



· 导读版 ·

Calculations for Molecular Biology and Biotechnology:

A Guide to Mathematics in the Laboratory

分子生物学 与生物技术中的计算： 实验室数学指南

Frank H. Stephenson



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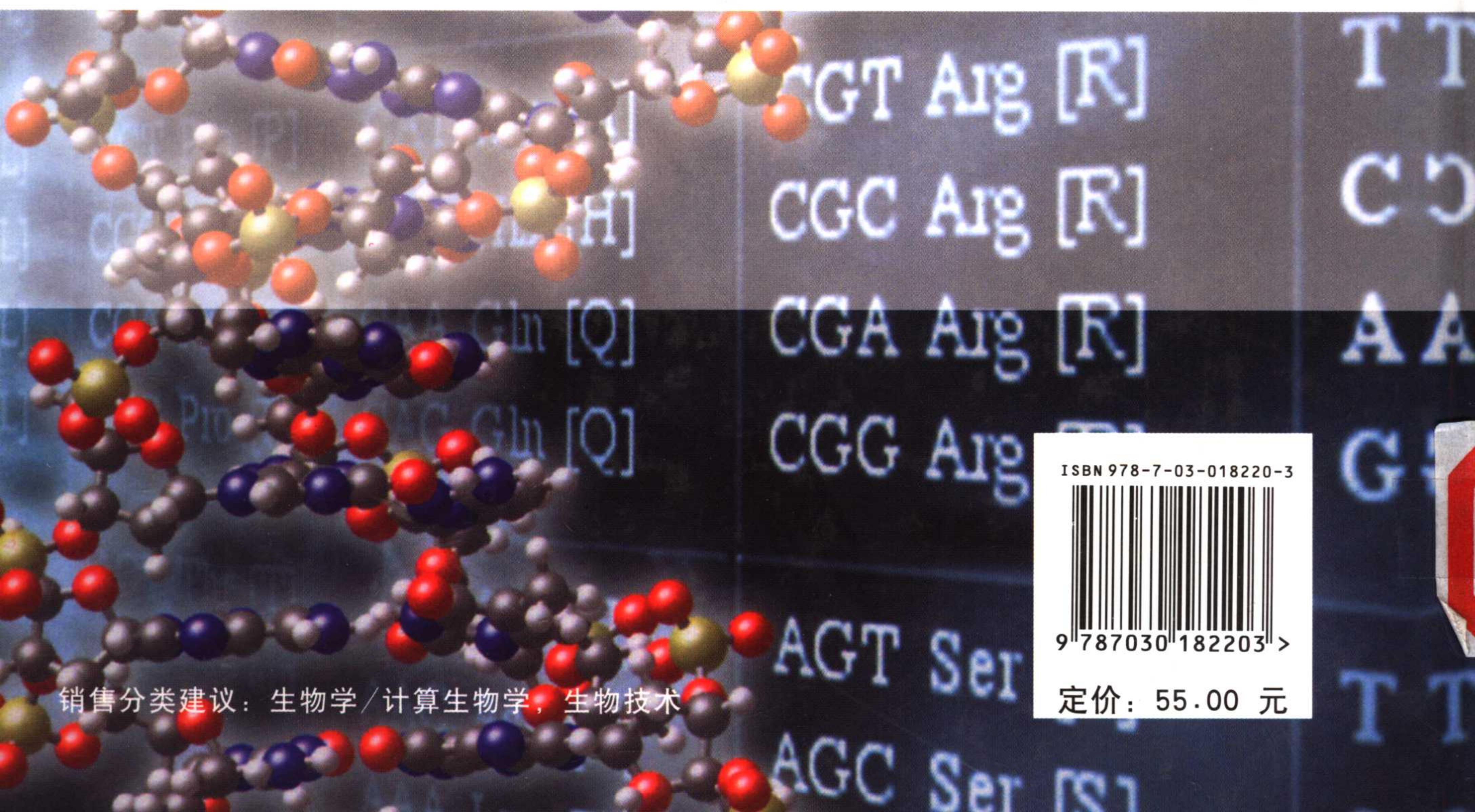
A Guide to Mathematics in the Laboratory

