翻譯以下各題，不必逐字翻譯，寫出關鍵概念與重點

第一題 (10%)

Thrust production by propulsive structures is a fundamental requirement for animal movement through air or water. Models of animal propulsion often emulate patterns that have been established for hydrofoils and airfoils and, as with these engineering-based models, animal propulsor models often assume a rigid structure that oscillates through the surrounding fluid with varying types of heaving and pitching motions. However, animal propulsors are not rigid, but instead, typically bend during motion. Attempts to evaluate the role of propulsor bending on thrust production have been met with conflicting results. For example, although some empirica, modelling and computational studies have indicated that flexible propulsors may permit higher thrust production than rigid counterparts, other evidence indicates that flexibility may sometimes lessen or prevent thrust production. Evaluation of these results has been complicated by a lack of common bending criteria to guide experimental design. Consequently, bending has been projected to occur both evenly over the full length and only over a limited portion of the propulsor. Most frequently, flexibility has been evaluated in terms of material properties such as elastic modulus or flexural stiffness of the propulsor rather than actual bending patterns. Experimental testing of the effects of bending on thrust production have been influenced by the inherent control possible with human-engineered propulsors so that most work on flexibility has been based on specifically engineered propulsors in laboratory conditions. Rarely have bending patterns of living animal propulsors, which have evolved over millions of years and among multiple taxonomic groups, been measured to inform experimental manipulations.

第二題 (15%)

The best way to manage forests to store carbon and to mitigate climate change is hotly debated. Trees absorb carbon dioxide from the atmosphere, and wood can be a substitute for fossil fuels and carbon-intensive materials such as concrete and steel. In the past few decades, the world's forests have absorbed as much as 30% (2 petagrams of carbon per year; Pg C year−1) of annual global anthropogenic $CO_2$ emissions1 — about the same amount as the oceans. Two-thirds of forests are managed.

Much has been learned about the carbon cycle in forests, but there are still too many gaps in our knowledge. New observations have called long-accepted theories into question: the finding that unharvested forests, for example, are absorbing more carbon than they release, accounting for half the sink, is contrary to the tenet of ecology, known as Odum's framework, that carbon flows in natural forests should be in equilibrium.

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This carbon-sink behaviour of mature forests is attributed to large-scale environmental changes that violate the assumption of the steady conditions underlying Odum's framework: higher atmospheric $CO_2$ concentrations are accelerating tree growth worldwide and nitrogen emitted by industry, agriculture and fossil-fuel burning is increasingly fertilizing managed forest soils in Europe, China and the eastern United States[3].

To make good decisions about how to cultivate forests for climate-change mitigation, such as whether it is better to harvest or conserve trees, we must better understand the cause and future behaviour of this *in situ* carbon sink. Until more is known, we propose that forestry management should prioritize 'win–win' strategies — those that increase both forest stocks and timber harvest, through measures such as protecting trees from animals, or replacing dying or low-productivity forests.

So far, most discussions about the impact of climate change on forests have focused on the rising rate of locally devastating events such as forest fires, infestations, droughts and storms. The past decade saw 410 million cubic metres of wood felled in four major storms in Europe, a decade's worth of Amazonian carbon sequestration lost in severe droughts in 2005 and 2010, a record heat wave with forest fires affecting 23,000 square kilometres in Russia in 2010, and the bark beetle pandemic that has affected 130,000 square kilometres and killed 435 million cubic metres of trees in British Columbia, Canada, since 2004.

Regionally, these events have had large socio-economic and ecological impacts. The windstorms that hit Europe in 1999, for example, destroyed one-third of the region's annual carbon sequestration[4] by forests, and halved the price of timber in France and other affected countries. But such events are insignificant over decades and at the global scale. The Pacific El Niño and La Niña climate oscillations — primarily the tropical forest

and peatland fires associated with them — are the only regional disturbances evident in globally averaged atmospheric $CO_2$ records[5].

At the same time, atmospheric records and forest inventories show that forests have been taking up ever more $CO_2$ in the past 50 years[1]. Experimental and modelling studies have established that currently, the global forest sink is driven mainly by changes in atmospheric $CO_2$ concentration and in nitrogen deposition. The competing explanation, that today's rapid tree growth is a recovery from ancient climate or harvesting losses, seems unlikely because it requires that regions around the globe, such as the Amazon and the Congo Basin, were simultaneously affected. Such a coincidence should have left traces of soot and enhanced $CO_2$ concentrations in air bubbles in glacial ice core samples, and these are not seen.

