普通高等教育创新规划教材
高等医学院校教材

Medical Humanities-oriented English Course

医学人文英语阅读

杜晓冰　李　响◎主编

知识产权出版社
全国百佳图书出版单位

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内容提要

本书主要选择与医学相关的社会和全球关注的前沿话题，从宏观上介绍医学人文和科技发展的进程。本教程设计新颖，注重培养学生在医学场景中实际的英语语言运用能力，旨在调动学生学习的主动性和积极性。本书力图使读者兼顾学习英语语言知识、了解医学专业发展动态和提升医学人文素质。

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前　言

随着医学教育的全球化及大学英语教学改革的逐步深入，将医学生的外语能力和医学专业知识相结合，日益成为众多专家学者关注的焦点。医学生及医务工作者都需要大量与医学知识相关的英语阅读为基础，才能进一步实现用英语撰写科技报告、学术论文或会议论文等以参与更多的国际学术交流和竞争。

《医学人文英语阅读》能够满足社会对于医学院校毕业生未来职业可持续发展的需求，是医学专业学生基础医学阶段的医学英语教材。本教材试图构建有效的教学机制，兼顾医学知识、语言和技能的相容相辅，让学生无论是在医学知识、语言习得和阅读技巧上，真正地学有所得。

医学人文学是一个探讨医学源流、医学价值、医学规范以及与医学有关的社会文化现象的学科体系。本书以医学人文内容为主要线索，构建了独具特色的医学英语学习框架，从宏观上介绍了医学人文方面的热点话题。

《医学人文英语阅读》共 15 个单元，涉及“人体基因组计划”“大脑功能”“全球流行病”“生活方式和健康”“抑郁与压力”“长寿”“急诊”“肥胖症”“顺势疗法”“医生，病人和医院”“公共和私人卫生服务”“环境与健康”“伦理：医学，法律和良知”“食品安全”以及“医疗保险”等热点。

每个单元分别由 2 个大部分组成：Preview：Tasks Before Class 和 Productive Reading。Preview：Tasks Before Class 用以调动学生自主学习的积极性，通过对重点词汇的“头脑风暴”（brainstorming）和焦点话题的讨论，激活、运用、构建和丰富大脑中的图式（schema）。而 Productive Reading 部分是每一个单元的核心内容，包括三篇精挑细选、原汁原味的文章，每篇文章都配有创新训练项目，并配有生词表。Section A 是主课文，是每一个单元学习的重点。

本书试图打破现有的教材编写体例，灵活驾驭用以实际提高阅读理解能力和英语语言运用能力的课程设计和题型安排，使学生在学习中能够兼顾掌握英语语言知识和技能、了解医学专业发展动态和提升医学人文素质。内容丰富、脉络清晰、信息面广，构成了医学人文英语学习的一个有机整体。

本书编者在编写过程中，参考了一些相关的国内外资料，在此谨向作者表示感谢。

医学人文英语教学尚在起步阶段，没有成熟的经验可循，由于时间和水平有限，编者唯恐挂一漏万，欢迎广大教师和同学提出宝贵意见，我们努力将本书打造成鲜活实用的优质教材。

编　者

2014 年 9 月

Contents

Unit 1 The Human Genome Project

Preview

A gene is a short piece of DNA. Genes tell the body how to build a specific protein. There are about 30,000 genes in each cell of the human body. Together, these genes make up the blueprint for the human body and determine how it works. In this unit, we are going to get a glimpse of advances in genetics. Section A introduces some advances in the Human Genome Project. Section B is that the Human Genome Project has yielded improvements in "genetic medicine". Section C covers the definition of the gene and its regulation and future direction.

Part I Preview: Tasks Before Class

I. Group Task: Words and Phrases Collection

Directions: This task is group-oriented so that students are required to form their own group to arrange the different roles to collect the useful words and phrases in Part II. Then, each group member should contribute to fill out the table below with the new words and phrases. The task is completed by finding an example sentence to help better define the meaning. Each group is required to submit a copy of this table before class.

No.	Words/ Phrases	Pronunciation	Part of Speech	English Meaning	Chinese Meaning	Example Sentences
1	catalyst	[ˈkætəlɪst]	*n.*	a substance that causes a chemical reaction to take place more quickly	[比喻] 触发因素；促进因素	Forgiveness is a powerful catalyst.
2						

II. Group Discussion

1. What is the idea of the Human Genome Project?

2. Is it possible for people to detect the risk of some diseases by gene testing? Give supporting details to defend your argument.

