* OpenAi provides quick access to the GPT model through their API
* Ex:

Suggest three names for an animal that is a superhero.

Animal: Cat

Names: Captain Sharpclaw, Agent Fluffball, The Incredible Feline

Animal: Dog

Names: Ruff the Protector, Wonder Canine, Sir Barks-a-Lot

Animal: Horse

Names:

Centaur, The Mighty Equine, Pegasus

* Setting Temperature above 0 causes different results for the given task, each iteration. Therefore, as you decrease temperature, the model takes less risks, and is more certain.
  + Temperature is a value between 0 and 1
  + Well-defined tasks should have temperature set to 0
* Playground (https://asknature.org/strategy/how-elephant-trunks-twist-and-twirl/):

Summarize this into a biological strategy.

Most muscles require bones to support them and joints to cantilever their movements. To raise your forearm from your side, you flex your biceps, which rotates the forearm across the hinge of your elbow. Muscular organs without bones and joints—like elephant trunks, snake tongues, and octopus arms—are called muscular hydrostats. They support themselves instead with a complex arrangement of muscle fibers. The most important feature of hydrostats, and what enables them to move without bones, is that the volume of water within them stays constant. An elephant trunk is composed almost entirely of water and muscle (which is itself mostly water). Because this volume of water stays constant, when the elephant moves its trunk in one direction, there will automatically be a compensating change in another direction.The muscle fibers that control these movements are arranged in three patterns: parallel to the length of the organ, perpendicular to its length, and obliquely wrapped down its length like candy cane stripes. In an elephant’s trunk, each fiber pattern controls specific actions or provides the support required to preserve its overall shape. In order to bend, longitudinal fibers on the outside of a trunk must contract and shorten on one side. But to prevent the trunk from folding in like a pinched hose, perpendicular fibers that are arranged radially throughout the cross-section must tense up to resist the compression of bending. When flexed, these radial fibers form a kind of “joint” like a solid ring around which the trunk can bend while maintaining a constant diameter. Because these fibers run the length of a trunk, an elephant can flex the “ring” muscles at many points, effectively having a movable joint that allows bending at nearly any location. Elephants can also twist their trunks because the oblique fibers coil like helices around them. If you looked down the end of a trunk, some helices would coil in a left-handed or counter-clockwise direction while others would be right-handed. The different orientations of these fibers enable elephants to twist their trunks in both left- and right-handed motions.

* Strategy generated:

The muscle fibers in an elephant's trunk are arranged in three patterns: parallel to the length of the organ, perpendicular to its length, and obliquely wrapped down its length like candy cane stripes. This arrangement of muscle fibers enables the elephant to flex and twist its trunk in a variety of ways.

* Strategy on Ask Nature:

Three muscle fiber patterns inside trunks work together to provide the strength, support, and resistance needed to bend and twist with extreme agility.

Brandon’s Prompts

A biological strategy is a characteristic, mechanism, or process that an organism or ecosystem exhibits to accomplish a particular function within a particular context.

The main elements of a biological strategy are:

* The organism or ecosystem
* The part of the organism
* Function (what it does or accomplishes)
* Mechanisms (how it does it)
* Context (environment, conditions, constraints, stressors)

Make sure your strategy is accurate, high-quality, written by an expert, and can be understood by a high school student.

Text: Harbor seal vibrissa morphology suppresses vortex-induced vibrations. Harbor seals (Phoca vitulina) often live in dark and turbid waters, where their mystacial vibrissae, or whiskers, play an important role in orientation. Besides detecting and discriminating objects by direct touch, harbor seals use their whiskers to analyze water movements, for example those generated by prey fish or by conspecifics. Even the weak water movements left behind by objects that have passed by earlier can be sensed and followed accurately (hydrodynamic trail following). While scanning the water for these hydrodynamic signals at a swimming speed in the order of meters per second, the seal keeps its long and flexible whiskers in an abducted position, largely perpendicular to the swimming direction. Remarkably, the whiskers of harbor seals possess a specialized undulated surface structure, the function of which was, up to now, unknown. Here, we show that this structure effectively changes the vortex street behind the whiskers and reduces the vibrations that would otherwise be induced by the shedding of vortices from the whiskers (vortex-induced vibrations). Using force measurements, flow measurements and numerical simulations, we find that the dynamic forces on harbor seal whiskers are, by at least an order of magnitude, lower than those on sea lion (Zalophus californianus) whiskers, which do not share the undulated structure. The results are discussed in the light of pinniped sensory biology and potential biomimetic applications.

Strategy:

The harbor seal has a specialized undulated surface structure on its whiskers that suppresses vortex-induced vibrations. This allows the seal to scan the water for hydrodynamic signals at high speeds without being hindered by vibrations.

Actual Strategy:

The harbor seal’s whiskers possess a specialized undulated surface structure that reduces vortex-induced vibrations as the whiskers move through water.

