I. Based on the following report from BBC, please provide a title and write a short summary of this scientific news in *English* (50%)

Hit: the important contributions/ discoveries based on the scientific work itself should be included

Scientists studying the DNA of Neanderthals say they can find no evidence that this ancient species ever interbred with modern humans. But our evolutionary cousins may well have been able to speak as well as us, said Prof. Svante Paabo from Germany's Max Planck Institute. He was speaking in Chicago, US, where he announced the "first draft" of a complete Neanderthal genome. The genetics information has been gleaned from fossils found in Croatia. Prof. Svante Paabo confirmed that Neanderthals shared the FOXP2 gene associated with speech and language in modern humans. A total of three billion "letters", covering 60% of the Neanderthal genome, have been sequenced by scientists from Max Planck Institute for Evolutionary Anthropology and 454 Life Sciences Corporation, in Branford, Connecticut. The majority of the sequence comes from bones from Vindija Cave in Croatia.

The draft genome can give us clues to the genetic regions which make us "uniquely human", Prof Paabo told BBC News.

"It was always a dream to look at the DNA of our closest evolutionary relatives.
"Now that we have the Neanderthal genome, we can look for areas in the human genome where a change seems to have swept rapidly through us since we separated from Neanderthals.
"There, something special may have happened in us. The cool thing is, now that we have the whole genome, we can look for these changes without bias."

Prof Paabo released details about the latest stage of his research at the annual meeting of the American Association for the Advancement of Science (AAAS).

Tongue twister
Neanderthals lived in Europe and parts of Asia until they became extinct about 30,000 years ago.
They were the closest relatives of currently living humans, sharing between 99.5% to 99.9% of our DNA sequence. Pinpointing the differences may reveal the crucial evolutionary changes that enabled modern humans to leave Africa and rapidly spread around the world, starting around 100,000 years ago.
Accordingly, Prof Paabo and his team have focused on genes of special interest in recent human evolution, such as FOXP2, which is involved in speech and language. Humans differ from chimpanzees at two key points in the FOXP2 gene. But the preliminary results suggest that Neanderthals shared these same variations.

"There is no reason to believe they couldn't speak like us," said Prof Paabo.
"But of course there are many other genes involved in speech and language, so there are many more studies to be done."

Breeds apart
Since Neanderthals lived side by side with modern humans in Europe for many thousands of

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years, it has been speculated that we may have inherited some Neanderthal DNA in our genome today, thanks to interbreeding. But Professor Paabo's team have found no evidence *for this. They focused on a gene implicated in brain development - microcephalin-1 - which* shows significant variation among present day humans. It has been suggested that a particular variant of the gene, found commonly in Europeans, was contributed by Neanderthals. But the Croatian Neanderthal fossils harboured an ancestral form of the microcephalin-1 gene, which today is also found among Africans. Overall, it seems that Neanderthals have contributed, at most, a "very limited" fraction of the variation found in contemporary human populations, said Prof Paabo.

"What is exciting now, is that we are beginning to look the other way - from early modern humans into Neanderthals."

Professor Chris Stringer, from the Natural History Museum, London, UK, commented: "If the the Neanderthal genome data show little evidence of potential hybridisation, that would fit with my view from the fossil evidence that, while interbreeding was probably possible, it may have occurred only rarely, with trivial impact on modern humans.
"The populations had been separate for hundreds of thousands of years and I think there would have been significant physical and behavioural differences between them. However, larger samples would be desirable to get a more complete picture, and hopefully those will follow soon."

Dead end
Prof Paabo said the team did not expect to find any clues which might help solve the riddle of the Neanderthals' demise.

"I don't think they became extinct due to something in their genome," he said.
"It was clearly something in their interaction with the environment or with modern humans that caused them to be extinct.
"That will not be something you can see from their DNA sequence."

And Prof Paabo was quick to pour cold water on any suggestion that the genome sequence would facilitate the cloning of a Neanderthal.

"We are talking about a very complex mammal," said the 53-year-old.
"I don't think that technology will improve fast enough to make this possible in my lifetime.
"It is more in the realm of science fiction than science."