3. From your perspectives, what will happen in the field of medicine in the next decades?

Part II Productive Reading

Section A Pre-assessment

I. True/False Questions

Indicate whether each sentence below is true (T) or false (F).

1. _____ Gene **sequencing** or DNA **sequencing** involves identifying the order in which the elements making up a particular gene are combined.

2. _____ A **catalyst** is a substance that causes a chemical reaction to take place more quickly.

3. _____ The word "**engender**" means "to put someone in danger".

4. _____ If you **decipher** a piece of writing or a message, you decode or work out what it says, even though it is very difficult to read or understand.

5. _____ **Viability** represents the ability to change.

6. _____ The noun form of "vary" is "**variant**".

7. _____ If you **bolster** something such as someone's confidence or courage, you decrease it.

8. _____ When something such as an organization or an industry **emerges**, it comes into existence.

9. _____ A **pilot** scheme or a pilot project is the one that is used to test an idea after deciding whether to introduce it on a larger scale.

10. _____ A **carrier** is a person or an animal that is infected with a disease and so can make other people or animals ill.

II. Missing Sentences

Read this editorial from a medical publication on The Human Genome Project: a new reality. The last sentences in some paragraphs have been removed. Read the sentences (A-H) carefully and decide where they must go in the text. One example is already done for you.

A. Eventually, in 1992, John Sulston submitted a grant application for an enormous £ 40 ~ 50 million to fund a new centre—the Sanger Centre—which was to form the British arm of the Human Genome Project's sequencing efforts.

B. The result: a physical human genome map that would be crucial for the sequencing efforts.

C. In Canada, researchers found five variants on the FAD gene, which together confer an almost 100 per cent risk of developing Alzheimer's disease.

D. By the end of that year, 87 scientists were working at the Sanger Centre, under the leadership of John Sulston, beginning to map and sequence the human genome.

E. Assembling the sequence from many short segments of sequence was a hugely intense compute task that depended on emerging technology and software to succeed.

F. Crucially, researchers were, at the same time, beginning to apply computing solutions to genetics and DNA sequencing, developing methods that would make feasible the task of generating and handling genetic data globally.

G. Even before the Human Genome Project began in earnest, some commentators feared that this project had "engendered a controversy... that involves personalities and politics."

H. Where the cloned fragments came from or which overlapped was not known at this point.

The Human Genome[1] Project: a new reality

In June 1985, as dusk[2] encroached[3] on the second millennium[4], meetings aimed at outlining the practical task of sequencing the human genome began at the University of California, Santa Cruz. The scientific and technological conditions of the 1980s had become a catalyst[5] for these discussions. DNA cloning and Fred Sanger's sequencing methods, developed in the mid-to-late 1970s, were being exploited by scientists who felt that sequencing the human genome seemed possible at an experimental level. 1. [F]

This grand, new concept—a "Human Genome Project" —had strong supporters, who argued that deciphering[6] the human genome would lead to new understanding and benefits for human health as well as determined detractors[7], who feared such a project would provide a product that would bear little explanatory[8] power for humans—perhaps merely a meaningless string of letters. 2. [ ]

The personalities, the politics and the controversy[9] were only just emerging.

The Human Genome Project launched[10] in 1990, through funding from the US National Institutes of Health (NIH) and Department of Energy, whose labs joined with international collaborators[11] and resolved to sequence 95% of the DNA in human cells in just 15 years. Meanwhile in the UK, John Sulston and his colleagues at the MRC's Laboratory of Molecular[12] Biology in Cambridge, had, for several years, been working at mapping the genome of the nematode[13] worm and had resolved that sequencing the entire genome of the worm was finally feasible[14].

As the Human Genome Project was progressing in the US, in the UK the MRC approached the Wellcome Trust suggesting they form a new partnership[15] to fund John's proposed worm sequencing, as a pilot for the Human Genome Project. From here things soon snowballed: the Wellcome Trust suggested that a much larger sequencing effort, to bolster[16] the Human Genome Project should be embarked[17] upon in the UK and appointed one of their senior administrators, Michael Morgan, to look into the viability[18] of such a sequencing initiative[19]. 3. [ ]

In 1993—with funding from the Wellcome Trust and MRC—the Sanger Centre was officially opened. One scientist recalls being struck by the scale of the task that lay ahead, on arriving at the Institute in 1993 Simon Gregory reflects: "it was just a huge lab, a huge empty lab, with boxes and boxes of equipment. It was all very exciting." 4. [ ]

To sequence the human genome as accurately as possible, researchers developed the "hierarchical[20] shotgun" method. Researchers agreed that this was the best way to achieve the Human Genome Project's target of 95% coverage[21] of the human genome by 2005.

