, feather-bodied forms.
5. Amorphous, blob-like organisms.
6. Multi-legged animals exhibiting screw-axis symmetry.

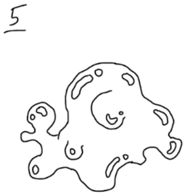
They also made some drawings of representative organisms from each of these six groups:





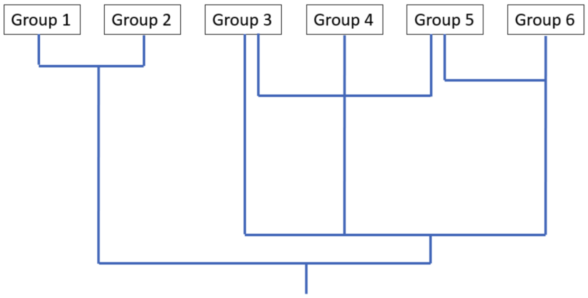






Meanwhile, the second team of biologists focused on genomic research. They quickly learned how to read the genetic code of local organisms, sampling 10–15 species from each of the six groups. By sequencing their genomes, they were able to reconstruct an evolutionary tree that traced all modern lineages back to a common—but now extinct—ancestor.

The tree is shown below.



How do you explain the architecture of this tree? Which evolutionary events could have led to this topology? Provide similar examples from the Earth's evolutionary tree. In your answer, assume that the evolution on that planet occurs mostly by the accumulation of mutations. Be specific.

Hint:

No hint this month.

Solution:

Symmetry in Body Structure

A key idea is the concept of symmetry in organisms. The structure and body plan of an organism can have a variety of symmetries, and this has a lot of implications for how the organism develops and how it functions. On Earth, most animals have **bilateral symmetry**, meaning their left and right halves are similar. On this planet, **radial symmetry** seems common, meaning that organisms' bodies have some sort of rotational symmetry. Groups 1 and 2 clearly diverged early in evolutionary history, and both share an odd-fold radial symmetry; this could be a conserved trait of their clade. However, note that another group (group 3) also has odd-fold radial symmetry, and that organisms from different evolutionary branches actually evolved into this group independently. Thus, we can guess that the organisms on this planet exhibited convergent evolution towards odd-fold radial symmetry.

An example of this phenomenon is the evolution of sponges, jellyfish, corals, and starfish. Sponges, jellyfish, and corals are very distant animals from humans, whose ancestors diverged early in evolutionary history; these are the canonical examples of radially symmetric organisms. By contrast, starfish ancestors diverged much later, and starfish are even more closely related to humans than other terrestrial animals like arthropods. Starfish, although technically bilaterally symmetric, are clearly able to develop body plans that appear five-fold symmetric, an example of **convergent evolution** towards an odd-fold symmetry body plan.

Modes of Evolution

Note that groups 3, 4, and 5 consist of organisms that developed from a common ancestor. This is an example of **evolutionary radiation**, a phenomenon where many new species rapidly evolve from a single species.

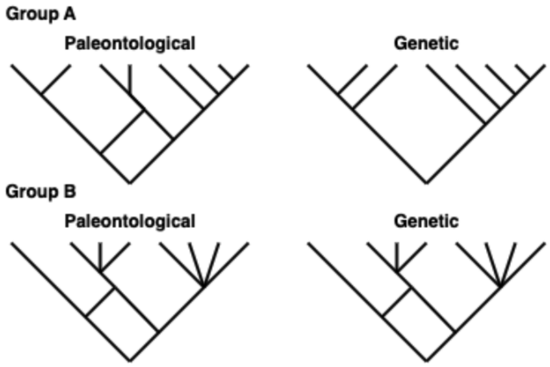
It is still likely that the organisms that share this ancestor have some common features, but they might be hard to see. In this example, we see that the ancestor diversified into multiple lineages, with many descendants more similar to unrelated organisms than to each other. A good example can be found in the evolution of lizards. Their modern descendants include snakes, other reptiles, and even birds. Birds, in particular, appear distinct, akin to group 4 standing alone. Some lizards may resemble amphibians, which are not lizards but still evolved from lobe-finned fish, akin to some organisms in group 3 resembling other group 3 organisms, which share a more distant common ancestor. Snakes resemble eels in structure, despite being very distantly related, akin to group 5.