分子生物学与生物技术中的计算： 实验室数学指南

本书是一本实验室数学指南，广泛介绍了遗传工程实验过程中所遇到的计算问题。本书主要适用于学生、技术人员和科研人员，为读者提供了具体的计算实例，这些实例多是在基因发现和分析过程中经常遇到的计算问题。全书所采用的计算实例的介绍形式，简单易懂，便于读者掌握。本书是从事DNA操作和分析人员不可或缺的完美的实验伙伴。

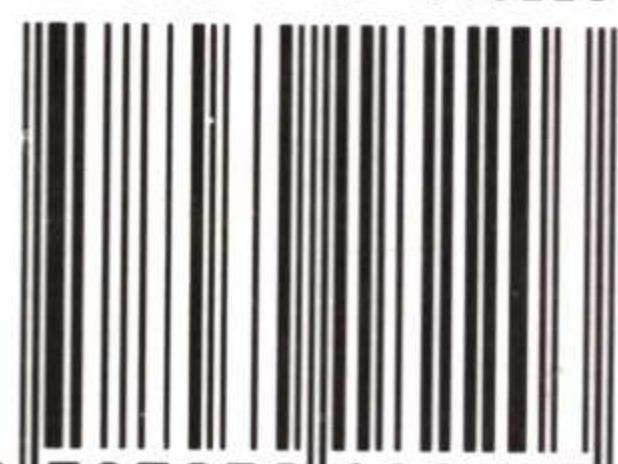
- 对基础研究实验过程中遇到的各种各样的计算问题给予了广泛的指导。
- 以一种贯穿实验始终的计算实例的形式介绍各种计算方法，非常浅显易懂。
- 重要的章节具体介绍了与细菌、噬菌体、PCR、放射性同位素、重组DNA、离心、寡核苷酸、蛋白质和法医学相关的实验工作中所遇到的计算问题。

本书读者对象主要是生物学相关专业的学生和实验技术人员，亦可作为经验丰富的科研人员的参考。



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Frank H. Stephenson

Applied Biosystems, Foster City, California

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Frank H. Stephenson

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To my wife, Laurie, and our beautiful daughter, Myla.

前言

回想我的高中化学老师,和当时的我自己罕有相似之处:他不同意我的穿着和头发,对我以网络冲浪为职业志向更是嗤之以鼻;我则回敬说他抽烟太多。但是不管怎么说,他教会了我计算溶液的浓度,我也完全同意了他关于数学在生物和化学科学中至关重要的看法。等我毕业走出课堂的时候,我感觉我似乎可以把光速转换成皮摩尔的单位来度量了。因为我所从事的是分子生物学的教学工作,在我每天的教学生活中,我在他的课上学到的东西,要远远比在其他课堂里学的东西实用。

数学是一门美丽优雅、条理性很强的科学。有人称它是世界语言。果真如此的话,那它肯定有很多方言。一个问题有多种解决方法,没有哪一种是最合理的。我经常发现一个有趣的现象,就是一些对数学充满热情的人们总是以自己独有的方式感受数学。或许有些人会问我,“你为什么用那种方式解决问题?”“显然,”我的评论者们继续说道,“如果你用这种方法的话,会更快捷,更合乎逻辑,更简便易行。这是解决问题的唯一途径。”或许对他们而言如此。但每个人思考问题的方式是不一样的。例如,在解决一个与浓度相关的问题的时候,人们往往很自然的就采用一个比例关系,或者用公式 $C_1 V_1 = C_2 V_2$, 或者采用本书介绍的其他方法。事实上,这些方法各有侧重,采用其中任何一种方法都可以得到你想要的答案。我想,这就是数学之美。