The first challenge was to create a map of the human genome—a set of index marks on the genome code, used to position the sequences of letters of code that would come later.

Researchers essentially broke many copies of the genome into fragments[22], each around 150,000 letters of code (or base-pairs) long. They inserted[23] the fragments into a bacterial[24] artificial chromosome[25] that could be grown in E. Coli bacteria[26] which divided, thereby replicating[27] the DNA samples to create a stable resource—a "library" of DNA clones. 5. [ ]

Using special enzymes[28], researchers could cut the individual clones into diagnostic[29] "fingerprint" of fragments defined by each clone's sequence. They could

then search among millions of fingerprints for shared fragments that would reveal overlaps among the clones. Researchers then assembled the clones into longer contiguous[30] regions and mapped these onto the human chromosomes. 6. [ ]

To generate sequence of the individual bases that make up the genome, scientists needed to break the cloned fragments into smaller, more manageable, chunks[31], each around 1,000 to 2,000 base-pairs long. Researchers sequenced these fragments of human DNA using the shotgun method developed by Fred Sanger and his colleagues a dozen years before. Much as in mapping, researchers used overlaps, this time in the letters of genetic[32] code itself, to reassemble the short stretches[33] of determined sequence. 7. [ ]

Gradually labs around the world began producing DNA sequence. By 1994, the Sanger Institute had produced its first 100,000 bases of human DNA sequence. Remarkably, researchers at the Institute had already produced ten times that amount from the nematode worm genome. The worm project was a trailblazer[34]—its methods, practices, collaborations and ethos[35] would be integral[36] to the development the social mores that would later lead to the successful completion of the Human Genome Project.

As the human sequence data was pouring out from centres across the globe, researchers were afforded glimpses[37] of the kind of power that the human genome sequence might have for medical advance. In 1995, researchers from the Sanger Centre, with international collaborators, located the BRCA2 gene, associated with increased risk of breast cancer. Elsewhere, as early as 1993, a US team had located the MSH2 gene, which increases the risk of colon[38] cancer for carriers. 8. [ ]

(997 words)

Notes:

1. MRC: Abbreviation for Medical Research Council in Britain (英国) 医学研究理事会

2. Wellcome Trust: The Wellcome Trust was established in 1936 as an independent charity funding research to improve human and animal health. The Trust has been described by the Financial Times as the United Kingdom's largest provider of non-governmental funding for scientific research and one of the largest providers in the world. 惠康基金会

3. hierarchical shotgun (sequencing): In hierarchical sequencing, also known as top-down sequencing, a low-resolution physical map of the genome is made prior to actual sequencing. From this map, a minimal number of fragments that cover the entire chromosome are selected for sequencing. In this way, the minimum amount of high-throughput sequencing and assembly is required. 层次鸟枪 (测序法)

4. base pair (bp): Two nitrogenous bases paired together in double-stranded DNA by weak bonds; specific pairing of these bases (adenine with thymine and guanine with cytosine) facilitates accurate DNA replication; when quantified (e.g., 8 bp), bp refers to the physical length of a sequence of nucleotides. 碱基对

5. BRCA2: BRCA2 are Tumor-suppressor genes associated with inherited forms of breast cancer and ovarian cancer. In women with mutations in either gene, there is a much higher risk of breast and certain other cancers than in women without such mutations.

Exercises

I. Comprehension of the Text

Answer the following questions by choosing the best from the 4 choices given below.

1. For scientists in the mid-to-late 1970s, the human genome sequencing were believed to be_____.
   A. dusk encroached
   B. be the outline of the practical task
   C. a catalyst
   D. at an experimental level
2. According to the timeline, which team justified that the entire genome sequencing of the nematode worm was feasible?
   A. NIH.
   B. Department of Energy.
   C. The UK team.
   D. Welcome Trust.
3. Hierarchical shotgun method was developed to improve the human genome sequencing's _____.
   A. accuracy
   B. achievement
   C. integrity
   D. efforts
4. What was the special enzymes' function in the process of mapping the human genome?
   A. They could be used to insert the base-pairs into a bacterial artificial chromosome.
   B. They could be used to cut the clones into diagnostic fingerprint of fragments.
   C. They could be used as the tool to assemble the clones into longer contiguous regions.
   D. They could be used to create a stable library of DNA clones.
5. In Paragraph 12, why did the author present that the worm project was a trailblazer?
   A. Because its methods contributed to the future successful completion of the

Human Genome Project.