Group 6 is clearly a unique group of organisms that nevertheless diverged fairly recently. Some good examples are marine/ocean mammals, like cetaceans (whales, dolphins), pinnipeds (seals, sea lions), and sirenians (manatees). Each of these groups evolved from a land species relatively recently, but obviously has a very different structure and ecology; cetaceans evolved from hoofed animals, pinnipeds from canines, and sirenians from elephant ancestors. This is an example of how intense evolutionary pressure can cause organisms to change their morphology very rapidly.

For more information about symmetry, visit this website.
For more examples and information about convergent evolution, visit this website.

10 points:

The Sigmanauts then traveled to another planet with life. They looked at two different groups of animals and similarly prepared two evolutionary trees for each group; one constructed only from paleontological data, and one from genetic analysis.



One of these groups of animals was extensively subjected to interspecific gene transfer early in its evolutionary history, and the other was not. Which is which?

Hint:

No hint this month.

Solution:

Featured Solution

by Giselle Kurbatova

https://youtube.com/watch?v=cD15wcFbBVM

Featured Solution

by Sofya Salova

https://www.youtube.com/watch?v=d8Ej5QGUZeE

Official solution below.

In both paleontological trees, we see two distinct branches converge into one. At first glance, this might suggest that two separate evolutionary lineages merged into a single species, but that interpretation is not entirely correct. The evolutionary tree can never fully converge: this would result in a species having two ancestors, which is the metaphorical equivalent of a child having two fathers. Despite this, certain phenomena can make it appear as if branches amalgamate, causing species that are evolutionarily distant to appear similar in morphology.

There are two main explanations for the apparent convergence:

Paleontological Convergence

Different species can sometimes be exposed to similar selective evolutionary pressure and evolve similar traits that increase fitness. For instance, bats and birds both evolved wings for flight, even though their last common ancestor (a small, early reptile-like amniote) did not have wings. In paleontological reconstructions, this can cause evolutionarily distant species to appear deceptively close. This had resulted in many mistakes by early zoologists, like the initial placement of sponges and ascidians in the same taxon.

This seems to be the case on Planet A. We can see that the organisms evolved very straightforwardly, with species branching off at a consistent rate. Unfortunately, the paleontological similarity led our scientists astray and to the assumption that some species were more closely related than they really are.

Genetic Convergence

While species cannot truly merge into one, genes can move laterally between species. This is a phenomenon known as **horizontal gene transfer** or **HGT**. This process is common in bacteria and sometimes seen across other species, particularly in viruses.

On Planet B, the convergence of branches on the genealogical tree suggests that interspecies genetic transfer occurred. HGT can make a lineage appear to have multiple distant ancestors if the genomic segments used for analysis include transferred genes. It can also cause evolution to happen in rapid bursts, as newly acquired genes that enable different traits suddenly expand adaptive potential.

Note about Bioinformatic Reconstructions

It is crucial to note that these genetic trees greatly depend on which portion of the genome is analyzed. Typically, scientists use highly conserved genes to reconstruct the "tree of life." Common examples of these include ribosomal RNA (such as 16S in prokaryotes and 18S in eukaryotes). Famously, Carl Woese used 16S rRNA to uncover the three domains of life: Bacteria, Archaea, and Eukarya. It is important to remember that different genes can tell different evolutionary stories, some reflecting vertical descent while others showcase a horizontal exchange. This is why, as scientists learn more and sequence more organisms, we are altering our current knowledge of the "Tree of Life" to create the most accurate understanding of the mosaic representation of evolutionary history.

For more information on gene transfer, visit this website.

Linguistics & Applied Sciences

5 points:

Here are phrases in an artificially constructed language and their translations, **not all in matching order**:

A. Ko gerazami rakoti juzati
B. Tiratizaju migeju
C. Ramirage ramizage
D. Tira mijuzako koge
E. Tiratiraza jugemi
F. Ko gerazara juzati gezamira
G. Timi mijutimi tira
H. Ko tiratiraza timirami gerazami

1. *A short rabbit*
2. *The dog runs quickly*
3. *A tall giraffe*
4. *The rabbit sees a cat*
5. *The sleepy cat runs*
6. *A slow car*
7. *I dance poorly*
8. *You calm me*

Match each phrase to its translation.

Translate the following phrase from the language into English:

> Ko tiratizaju timirami geko

Translate the following phrase from English into the language:

> *The sleepy dog worries you*

Hint:

Here are 3 matches: A5, F2, H4

Solution:

Answer:
Matches - A5, B3, C6, D7, E1, F2, G8, H4

Translations -
- Ko tiratizaju timirami geko → *The giraffe sees well*
- *The sleepy dog worries you* → Ko gerazara rakoti mitijumi timi

Explanation:

Note “ko” appears 3 times on the left and “the” appears 3 times on the right. ”A” on the right which also appears 3 times on the right is ruled out as its sentences are shorter.