※本大題請於試卷內之「選擇題作答區」依序作答。

II. Multiple-choice Questions (each question 2% for a total of 50%)

The emergence of infectious diseases is a hallmark of the twentieth century, along with the resurgence of diseases thought to have been "conquered".   This continuing problem is global in scope, involves humans (e.g. AIDS, hantavirus pulmonary syndrome, and tuberculosis), domestic animals (e.g. bovine spongiform ecephalopathy "mad cow disease", Nipah virus infections, and foot-and-mouth disease), and wildlife (e.g. mobillivirus infections, chronic wasting disease, and inclusion body disease of cranes).   The emergence of diseases in wildlife involves virtually all classes of vertebrates and is occurring in all types of habitats. The number of diseases involved and the magnitude of losses are such that disease emergence and resurgence are posing an unprecedented challenge for the conservation of wildlife, including some waterbird populations.

1. According to the paragraph, which of the following statement is correct?
   A. Many diseases were eliminated by human.
   B. Nipah virus infects human.
   C. The diseases in wildlife are limited to some vertebrates.
   D. The emergence of infectious diseases has caused losses in money and lives.

2. According to the paragraph, wildlife conservation faces serious challenges due to
   A. habitat loss
   B. predator problem
   C. infectious disease emergence and resurgence
   D. declining population

Agricultural practices in southern China provide an abundance of avian influenza viruses in the environment through the medium of the domestic duck.   This is the backdrop to a series of remarkable genetic changes by the recently recognized Asian lineage of highly pathogenic H5N1 virus involving multiple poultry hosts, particularly the chicken, and in the case of the 2003/2004 outbreak in east and south-east Asia, the domestic duck as well as the chicken. While there is little evidence to support the role of migratory birds in the spread of this outbreak, the widening range of hosts suggests that they could in the future.   The implications arising from the spread of the H5N1 virus for humans, poultry and wildlife in the Asian region and beyond are great.   Ornithologists have much to contribute in dealing with these issues.

3. According to the paragraph, the avian influenza viruses for humans in China originated from
   A. the domestic duck
   B. the waterfowl
   C. human transfer .
   D. migrant wild bird

4. According to the paragraph, the 2003/2004 pathogenic H5N1 virus outbreak in east and south-east Asia was due to
   A. the chicken
   B. the duck
   C. the waterfowl
   D. the domestic duck and the chicken

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Wetlands are more threatened than any other ecosystem type, with losses exceeding 50% of their original extent worldwide. Despite the small portion of the Earth's surface that they comprise, wetlands contribute significantly to global ecosystem services. In this study, we tested the hypothesis that the location and rate of change in wetland amount in the Tempisque Basin of northwest Costa Rica is predictable from landscape setting. Our results demonstrate that a strong potential exists for developing predictive models of wetland conversion based on an understanding of wetland location and surrounding trends of land use. We found that topography was the single most important predictor of wetland conversion in this area, entraining other conversion processes, and that spatial patterns of wetland loss could consistently be predicted from landscape-level variables. Areas with highest *probabilities of conversion were found in the most accessible, non-protected regions of the* landscape. While Palo Verde National Park made a substantial contribution to wetland conservation, our results highlight the dependence of lower-lying protected areas on upland processes, adding a little-addressed dimension of complexity to the dialogue about protected area management. Conservation strategies aimed at reducing wetland loss in tropical habitats will benefit from careful analysis of the dominant land use system(s) at a relatively broad scale, and the subsequent development of management and policy responses that take into account dynamic opportunities and constraints in the landscape.

5. According to the paragraph, which of the following statement is NOT true?
    A. Wetlands are threatened ecosystems.
    B. Current worldwide wetland losses exceed 50% of their original extent.
    C. The most accessible wetlands were wuickly converted into human related landscape.
    D. Palo Verde National Park did not contribute to wetland conservation.

6. According to the study, which factor contributed most to the prediction of wetland conversion?
    A. climate
    B. topography
    C. temperature
    D. spatial pattern

Monitoring programs are an essential component of successful waterfowl management in North America. Five major categories of waterfowl monitoring efforts are conducted annually: population surveys; production surveys; habitat surveys; banding and marking programs; and harvest surveys. These surveys and programs are cooperative in nature, and rely on integrated partnerships between federal, state, and provincial agencies, as well as private organizations throughout the continent. Results from these surveys provide estimates of waterfowl population size, recruitment, survival rates, and harvest, as well as a means of evaluating habitat quality. Quantitative assessments of these key parameters provide the foundation for understanding waterfowl population dynamics and making and evaluating harvest management decisions.