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第三題 (15%)

Newborn mammals rely on their mother's milk not only for the nutrients critical for growth and survival, but also for key immunological factors. Milk-transmitted compounds protect newborns against environmental pathogens until the developing immune system has sufficiently matured and can defend against infectious agents on its own. In adult animals, many of these same immunological factors have also been observed in the brain, which raises the question of whether immunological factors in the mother's milk influence the development or function of the nervous system as well. A report by Liu et al. in this issue suggests that milk-transmitted cytokines do in fact alter the course of hippocampal development and have a lasting effect on the cognitive function of the offspring as adults.

Tumor necrosis factor-$\alpha$ (TNF$\alpha$), a key factor in the immune response, is also produced by glial cells in the brain. Although chronically elevated TNF$\alpha$ has been associated with neurodegenerative disease, TNF$\alpha$ is also present at low levels in the brain under normal conditions, suggesting a physiological function in the CNS. Two previous studies that examined cognitive function in TNF$\alpha$ knockout mice reported conflicting data. But Liu et al. observed that different types of control mice, namely wild-type littermates and wild-type non-littermates, were used in these studies, prompting the authors to explore whether parental TNF$\alpha$ differences might explain these inconsistent effects on the cognitive performance of the offspring. Using standard Morris water maze and fear-conditioning tasks, they found that the offspring of parents that were either heterozygous or homozygous for the TNF$\alpha$ knockout allele had enhanced spatial and contextual memories compared with the offspring of wild-type parents. Surprisingly, the genotype of the offspring themselves did not appear to affect performance. These findings supported the authors' hypothesis that parental TNF$\alpha$ can affect the cognitive function of offspring: specifically, reduced parental TNF$\alpha$ conferred enhanced memory.

Next, the authors asked whether the parental effects of TNF$\alpha$ originated from their mothers and, if so, whether from the immune system or nervous system of the mothers. Using Cre-loxP conditional knockout mouse lines, the authors generated mother mice with a TNF$\alpha$ deficiency in either the nervous system or the immune system. Behavioral assessment of wild-type offspring revealed that memory improvement was only detected in the offspring of mothers with TNF$\alpha$ deficiency in the immune, but not nervous, system, suggesting that the lack of TNF$\alpha$ in the maternal immune system alone can facilitate memory enhancement in offspring.

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The hippocampus is a brain region involved in both spatial and associative memory and is one of the few brain regions with continuous neurogenesis throughout life. Extensive studies have established a role for neurogenesis in the hippocampal dentate gyrus in spatial and contextual memory. To explore whether enhanced neurogenesis in the dentate gyrus could be a potential mechanism for the memory enhancement induced by a maternal TNFα deficit, Liu et al. examined how maternal TNFα mutations affected neural progenitor proliferation in the dentate gyrus. Using BrdU labeling at several time points during postnatal dentate gyrus development, they found that reduced maternal TNFα increased neural progenitor proliferation in the dentate gyrus, but not in the subventricular zone, at postnatal day 14 (P14). The enhanced neural progenitor proliferation was transient and was not detected at P5 or in adulthood. The authors further found that this transient effect was mainly driven by increased proliferation of transit-amplifying progenitors, but not the more stem cell–like quiescent progenitors, and that it did not result in a net increase in neuronal production in the dentate gyrus. In addition, there were no changes in the density of astrocytes or microglia in the hippocampus.

第四題 (15%)

Two types of skeletal systems are recognized in vertebrates, the exoskeleton composed of the dermal bones and the cartilaginously preformed endoskeleton. For the past 200 years, the origin of the turtle carapace has remained unclear, and several different hypotheses about incorporation of the exoskeletal components into the costal and neural plates (Fig. 1, Supplementary Fig. S1) have been proposed although the exoskeletal origin of the accessory bones that surround the costo-neural plates marginally, namely the nuchal, peripheral, suprapygal and pygal plates, is widely accepted. One hypothesis assumes that costo-neural elements contain both the endo- and exoskeletal materials—in particular, dermal elements called the osteoderm. For shell acquisition, the osteoderms of the ancestral animal was thus thought to have fused with the axial skeletal elements (ribs and vertebrae) underneath. Osteoderms are also seen in other tetrapods (for example, crocodilians and armadillos), and the most conspicuous examples are found in extinct animals, namely the mammalian glyptodontids, in which exoskeletal elements form a thoracic shell. However, in contrast to the completely immovable shell seen in the turtle, the shells of the above-mentioned armoured tetrapods are not linked directly to the vertebral column or the rib cage, allowing free movement of the rib cage with the surrounding intercostal muscles.