B. Because its integrity contributed to the future successful completion of the Human Genome Project.

C. Because its practices contributed to the future successful completion of the Human Genome Project.

D. Because its collaboration contributed to the future successful completion of the Human Genome Project.

II. True/False Questions

Decide whether the following statements are true (T) or false (F) according to the text.

1. ( ) The supporters of "Human Genome Project" concerned the potential failure in the explanatory power for human.
2. ( ) To fund a pilot for the Human Genome Project, the Welcome Trust believed that this project should be only developed and embarked upon in the USA.
3. ( ) By the end of 1993, 87 scientists were successful in the mapping and sequencing the human Genome.
4. ( ) Without special enzymes, individual clones could not be separated into diagnostic fingerprint of fragments characterized by each clone's sequence.
5. ( ) BRCA2 gene can be located to detect the increase risk of breast cancer, while five variants on the FAD were characterized as almost 100 per cent risk of Alzheimer's disease.

III. Translation Exercises

Translate the Chinese words in the brackets into English, and write them down on the gaps.

1. The Human Genome Project's strong supporters argued that deciphering the human genome would lead to _____ (对人类健康的崭新理解及其相应益处) as well as _____ (坚定的反对者) feared such a project would provide a product that would _____ (不具有解释力) for humans.
2. Even before the Human Genome Project began _____ (认真地), some commentators feared that this project had "_____ (引起争议)... that involves personalities and politics."
3. As the human sequence data was _____ (蜂拥而来) from centres across the globe, researchers were afforded _____ (初步感受这种力量) that the human genome sequence might have for medical advance.
4. Assembling the sequence from many short segments of sequence was _____

_____（是一项依赖于新型科技及软件成功成果的高强度计算任务）.

5. Crucially, researchers were, at the same time, beginning to apply computing solutions to _____（遗传和 DNA 的排序）, developing methods that would _____（使全球化产生和处理遗传数据的任务变得可行）.

Translation Tips:

鉴于中英文思维的不同，中英文之间的翻译可以遵循以下逻辑。

中文习惯把重要的信息留在后面说，例如："……的任务"；而英文则习惯于将最重要的信息放在句子前面，譬如英文中的定语从句、定语后置，都说明其语言习惯。例如：a task of... /that...。因此在做翻译练习时，应该考虑这种语言文化上的差异，对语序进行调整，尽量在翻译前对翻译目标进行逻辑上的分析。

Vocabulary

[1] genome [ˈdʒɪːnəʊm] *n.* 基因组，染色体组
[2] dusk [dʌsk] *n.* 黄昏，傍晚；幽暗
[3] encroach [ɪnˈkrəʊtʃ] *vi.* 侵犯；侵占
[4] millennium [mɪˈlenɪəm] *n.* 一千年；千年期；千禧年
[5] catalyst [ˈkætəlɪst] *n.* 催化剂；刺激因素，触发因素
[6] decipher [dɪˈsaɪfə(r)] *vt.* 破译（密码）
[7] detractor [dɪˈtræktə(r)] *n.* 贬低者
[8] explanatory [ɪkˈsplænətrɪ] *adj.* 解释的；说明的
[9] controversy [ˈkɒntrəvɜːsɪ] *n.* 公开辩论；论战
[10] launch [lɔːntʃ] *vt.* 开展（活动、计划等）
[11] collaborator [kəˈlæbəreɪtə(r)] *n.* 协作者，合作者
[12] molecular [məˈlekjələ(r)] *adj.* 分子的，由分子组成的
[13] nematode [ˈnemətəʊd] *n.* 线虫类
[14] feasible [ˈfiːzəbl] *adj.* 可行的；可用的
[15] partnership [ˈpɑːtnəʃɪp] *n.* 伙伴关系；合伙人身份
[16] bolster [ˈbəʊlstə(r)] *vt.* 支持；支撑
[17] embark [ɪmˈbɑːk] *vi.* 着手，从事
[18] viability [ˌvaɪəˈbɪlətɪ] *n.* 生存能力，发育能力
[19] initiative [ɪˈnɪʃətɪv] *n.* 主动性；主动精神；主动权；倡议
[20] hierarchical [ˌhaɪəˈrɑːkɪkl] *adj.* 按等级划分的，等级（制度）的