That leaves us with:

- 2. *The dog runs quickly*
- 4. *The rabbit sees a cat*
- 5. *The sleepy cat runs*
- A. Ko gerazami rakoti juzati

- F. Ko gerazara juzati gezamira
- H. Ko tiratiraza timirami gerazami

We see juzati and gerazami appear twice, so one is *cat* and one is *runs*. Gerazami is *cat* as it has a similar word gerazara, which will then be *dog*. that means tiratiraza is *rabbit*, and the general structure is "SUBJECT [EVERYTHING ELSE]."

Since juzati is runs that means the rakoti in A is *sleepy* and the gezamira is *quickly*, leaving timirami as *sees*. From this we conclude the structure is "SUBJECT (ADJECTIVE) VERB (ADVERB) (OBJECT)" (parentheses mean optional component).

The rest of the matches can be made from there, noting some common prefix patterns and unique words.

For the first translation, we know ko tiratizaju is *the giraffe*, and domiremi is *sees*. We also note that migeju is *tall* while jugemi is *short*, and that gezamira is *fast/quickly* while ramizage is *slow*. From this we conclude reversing the order of an adjective inverts its meaning, so geko is the opposite of koge. Since koge means *poorly*, we conclude *geko* means *well* and get the phrase *The giraffe sees well.*

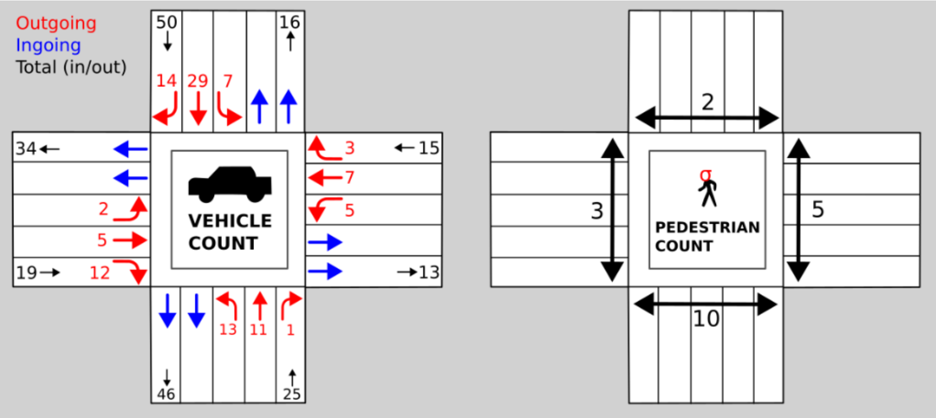
For the second translation, we extend the same rules to verbs, this time inverting mijutimi=*calm* to get Ko gerazara rakoti mitijumi timi.

Note:

The language in this problem is a substituted version of Symmetric Solresol, a language constructed from the 7 musical syllables (do, re, mi, fa, sol, la, si). Check it out!

10 points:

SigmaCity's planning committee is updating the Sigma St & 2025 Ave intersection, citing historically bad congestion. Each side of the fourway intersection has 5 lanes and a pedestrian crossing.

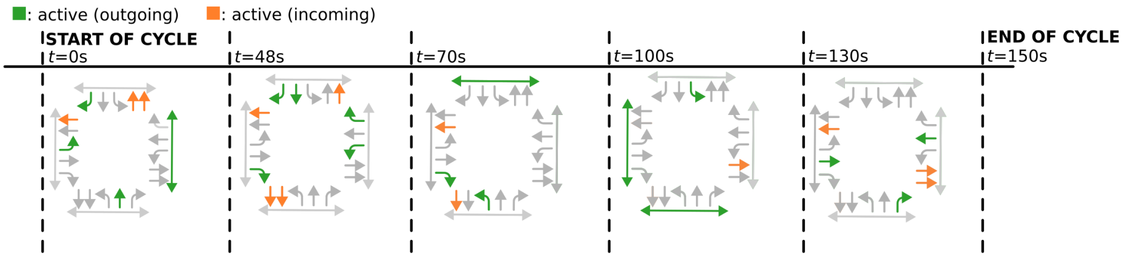


It takes $T = 28 + 2N$ seconds for N pedestrians to cross the street. In 30 seconds, 5 cars can make a turn and 7 cars can go straight across. Remember that 2 lanes can not zipper merge into 1 lane.