The second hypothesis assumes the endoskeletal origin of the costo-neural carapace, maintaining that the costal and neural plates were simply acquired by modification of the axial skeleton and, therefore, that the major parts of the carapace were formed solely from the endoskeleton.

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Lastly, in the third hypothesis, superficially translocated endoskeletal elements were thought to induce heterotopically exoskeletal osteogenesis of the carapace. Recent observations of the embryonic turtle suggest that heterotopic shifts of the ribs occur during development: rib primordia translocated into the dermis induce membranous ossification to differentiate flanges on the craniocaudal aspects of the rib shafts and thus complete the costal plate. The superficial shift of the ribs, initially arising endochondrally, is thought to cause a new tissue interaction in the new location (that is, the dermis).

Here through a comparative developmental analysis, we demonstrate that the costal and neural plates are assigned to be hypertrophied ribs and vertebrae, respectively. These results indicate that the major part of the turtle carapace evolved solely by modification of the endoskeleton (that is, second hypothesis). Furthermore, in the fossil record, we recognized that precursors of carapace in some non-turtle diapsid reptiles developed also as an endoskeleton. The ribs of these reptiles are not only expanded in shape, as seen for examples, in extant anteaters or a Permian reptile Eunotosaurus, but also laterally (nearly horizontally) projected as in the turtles. The genetic basis relevant to the carapace evolution is, therefore, likely to have deeper history than the split of the turtle lineage.

第五題 (15%)

Plants can be attacked by a vast range of pathogen classes, causing substantial agricultural losses. The Phytophthora (meaning "plant killer") genus is a particularly destructive pathogen that causes root and stem base decay in a wide range of plants. Phytophthora infestans, which precipitated the Irish potato famine, originated in Central Mexico and is closely related to other Phytophthora species with distinct host ranges. Pathogen effectors that are secreted during infection play a key role in disease biology, but effector-induced adaptation to new hosts is an understudied topic. On page 552 of this issue, Dong et al. investigate how Phytophthora effector proteins evolve the ability to specialize on new hosts (see the figure).

Phytophthora is a genus of oomycetes that exhibit filamentous growth on plants. Oomycetes share some phenotypes with fungi, but are phylogenetically related to photosynthetic brown algae and are thought to have initially emerged from marine environments. The Phytophthora genus comprises 10 main lineages designated as clades 1 to 10. Clade 1c, a subdivision of clade 1, includes P. infestans (infecting potato and tomato) and P. mirabilis (infecting 4 o'clock weeds), indicating that these species share a recent common ancestor (2). Genome comparisons between P. infestans and P. mirabilis highlight alterations and patterns of selection in repetitive DNA containing rapidly evolving families of virulence genes (such as effectors).

The 82 effectors undergoing positive selection between P. infestans and P. mirabilis are promising candidates shaping host specialization. Dong et al. focused their efforts on the EPIC1 effector, which is abundantly secreted during infection of tomato and inhibits extracellular papain-like proteases (including RCR3) that are involved in plant immune perception.

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Dong et al. now report that the P. mirabilis epiC1 ortholog (PmepiC1) shows signatures of positive selection, suggesting that this effector has evolved to function in Mirabilis jalapa, the 4 o'clock plant, following the split between P. mirabilis and P. infestans. Using activity-based profiling with a probe that targets papain proteases, the authors demonstrate that recombinant EPIC1 from P. infestans effectively inhibits tomato and wild potato RCR3 proteases, whereas PmEPIC1 does not. The authors identify two PmEPIC1 M. jalapa targets with homology to RCR3 (MRP1 and MRP2). Subsequent experiments confirmed that MRP2 is an active protease and can be effectively inhibited only by PmEPIC1. Thus, EPIC1 effectors function more effectively on their respective hosts, supporting the hypothesis of effector specialization after a host jump.

第六題 (15%)

In Arabidopsis, a small group of undifferentiated stem cells in the center of the floral meristem give rise to the flower. These stem cells produce daughter cells that differentiate into the four whorls of organs (sepals, petals, stamens, and carpels) underlying the basic flower structure. The different organ identities are determined by the complex interplay of floral organ identity genes, most of which are transcription factors. On page 10.1126/science.1248559 in this issue, Sun et al. describe an elegant timing mechanism that allows transcriptional changes specified in the stem cells to be executed only in daughter cells and only after a predefined number of cell divisions.