Sorry for so many questions, but within the first prompt you sent, are we supposed to have this part within it:

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Strategy: A harbor seal’s whiskers possess an undulated surface structure that reduces vortex-induced vibrations while moving through the water

Organism: harbor seal

Part of: whiskers

Function: reduces vortex-induced vibrations

Mechanisms: undulated surface structure

Context: moving through water

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Because then, the output matches this word for word when I run it in the GPT playground, which does not seem correct.

among the wealth of microbial organisms inhabiting marine environments, cyanobacteria (blue-green algae) are the most abundant photosynthetic cells. prochlorococcus and synechococcus, the two most common cyanobacteria, account for 30% of global carbon fixation (through the photosynthetic process in which sugars are manufactured from carbon dioxide and water). by drawing on natural resources, these microbes use photosystems (ps) i and ii (the two reaction centers in photosynthesis) to harness energy. \r\n\r\nintriguingly, some viruses that infect cyanobacteria (called cyanophage), carry genes that encode two psii core reaction-center proteins: psba (the most rapidly turned over core protein in all oxygen-yielding photosynthetic organisms) and psbd (which forms a complex with psba). by expressing their own copies of psba and psbd during infection, these cyanophages have managed to co-opt host genes to suit their own purposes: enhancing photosynthesis. it seems likely that they do this in the interests of their own fitness, since cyanophage production is optimal when photosynthesis is maintained during infection. \r\n\r\nuntil recently, only a small sample of cyanophages had been examined, leaving open the questions of how widespread psii genes are in these organisms and where the genes came from. to answer these questions, matthew sullivan, debbie lindell, sallie chisholm, and colleagues examined a pool of 33 cyanophage isolates (cultured from samples collected from the sargasso sea and the red sea), along with data already available for nine other cyanophages, for the presence of psba and psbd genes. they found psba was present in 88% and psbd in 50% of the cyanophages studied. by analyzing the sequences of these genes along with those from prochlorococcus and synechococcus host genes, they reconstructed the evolutionary history of how the psii genes entered the phage genomes. \r\n\r\ncyanophages are divided morphologically into three main families (podoviridae, myoviridae, and siphoviridae). looking at the distributions of the psii genes across the different families, sullivan, lindell, et al. saw that psba was present in all myoviruses and all prochlorococcus podoviruses, but not in prochlorococcus siphoviruses or synechococcus podoviruses. the high levels of sequence conservation between the different cyanophages suggest that this gene is probably functional and that it is likely to increase the reproductive fitness of the phage. the length of the latent period may impact the distribution pattern of psba among these phage groups. however, more information about the physiological characteristics of cyanophages is needed to further investigate these possibilities. \r\n\r\nthe second gene, psbd, was less prolific but was seen in four of the 20 prochlorococcus myoviruses and 17 of the 20 synechococcus myoviruses examined\u2014all of which also encoded psba. myoviruses are known to infect a wider range of cyanobacteria than the other cyanophage families. indeed, when investigated, the psbd-encoding myoviruses correlated with those known to have a broader host range. perhaps the co-opting of both psii genes ensures a functional psba\u2013psbd protein complex to enhance infection for these cyanophages that are able to infect a wider range of hosts. \r\n\r\nto determine when the psii genes had been transferred into the phage and from where, sullivan, lindell, et al. investigated the nucleotide sequences of psba and psbd from both prochlorococcus and synechococcus host and cyanophage. using meticulous sequence analyses and standard statistical methods, they generated phylogenetic trees to explain the evolutionary history of these two psii genes. \r\n\r\nby analyzing the clusters of sequence types within the resulting tree, the authors saw evidence that psba was transferred from the cyanobacteria host genome into the phage genome on four independent occasions and two separate occasions for psbd. exchange events were generally host-range specific, meaning that prochlorococcus genes transferred to prochlorococcus phages, and so on. however, a few intriguing exceptions, where genes did not cluster with their hosts, were observed; these might result from genetic exchange between members of two different phage families (one of broader host range) during co-infection of the same host. \r\n\r\nsullivan, lindell, et al. were also able to use their dataset to investigate a previous suggestion that alterations in the nucleotide distributions within individual psii genes (creating a kind of patchwork gene) demonstrate that intragenic recombination has taken place. indeed, they confirm that this occurs among synechococcus myoviruses and prochlorococcus podoviruses. in some cases involving synechococcus, intragenic recombination appears to have happened in both host-to-phage and phage-to-host directions for both genes; and, for some prochlorococcus genes, dna from an unknown source also seems to have been inserted. occasionally, intragenic exchanges are also seen between synechococcus hosts. \r\n\r\nthe authors compare their cultured results to those from wild phage sequences from the pacific ocean and see that much of the natural diversity is similar to the sequences from the cyanophage isolates, despite their origination from different ocean basins. overall, therefore, a considerable amount of genetic shuffling takes place within these two psii genes in cyanophages, and this creates a reservoir of photosynthetic diversity from which both host and phage are likely to benefit. this study offers a compelling example of global-scale microbial and phage co-evolution that likely influences the biological success of these prolific marine organisms.