A proposed schedule is shown below:

(a) Identify as many problems with the proposed schedule as you can.

(b) Adjust the cycle of the lights to safely allow the number of vehicles/pedestrians indicated in the first figure above to pass the intersection in one cycle (i.e. in one cycle 50 vehicles from the top should get through, 19 from the left, etc. . .).



(c) Design your own schedule that minimizes the duration of the cycle while allowing for the same number of cars and pedestrians.

Explain any additional assumptions you made about the vehicles and the pedestrians.

Note: you do not have to specify your design the same way as the proposed schedule, but it must be clear what lanes/crossings are active at what times, and what the length of your cycle is.

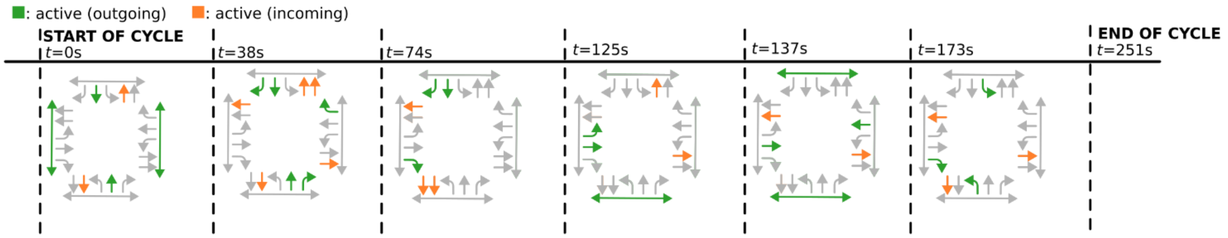
Hint:

No hint this month.

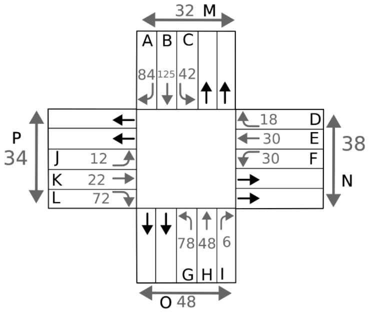
Solution:

(a) There are a lot of issues depending on how you look at it, but the main ones are that not all the cars get through, not all the pedestrians get through, and at $t = 48$s three lanes would merge into two (not allowed by problem statement). Additionally the cycle time is clearly too short for this set up, as we will show in part c.

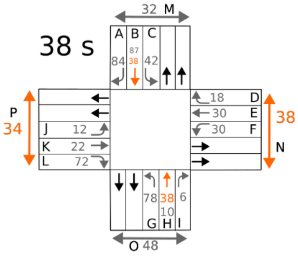
(b) Here is one schedule, there are infinitely many acceptable answers for this part since there isn't an upper limit on time:

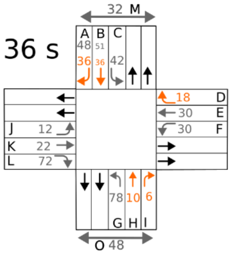


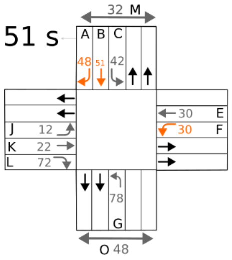
(c) We will convert from the counts of cars and pedestrians to the time each lane must be "active," rounding up (letters are also added as labels to each lane):



First, we can find any schedule will be at least 251 seconds long, as $B + G + O = 251$, and none of B/G/O can be active at the same time. Therefore, we will structure our schedule around when each of those 3 parts is active, which should at least get us close to an optimal solution. We will start with B arbitrarily (in this figure the time represents the cycle duration) Note that we are careful to keep lanes active on consecutive cycles only without gaps, as otherwise we would have to make round down the number of cars:

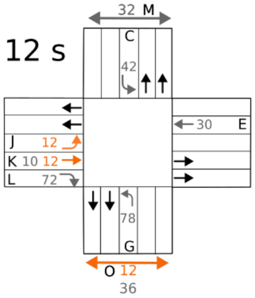


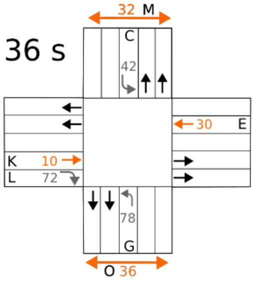




Crossing P and N have very similar times, so it makes sense to run them at once, and then let the north and south bound lanes at once. The second period uses several of the available right turns which rarely interfere with other traffic (L is left for later as it will have a good opportunity, while here it would prevent B+F). The third takes care of F which can not happen with G or O active.

