

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.

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