我一直在思索如何解决分子生物学实验室的常见问题。直到去年,我才想到一个办法,把这些问题汇总在一起,统称为“因次分析”。也叫 Canceling terms,这个提法更易于理解。很多人建议我用公式 $C_1 V_1 = C_2 V_2$,但都没能说服我。为此,我也没少受嘲笑和奚落。可也有很多人支持我。当我想到我可以用“因次分析”把这些问题都归拢在一起时,我觉得我的感觉,就像病人在向医生叙述难以名状的病情时的那种焦躁不安的情绪,但是当医生把这种病情用非常专业的词汇表达出来时,病人一下子就平静下来了。至少病人知道了其他人也曾经得过这种病,有过类似的痛苦经历,医生们也在研究它,而且这种病有可能治愈。

如果对本书所涉及的每一问题的所有可能的解决办法都要讨论一遍的话,那将是一件十分繁琐的事情。我毫不同情那些认为每一问题都应该有其他更好的解决方法的人。如果把本书作为实验室常用参考书,当你们用自己的实验数据去代替本书中所用到的数值时,我肯定你们的实验做不好。你们必须有适合你们需要的数值,只有这样,你们才不会把盐加得太少以至于你们培养的细胞受到渗透压胁迫,也只有这样,你们才不会把盐加得太多以至于你们在酶切 DNA 时 *EcoRI* 有星号活性。

衷心感谢我的同事 Maria Abilock 认真阅读了我的书稿并提出中肯的意见,尽管她觉得她的解决办法比我的要好。

Frank H. Stephenson

(孙红梅 译)

Foreword

It was sometimes difficult for me to find a common ground with my high school chemistry teacher. We couldn't agree on what was appropriate attire or hair length for a sophomore. He had no respect for the notion that surfing is a viable career goal. He smoked way too much. But it was either in spite of him or because of him that I learned the mathematics involved in calculating the concentration of solutions, and I eventually agreed with him on the importance of numbers in the biological and chemical sciences. By the time I got out of that class, I was feeling as though I could have converted the speed of light into picomoles. As I undertook a career in molecular biology and teaching, it was what I learned in that class, more than in any other, that I have used on almost a daily basis.

Mathematics is a beautiful and elegant way of expressing order. I have heard it called a universal language. If true, then there are many dialects. There are any number of ways to approach a problem, no one of them necessarily more legitimate than another. I have always found interesting the passion and fervor people attach to their particular approach to mathematics. "Why do you do the problem **that** way?" I might be asked. "Clearly," my critic continues, "if you solve the problem **this** way, it's much quicker, more logical, and easier to follow. This is the only way that makes any sense." Well, maybe to them. Not everyone's brain works in the same way. In solving a problem in concentration, for example, it is probably amenable to solution by using a relationship of ratios, or $C_1V_1 = C_2V_2$, or the approach most often taken in this book. In actuality, they are all variations on a theme. Any one of them will get you the answer. Therein, I believe, lies the very beauty of mathematics.

It wasn't until this last year that I discovered the approach that I take to most of the problems encountered in the molecular biology laboratory has a name. It is called **dimensional analysis**. I always thought of it as "canceling terms." My brain is comfortable with this method. Many have tried to convert me to the use of the $C_1V_1 = C_2V_2$ approach, but all have failed. I have been chided and ridiculed by some for the manner in which I solve problems. I have been applauded by others. When I learned that the approach I take has the name **dimensional analysis**, I felt, in a way, like the person who visits the doctor with some inexplicable malady and who is reassured when the doctor attaches some Latin-sounding name to it. At least then, the

individual knows that other people must also have the affliction, that it has been studied, and that there may even be a cure.

To present every possible way that each problem in this book could be solved would have made it too cumbersome. I make no apologies to those who might think that any one problem is better solved in another manner. To those of you who use this book as a companion in the laboratory, if you replace your values with the ones I have used in the example problems, you will do fine. You will have the numbers you need such that, for example, you will not be adding too little or too much salt that will send your cultured cells into osmotic shock or give you *EcoRI* star activity when digesting DNA.

My appreciation goes to my colleague Maria Abilock for bringing her critical eye to bear on this manuscript. She agreed to critique the draft in spite of the fact that she feels her way of solving problems is better than mine.

Frank H. Stephenson, Ph.D.

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(孙红梅 译)

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