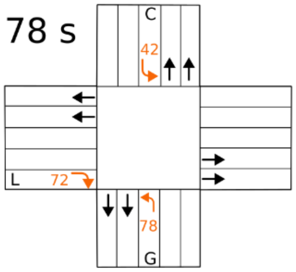
Next we have crossing O active:



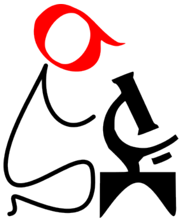


Once more, it is nice to have opposing crosswalks active, though J needs 12 seconds first to clear.

Finally, we clear C, L and G, none of which interfere:



The resulting schedule is the same as the one shown in part (b).



Project (30 points)

Mathematics and Computer Science

This project will ask you to explain some of the theory behind the Fibonacci sequence and related sequences, and to implement algorithms for calculating them. Some of the questions are introductory and others are more involved. We recommend that you consider all the questions in the order they are written, but you are not required to solve any earlier questions to present later ones.

There are many parts and subparts to the project. You may choose to implement the algorithms and/or provide a theoretical answer to any of them. You are not expected to answer and/or implement all of them to get a full score. The theoretical and coding portions will be graded separately. In particular, code with a minimal mathematical explanation, or a theoretical explanation without any accompanying code will both score points.

Given the open nature of some of the questions, the exact scoring will be determined after all submissions are collected and reviewed. As a general guidance, the mathematical part and the implementations will each be worth 15 points total.

The *standard Fibonacci* sequence is a sequence which starts with $1, 1, \ldots$ and where each successive element is the sum of the two elements that precede it. Namely, if we let F_n be the n-th Fibonacci number, we have $F_1 = 1$, $F_2 = 1$, and for each subsequent number $n > 2$, we define $F_n = F_{n-1} + F_{n-2}$. As you most likely have seen before, the first few elements of this sequence are $1, 1, 2, 3, 5, 8, 13, \ldots$

The main goal for this project is to describe and implement algorithms to find F_n and related numbers for large and very large n as quickly and precisely as possible.

There are terms related to the Fibonacci sequence, other similar sequences, and methods to compute these sequences throughout this problem. You are encouraged to use any available sources of information to learn about these terms, ideas, and methods.

The project consists of two parts: Part A is concerned with the Fibonacci sequence, and Part B is concerned with its generalizations. **You do not need to complete all questions to get full points**; for example, you can solve any three questions from Part A and any two questions from part B, or provide partial solutions for all 7 questions.

Part A: Fibonacci sequence

You may choose 3 out of 4 questions to complete in Part A to receive full credit.

1. Besides the standard recursive definition $F_n = F_{n-1} + F_{n-2}$, there are other clever ways to compute Fibonacci numbers. Pick one of these options, research it, and explain how and why it works:

- an explicit formula for F_n using the golden ratio (aka *Binet's formula*);
- matrix multiplication;
- anything else you can find or think of, that is not a straightforward implementation of the definition by a recursive or iterative algorithm.

2. Implement (using Python or Java) **at least two** of the following options for the standard Fibonacci sequence. Your program should output F_n for any n (including large n, up to $n = 10{,}000$), where n is given as input. The possible methods include: recursion, a `for` loop without recursion, matrix multiplication, an explicit formula for F_n using the golden ratio (aka *Binet's formula*), or anything else you can find or think of.

If any of your solutions do not use the recursive definition directly and were not explained before, explain why your program is computing F_n with any needed mathematical details.

3. Using one of the algorithms you wrote in Question 2, or an online list of Fibonacci numbers, determine the number of decimal digits in each of the 20 numbers $F_{100}, F_{200}, \ldots, F_{2000}$.

Create a plot of the number of digits in F_n vs. n; you should see a straight line. What is the slope of this line? Can you connect the slope to the numbers in the explicit formula for F_n?

4. A central concern of algorithms is *runtime*: how long an algorithm takes to run. Any algorithm which finds F_n given n has some runtime $T(n)$. Describing the runtime $T(n)$ exactly is often hard, so we instead focus on the general "shape" of the runtime.