7. In North America, waterfowl were NOT monitored by
    A. population surveys
    B. habitat surveys
    C. harvest surveys
    D. stable isotope survey

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8. Which of the following statements is not true?
   A. Monitoring programs are an essential component of successful waterfowl management.
   B. There are at least 5 categories of waterfowl monitoring efforts are conducted annually.
   C. These waterfowl surveys and programs are cooperative in nature.
   D. The waterfowl monitoring programs take lots of time and money, but do not provide important information.

9. The results of waterfowl monitoring programs do not provide the information about
   A. survival rates
   B. recruitment
   C. population size
   D. species diversity

Use of stable nitrogen isotope ratios is one method that has been proposed to indicate anthropogenic nutrient enrichment in estuarine systems. However, the role of stable isotopes as a tool in long-term ecosystem monitoring has not been fully developed. Resident producer and consumer species were collected from marshes dominated by *Spartina alterniflora* and subject to a range of anthropogenic impacts in Cape Cod, Massachusetts, and in Great South Bay and Jamaica Bay, New York. Tissue isotope ratios of *Spartina alterniflora, Ulva lactuca, Fundulus heteroclitus,* and *Geukensia demissa* were analyzed in order to determine which organisms are the most sensitive indicators of changes in anthropogenic nitrogen source and loading. Power analysis was used to determine the sample sizes necessary to detect change in nutrient source using the species sampled. Relationships between the $\delta^{15}N$ values of the species sampled and watershed population density and residential development were evaluated. Population density was a better indicator of anthropogenic nitrogen impact than residential development, since most anthropogenic nitrogen in the study marshes was derived from wastewater. Consumer species demonstrated lower within-site variability than producer species and would therefore require smaller sample sizes to detect changes in nitrogen source and loading.

10. Which of the following studies may not be the applications of stable isotope
    A. anthropogenic nutrient enrichment in an ecosystem
    B. long-term ecosystem monitoring
    C. food chain related studies
    D. population estimates

11. The use of power analysis is to
    A. evaluate residential development.
    B. estimate watershed population density.
    C. decide how large a sample is needed to enable accurate and reliable statistical judgments .
    D. estimate anthropogenic nutrient enrichment in an ecosystem.

12. Which of the following statements is NOT true?
    A. To detect changes in nitrogen source and loading, consumer species take smaller sample sizes.
    B. Comparing to residential development, population density was a better indicator of anthropogenic nitrogen impact.

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C. Many applications of stable isotope have been developed.
D. The use of stable isotope is a panacea in ecological research.

Collisions between aircraft and birds, so-called "bird strikes," can result in serious damage to aircraft and even in the loss of lives. Information about the distribution of birds in the air and on the ground can be used to reduce the risk of bird strikes and their impact on operations en route and in and around air fields. Although a wealth of bird distribution and density data is collected by numerous organizations, these data are not readily available nor interpretable by aviation. This paper presents two national efforts, one in the Netherlands and one in the United States, to develop bird avoidance models for aviation. These models integrate data and expert knowledge on bird distributions and migratory behavior to provide hazard maps in the form of GIS-enabled Web services. Both models are in operational use for flight planning and flight alteration and for airfield and airfield vicinity management. These models and their presentation on the Internet are examples of the type of service that would be very useful in other fields interested in species distribution and movement information, such as conservation, disease transmission and prevention, or assessment and mitigation of anthropogenic risks to nature. We expect that developments in cyber-technology, a transition toward an open source philosophy, and higher demand for accessible biological data will result in an increase in the number of biological information systems available on the Internet.

13. 'Bird strikes' means
    A. birds collide building walls
    B. birds strike tall tower
    C. birds hit wind towers
    D. a collision between a bird and an aircraft in flight

14. Bird avoidance models were developed to
    A. integrate data and expert knowledge on bird distributions
    B. enhance the risk of bird strike
    C. reduce the potential of bird collision
    D. help flight planning and flight alteration and for airfield and vicinity management

15. The word 'cyber-technology' means
    A. biological information technology
    B. bioinformatics
    C. the Internet technology
    D. ecoinformatics

Tetraclita squamosa, T. kuroshioensis, T. japonica and *T. formosana* are common intertidal barnacles on exposed to semi-exposed shores in the Pacific waters. Their geographical distribution is often reported qualitatively and this has resulted in confusion of the patterns addressed and has made it difficult to compare abundance between locations. Using stratified transect surveys along the latitudinal gradient from the Japan mainland, Okinawa, Taiwan, Xiamen and Hong Kong, *Tetraclita* showed variations in the horizontal and vertical distribution patterns which appear to result from the interactions of the climate and oceanographic patterns. In Japan and northern Taiwan, *T. kuroshioensis, T. formosana* and *T. japonica* co-exist and occur over the same vertical range while in Hong Kong and Xiamen, *T. squamosa* and *T. japonica* occupy different tidal levels. *T. formosana* and *T.*