[21] coverage [ˈkʌvərɪdʒ] *n.* 范围，规模
[22] fragment [ˈfrægmənt] *n.* 碎片
[23] insert [ɪnˈsɜːt] *vt.* 插入；嵌入
[24] bacterial [bækˈtɪərɪəl] *adj.* 细菌的；细菌性
[25] chromosome [ˈkrəʊməˌsəʊm] *n.* [生] 染色体
[26] bacteria [bækˈtɪərɪə] *n.* 细菌（bacterium 的名词复数）
[27] replicate [ˈreplɪkeɪt] *vt.* 复制，复写
[28] enzyme [ˈenzaɪm] *n.* [生化] 酶
[29] diagnostic [ˌdaɪəgˈnɒstɪk] *adj.* 诊断的，判断的；特征的
[30] contiguous [kənˈtɪgjʊəs] *adj.* 接触的；邻近的；共同的
[31] chunk [tʃʌŋk] *n.* 厚厚的一块
[32] genetic [dʒəˈnetɪk] *adj.* 遗传的；基因的
[33] stretch [stretʃ] *n.* 伸展；延伸
[34] trailblazer [ˈtreɪlbleɪzə(r)] *n.* 开路的人；先驱者；开拓者
[35] ethos [ˈiːˌθɔs] *n.* 民族精神
[36] integral [ˈɪntɪgrəl] *adj.* 完整的
[37] glimpse [glɪmps] *n.* 一瞥，一看
[38] colon [ˈkəʊlən] *n.* 冒号；[解] 结肠

Section B

Exercises

I. Blanks Filling

Read the following passage with missing words and fill in the blanks with the best choice from the box provided.

refer	regardless of	elevated	recurrent	derived from
advances	result in	associated with	free of	prompts

Genomic Medicine—An Updated Primer—NEJM

Cathy, a 40-year-old mother of three, arrives in your office for her annual physical. She has purchased a commercial genomewide scan, which she believes measures the clinically meaningful risk that common diseases will develop, and has completed her family history online using My Family Health Portrait, a tool developed for this purpose by the U. S. Surgeon General. Her genomewide scan suggests a slightly

1. _____ risk of breast cancer, but you correctly recognize that this information is of unproven value in routine clinical care. On importing Cathy's family-history file, your office's electronic health record system alerts you to the fact that Cathy is of Ashkenazi Jewish heritage and has several relatives with breast cancer, putting her at heightened risk for the hereditary[1] breast and ovarian[2] cancer syndrome.

The system 2. _____ you to discuss Cathy's risk of breast and ovarian cancer during the visit. Considering both her family history and ancestry, you 3. _____ Cathy to a health care professional with advanced genetics training for consultation.

In the coming months Cathy elects to have her DNA tested for mutations in BRCA1 and BRCA2, the genes 4. _____ hereditary breast and ovarian cancer syndrome, and to undergo a mammographic[3] examination. Although the results of her genetic tests are negative, her mammogram reveals a suspicious abnormality[4]. A biopsy[5] is performed, and breast cancer is detected. Surgery is successful. Pathological[6] examination of tissue from the excised tumor reveals that it is positive for estrogen[7]-receptor[8] protein and negative for human epidermal[9] growth factor receptor type 2 (HER2); the lymph[10] glands[11] are 5. _____ cancer cells. Genetic-expression profiling[12] of the tumor indicates a relatively high risk of 6. _____ cancer, and Cathy elects to receive adjuvant[13] chemotherapy[14] followed by treatment with tamoxifen[15]. Five years later, the cancer has not recurred.

Remarkable 7. _____ have been made in understanding the human genome's contribution to health and disease since the first Genomic Medicine series was launched in the Journal in 2002. The vignette[16] about Cathy illustrates the strengths and limitations of these advances. Completion of the Human Genome Project in 2003, was a major driver for the current period of biomedical[17] discovery, and the pace continues to accelerate. This project spurred the development of innovations with extraordinary benefits.

Initially, clinically useful discoveries 8. _____ the Human Genome Project yielded improvements in "genetic medicine" —that is, the use of knowledge about single genes to improve the diagnosis and treatment of single-gene disorders. However, our increased understanding of the interactions between the entire genome and nongenomic factors that 9. _____ health and disease is paving the way for an era of "genomic medicine," in which new diagnostic and therapeutic approaches to common multifactorial[18] conditions are emerging.

As a result of genomic discoveries, increasing numbers of clinical guidelines now