For example, if an algorithm takes some constant time c_{start} to initialize, then loops n times with each loop taking c_1 time at each step, then the total runtime of the implementation is $T(n) = c_{start} + c_1 n$. As n grows, the runtime $T(n)$ becomes almost proportional to n, and we say the runtime is linear. (This notion of *asymptotic* behavior of $T(n)$ as n gets very large is formalized using *big-O notation*, which you may use, but it is not required.)

(a) Before making empirical measurements, make a theoretical prediction for the runtime of two or more of your algorithms in Question 2. Is the runtime proportional to n? To n^2? Some other function of n? Be sure to consider very large n; the runtime depends on the behavior of your algorithm as n grows.

(b) Now, let's validate your prediction with measurements. In Python, this can be done with the `time` package. Here's an example of how you can use it:

```
import time
def fib(n):
    ...
def time_fib(n):
    t0 = time.time()
    fib(n)
    t1 = time.time()
    print("My code runs in" + t1-t0 + "seconds")
```

In Java, you can time your code using the `System.currentTimeMillis()` function.

Create scatter plots of the amount of time it takes your algorithms to evaluate F_n for at least 20 values of n covering the range $1 < n < 20,000$. Do the graphs validate your predictions? (If you are using Python, you are likely to be surprised at this step.)

Part B: Generalizations

You may choose 2 out of 3 questions to complete in Part B to receive full credit.

5. We can define different sequences (sometimes called Lucas sequences) by using the same equation $L_n = L_{n-1} + L_{n-2}$ for $n > 2$, but different initial conditions $L_1 = p_1$, $L_2 = p_2$. For the standard Fibonacci sequence, $p_1 = p_2 = 1$.

(a) Using *generating functions* (see any of the links here, in particular this one), *characteristic polynomials*, or any other method of your choosing, derive the explicit formula for the case $p_1 = 3$, $p_2 = 10$. Use it to find L_{10}; confirm your result by implementing a recursive or iterative algorithm to compute it.

(b) Let us go a bit farther and change the equation. For example, if $L_n = 2L_{n-1} + 3L_{n-2}$ for $n > 2$, $L_1 = L_2 = 1$, what is the explicit formula? Use it to find L_{10}; confirm your result by implementing a recursive or iterative algorithm to compute it.

6. To generalize even further, we can have a recurrence relation that goes more than 2 terms back, the most famous being $T_n = T_{n-1} + T_{n-2} + T_{n-3}$ (sometimes called tribonacci numbers). We will define the P-numbers p_n, which start with 1, 2, 3, … and follow the recursive relation $p_n = 2p_{n-1} + p_{n-2} - 2p_{n-3}$.

The characteristic polynomial for $p_n = 2p_{n-1} + p_{n-2} - 2p_{n-3}$ has easy-to-guess roots. Using it, or some other method (like generating functions), derive an explicit formula for p_n, given that $p_1 = 1$, $p_2 = 2$, $p_3 = 3$, use it to find p_{10}, and confirm your result by implementing a recursive or iterative algorithm to compute it.

7. In this question, use any of the techniques you have learned to compute elements of a general constant coefficients recurrence relation. Namely, consider a sequence defined by $p_n = a_1 p_{n-1} + \cdots + a_k p_{n-k}$ for some fixed k and for all $n > k$, with given values of $p_1, \ldots, p_k$.

Create a function in your program named `general_recurrence()` that reads a file `input.txt` that contains 4 lines:

- The first line will contain the number k.
- The second line will contain k numbers $a_1, \ldots, a_k$.
- The third line will contain k numbers $p_1, \ldots, p_k$.
- The fourth line will contain a single positive integer n.

Your program will then compute and output a single number p_n in an output file `output.txt`.

Project Submission Instructions

- Submit a **video at most 6 minutes long** describing your solutions to all the questions you answered (both theoretical and coding). Explain your answer, how you arrived at it, and what resources you used. For coding questions, explain how your code works, as well as any intricacies about your code that we should know when reading it.
- For the theoretical questions, submit **a single PDF file** containing your solutions.
- For the coding questions, submit **a single Python-3 or Java code file** containing all of the coding parts with each question in a different function.

Hint:

No hints this month.

Solution:

Featured Solution

by Alice Cheremukhina

https://youtube.com/watch?v=fAtgfCiVpL8

Featured Solution

by Avitel Gaidukova

https://youtube.com/watch?v=Ywr7zg3vcqk