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kuroshioensis are abundant on the west Pacific waters suggesting the larval pool is associated with the Kuroshio Current.   *T. squamosa* had the distribution in the South China Sea and it is possible the larvae is transported mainly by the South China Sea Surface Current.   *T. japonica* had high abundance in both the Japanese Mainland and the in southern locations (Hong Kong and Xiamen) but with very low abundance at shores in between these two locations.   There may be a physical and genetic boundary between the northern and southern populations in the Pacific Ocean and further studies should focus on population genetics of *Tetraclita* in the Asian region.

16. Barnacles are
    A. a group of terrestrial plants
    B. a group of small invertebrate animal with a shell that clings to rocks and ships
    C. a group of marine parasites
    D. a group of marine vertebrates

17. Which of the following is not included in the study areas?
    A. Okinawa
    B. Taiwan
    C. Xiamen
    D. Vietnam

18. According to this study, the barnacle distribution patterns are an interaction result of
    A. the oceanographic patterns
    B. the climate patterns
    C. the climate and oceanographic patterns
    D. tidal influence

19. The study suggested further work may investigate
    A. the distribution pattern of barnacle
    B. the interaction of climate and oceanographic patterns
    C. the population genetics
    D. the abundances of different barnacle populations

Predicting species distribution and identifying hotspots are essential in designing conservation strategies.   Because of different spatial scales and/or species characteristics, uncertainty still exist on which species prediction model is the best to use.   Several models have been proposed to calculate the probability of species occurrence, predict biodiversity hotspots and decide importance levels of biodiversity hotspots.   We constructed predictive distribution models for 14 endemic bird species in Taiwan by using fine resolution (1×1 km) breeding bird distribution dataset compiled over the past decade as well as environmental variables.   We compared performances of four models: logistic regression (LR), multiple discriminant analysis (MDA), genetic algorithm for rule-set prediction (GARP) and artificial neural networks (ANN).   Maps for biodiversity hotspots were generated based on the species distribution from the four models.   To account for the potential uncertainty we constructed hotspot maps by the frequency histogram and the probability density function approaches.   Based on distribution maps and the area under the curve (AUC) of the receiver operating characteristic, all of our models predicted well for each species (all AUC > 0.75). Non-linear models (GARP, ANN and LR) predicted better than linear (MDA) model. GARP was the most consistent model when evaluated with kappa, sensitivity, accuracy and

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specificity for each species and the three species categories. The prevalence of all species did not affect the final predictive performance. The five biodiversity hotspot maps derived from the frequency histogram approach showed a relatively similar pattern while the maps generated by the probability density function indicated that area of mid- to-high elevation had higher probability. In spite of some inconsistency, the hotspot maps identified from these two approaches were fairly representative when evaluated with currently known hotspots. A GAP analysis indicated only 25% of the hotspots were protected by national parks. We conclude LR, GARP, ANN and MDA are all feasible to model species distribution. Though with some limitations, we suggest using a combination approach to identify common features and conservation priority of biodiversity hotspots.

20. Species prediction models are models that
    A. predict the potential carrying capacity
    B. predict the possible outcome of a specific event
    C. forecast a trend
    D. predict the potential spatial distribution

21. Which of the following models was not used in this study?
    A. multiple discriminant analysis
    B. genetic algorithm for rule-set prediction
    C. artificial neural networks
    D. maximum entropy

22. According to this study, which species prediction model is the most reliable?
    A. multiple discriminant analysis
    B. logistic regression
    C. artificial neural networks
    D. genetic algorithm for rule-set prediction

23. The study found that the hotspots for endemic bird species in Taiwan was located in
    A. low-elevation areas
    B. mid- to-high elevation region
    C. eastern region
    D. western region

24. An endemic species is
    A. one found in many different geographic areas.
    B. one found naturally in just one geographic area.
    C. one found only on islands.
    D. one that has been introduced to a new geographic area.

25. The word 'hotspot' means
    A. a spring of water heated by geothermal energy
    B. a camera accessory used to connect the camera and an electric flash
    C. an impressive, attractive, exciting, or important person or thing
    D. a place where a lot of activity of a particular type takes place

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