The meristem identity gene WUSCHEL (WUS) is required to maintain the stem cell population in the floral meristem. The transcription factor AGAMOUS (AG) drives differentiation of the stem cells into stamens and carpels and is induced by both the floral activator LEAFY (LFY) and WUS in early flowers (stage 3). At a later stage (stage 6), AG represses WUS in a negative feedback loop to convert the stem cells to organ primordia (see the figure). Although AG induction by WUS, and WUS repression by AG, both occur in the same stem cell population, the two events are temporally separated, with WUS being completely repressed ~2 days after AG induction. The precise timing of WUS repression allows the correct number of cells to be produced for reproductive organ formation. Too early and flowers have fewer stamens and no carpel; one day too late and flowers become partially indeterminate with additional and abnormal organs. Sun et al. now explain how the 2-day delay is achieved, through linking cycles of cell division to transcriptional derepression.

A key component in the WUS-AG pathway is the transcriptional repressor KNUCKLES (KNU), which represses WUS in stage 6 flowers. KNU is repressed by histone H3 lysine 27 trimethylation (H3K27me3), a repressive modification established by the Polycomb repressive complex 2 (PRC2). In developing flowers, AG activates KNU by binding to its promoter, but KNU expression only becomes detectable ~2 days after the initial AG binding, resulting in a substantial decrease in WUS expression. The delay in KNU activation is likely caused by the gradual loss of the repressive H3K27me3 mark at the KNU gene.

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Sun et al. observed that the ~2-day delay depends on cell-cycle progression, suggesting that the "timer" may be a "counter" that monitors the number of cell divisions. The authors hypothesized that AG binding interferes with the maintenance of H3K27me3 at KNU: Incorporation of unmodified H3 after roughly two rounds of cell divisions sufficiently dilutes the preexisting H3K27me3 to allow KNU expression. Indeed, a short region in the KNU promoter immediately adjacent to the AG binding site was found to be necessary and sufficient for recruiting a core component of the PRC2, FERTILIZATION-INDEPENDENT ENDOSPERM (FIE). Critically, Sun et al. show that AG binding leads to the immediate eviction of FIE.

第七題 (15%)

In contrast to the careful preplanning and regimentation that characterize human construction projects, animals that build in groups do so in a reactive and decentralized way. The most striking examples are mound-building termites, colonies of which comprise millions of independently behaving insects that build intricate structures orders of magnitude larger than themselves (Fig. 1, A and B). These natural systems inspire us to envision artificial ones operating via similar principles, with independent agents acting together to build elaborate large-scale structures, guided by reacting to the local situations they encounter. Such systems could enable construction in settings where human presence is dangerous or problematic, as in disaster areas or extraterrestrial environments.

Engineering an automated construction system that operates by termite-like principles rather than human-like ones requires an ability to design complex systems with desired collective behavior (e.g., producing a particular user-specified building). The hallmark of complex systems of independent agents is unexpected collective behavior that emerges from their joint actions, not readily predictable from knowledge of agent rules. If a specific collective behavior is desired, no method in general is known to find agent rules that will produce it.

We present a decentralized multi-agent system for automated construction of user-specified structures, thereby providing a solution to such a problem of complex system design. An arbitrary number of independent robots follow an identical set of simple, local rules that collectively produce a specific structure requested by a user. The rules are automatically generated from a high-level representation of the final target structure and provide provable guarantees of correct completion of that structure. The challenges associated with engineering a complex system are addressed by using principles drawn from social insects—in particular, indirect coordination through manipulation and sensing of a shared environment (stigmergy), and behavioral regularities that constrain the space of possible outcomes—which together make analysis and execution tractable. We first present the theoretical foundation for this work, followed by a physical implementation with three independent robots demonstrating autonomous construction.

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The independence of individual robots stands in contrast to other work on automating construction with single or multiple robots with centralized sensing and/or control. Centralized systems that provide a global computing authority and/or precise positioning information during run time, in settings where such features are feasible, can have advantages in aspects such as efficiency and run-time flexibility. Conversely, decentralization provides advantages including opportunities for greater scalability (no coordinating authority that can become overloaded) and robustness (no single point of failure).

We distinguish between two types of building processes. A system may produce a predetermined outcome, in which many possible system trajectories all lead to the same guaranteed final state. Alternatively, variation during the process may lead to a variable outcome, in which the final state is determined during the course of construction and can change if the process is rerun. In the context of human construction, single buildings are built via the first type of process, in which the order of operations might vary but the final result always matches a blueprint; cities develop via the second type of process, in which choices are contingent on previous decisions such that many distinct results are possible. Here, we focus on designing processes with fixed outcomes, but also show how our system can be used to generate structures that vary each time robots construct them.

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