2025 年度
創価大学 大学院 理工学研究科【生命理学専攻】
博士後期課程　一般選抜試験問題

英　　語

開始時刻　午前 10 時 00 分
終了時刻　午前 11 時 00 分

【注意事項】

１．解答用紙には受験番号、氏名を必ず記入してください。
２．試験終了後、答案用紙は必ず提出してください（問題用紙は提出しなくてよい）。
３．問題番号が明記された答案用紙を使用し、解答してください。

問題 1

次の科学ニュースの英文を読んで問 1〜4 に答えなさい。

[**Title**]

Ageing seems to affect cellular processes in the same way across five very different kinds of life — humans, fruit flies, rats, mice and worms — according to a study published in Nature on 12 April 2023. The findings could help to explain what drives ageing and offer suggestions for how to reverse it. “It opens up a really fundamental new area of understanding how and why we age,” says a biochemist at the University of New South Wales Sydney in Australia. As animals age, a variety of molecular processes inside cells become less reliable — gene mutations become more frequent, and the ends of chromosomes snap off, making them shorter. Many studies have explored ageing’s effects on gene expression, but few have investigated how it affects transcription — the process whereby genetic information is copied from a blueprint DNA strand to RNA molecules — says a computational biologist at the University of Cologne in Germany. (1)

Careless copying: To find out, the researchers analysed genome-wide transcription changes in five organisms: nematode worms, fruit flies, mice, rats and humans, at different adult ages. The researchers measured how ageing changed the speed at which the enzyme that drives transcription, RNA polymerase II (Pol II), moved along the DNA strand as it made the RNA copy. They found that, on average, Pol II became faster with age, but less precise and more error-prone across all five groups. “We saw more mismatches between the reads and reference genome,” says the primary investigator. Previous research had shown that restricting diet and inhibiting insulin signalling can delay ageing and extend lifespan in many animals, so the researchers then investigated whether these measures had any effect on the speed of Pol II. In worms, mice and fruit flies that carried mutations in insulin signalling genes, Pol II moved at a slower pace. The enzyme also travelled more slowly in mice on a low-calorie diet. But the ultimate question was whether changes in Pol II speed affected lifespan. The research team tracked the survival of fruit flies and worms that carried a mutation that slowed Pol II down. These animals lived 10% to 20% longer than their non-mutant counterparts. When the researchers used gene editing to reverse the mutations in worms, the animals’ lifespans shortened. “That really established a causal connection,” says the primary investigator.

(Nature NEWS 12 April (2023) doi: https://doi.org/10.1038/d41586-023-01040-x から改変)

問 1. 下線(1)の文章を和訳しなさい。

問 2. 下線(1)の文章の内容に相応しい題名[Title]を日本語と英語で書きなさい。

問 3. Careless copying: の段落で述べられている RNA ポリメラーゼ II の移動速度と寿命の関係を日本語で簡潔に説明しなさい。

問 4. 人の老化防止になると期待できる食品あるいは生活習慣について、自分の可能な考えを英文で簡潔に理由も含めて説明しなさい。

問題２

以下の文章を読んで、下の問 1〜問 5 に答えなさい。

A riddle: how does a protein find its unique structure?

Christian Anfinsen, an American scientist, made an early discovery. Using various chemical tricks, he managed to make an existing protein unfold and then fold itself up again. The interesting observation was that the protein assumed exactly the same shape every time. In 1961, he concluded that a protein's three-dimensional structure is entirely governed by the sequence of amino acids in the protein. This led to him being awarded the Nobel Prize in Chemistry in 1972. However, Anfinsen's logic contains a paradox, which another American, Cyrus Levinthal, pointed out in 1969. He calculated that even if a protein only consists of 100 amino acids, in theory the protein can assume at least 10^{47} different three-dimensional structures. If the chain of amino acids were to fold randomly, it would take longer than the age of the universe to find the correct protein structure. In a cell, it just takes a few milliseconds. So how does the string of amino acids actually fold?

Throwing down the gauntlet① **for the great challenge of biochemistry**

The above insights led to another decisive realisation – if chemists know a protein's amino acid sequence, they should be able to predict the protein's three-dimensional structure. This was an exciting idea. If they succeeded, they would no longer have to use fiddly X-ray crystallography and could save masses of time. They would also be able to generate structures for all the proteins where X-ray crystallography was not applicable. These logical conclusions threw down the gauntlet① for what has become the great challenge of biochemistry: the prediction problem. To encourage more rapid development in the field, in 1994 researchers started a project called Critical Assessment of Protein Structure Prediction (CASP), which developed into a competition. Every other year, researchers from around the globe (1) were given access to sequences of amino acids in proteins whose structures had just been determined. However, the structures were kept secret from the participants. The challenge was to predict the protein structures based on the known amino acids sequences. CASP attracted many researchers, but solving the prediction problem proved incredibly difficult. The correspondence between the predictions researchers entered in the competition and the actual structures hardly improved at all. The breakthrough only occurred in 2018, when a chess master, neuroscience expert and pioneer in artificial intelligence entered the field.

Boardgame master enters the Protein Olympics (2)

Let's take a quick look at Demis Hassabis' background: he started playing chess at the age of four and achieved master level as a 13-year-old. In his teens, he started a career as a programmer and successful games developer. He began exploring artificial intelligence and took on neuroscience, where he made several revolutionary discoveries. He used what he learned about the brain to develop better neural

networks② for AI. In 2010 he co-founded DeepMind, a company that developed masterful AI models for popular boardgames. The company was sold to Google in 2014 and, two years later, DeepMind came to global attention when the company achieved what many then believed to be the holy grail③ of AI: beating the champion player of one of the world's oldest boardgames, Go.(3) However, for Hassabis, Go was not the goal, it was the means for developing better AI models. After this victory, his team were ready to tackle problems of greater importance for humanity, so in 2018 he registered for the thirteenth CASP competition.

An unexpected win for Demis Hassabis' AI model

In previous years, the protein structures that researchers predicted for CASP had achieved an accuracy of 40 per cent, at best. With their AI model, AlphaFold, Hassabis' team reached almost 60 per cent. They won, and the excellent result took many people by surprise – it was unexpected progress, but the solution was still not good enough. For success, the prediction had to have an accuracy of 90 per cent when compared to the target structure. Hassabis and his team continued developing AlphaFold – but, however hard they tried, the algorithm never quite went all the way. (4) The hard truth was that they had come to a dead end. The team was tired, but one relatively new employee had decisive ideas about how the AI model could be improved: John Jumper.

ノーベル財団 HP「The Nobel Prize in Chemistry 2024 – Popular Science Background」より改変

① throw down the gauntlet：挑戦する
② neural network：人間の脳に似た方法で意思決定を行う機械学習プログラム
③ holy grail：聖杯

問１． 下線（１）の globe を別の単語で言い変えるとすると、どのような単語が最適か。
問２． 下線（２）Protein Olympics とは何のことか。
問３． 下線（３）を日本語に訳しなさい。
問４． 下線（４）を日本語に訳しなさい。
問５． ノーベル賞受賞者 Demis Hassabis の経歴を日本語で説明せよ。

問題３

これまでの自分が行ってきた研究の成果と今後の研究計画の概要を簡潔に英文で記述しなさい。