
Modeling and Computational Engineering

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(Work in Progress) The purpose of this document is to explain how computers solve mathematical models. Many of the most common numerical methods is presented, we show how to implement them in Python, and discuss the limitations. The mathematical formalism is kept to a minimum. All the material is available at github^a. For each of the chapter there is a Jupyter notebook^b. This makes it possible to run all the codes in this document. We strongly recommend to install Python from Anaconda^c. All documents have been prepared using doconce^d.

Code Examples in this Book

The code examples in this book are not optimized for speed. This is book is not meant as an introduction to good Python practice, we use Python to implement the algorithms. The choice has been made to focus on clarity rather than speed, once you get familiar with Python you can easily optimize the code examples presented here.

^a<https://github.com/ahiorth/CompEngineering>

^b<https://github.com/ahiorth/CompEngineering/tree/master/pub/chapters>

^c<https://www.anaconda.com/>

^d<https://github.com/ahiorth/CompEngineering/tree/master/pub/chapters>

Preface

What does computers do better than humans? What is it possible to compute? These questions have not been fully answered yet, and in the coming years we will most likely see that the boundaries for what computers can do will expand significantly. Many of the fundamental laws in nature have been known for quite some time, but still it is almost impossible to predict the behavior of water (H_2O) from quantum mechanics. The most sophisticated super computers runs for days and are only able to simulate the behavior of molecules in a couple of seconds, almost too short to extract meaningful thermodynamic properties. This leads to another interesting question: What does humans do better than machines? A large part of the answer to this question is *modeling*. Modeling is the ability to break a complicated, unstructured problem into smaller pieces that can be solved by computers or by other means. Modeling requires *domain knowledge*, one need to understand the system well enough to make the correct or the most efficient simplifications. The process usually starts with some experimental data that one would like to understand, it could be the increasing temperature in the atmosphere or sea, it could be changes in the chemical composition of a fluid passing through a rock. The modeler then makes a mental image, which includes a set of mechanisms that could be the cause of the observed data. These mechanisms then needs to be formulated mathematically. How can we know if a model of a system is good? First of all, a good model is a model that do not break any of the fundamental laws of nature, such as mass (assuming non relativistic effects) and energy conservation. Even if you are searching for new laws of nature, you have to make sure that

your model respect the existing laws, because then a deviation from your model and the observations could be a hint of the new physics you are searching for. Secondly, the model must be able to match the observable data, with a limited set of variables. The variables should be determined from data, and then the model should be able to make some predictions that can be tested. Thus, the true purpose of the model is not only to match experimental data, but serve as a framework where the underlying mechanisms of the process can be understood. This is done by making model predictions, test them, and improve the model.

In this course our main focus will be on how to use computers to solve models. We will show you through numerical projects how a mathematical model of a physical system can be made, and you will have the possibility to explore the model. Computers are extremely useful, they can solve problems that would be impossible to solve by hand. However, it is extremely important to know about the limitations and strength of various algorithms. One need to have a toolbox of various algorithms that can be employed depending on the problem one are studying. Sometimes speed is not an issue, and one can use simpler algorithms, but in many cases *speed is an issue*. Thus it is important to not waste computational time when it is not needed, we will encounter examples of this many times in this course.

Why should you spend time learning about algorithms that have been implemented already in a software that most likely can be downloaded for free? There are many answers to this question, some more practical and some that goes deeper. Lets start with the practical considerations: Often you encounter a problem that needs to be solved by a computer, it could be to fit an analytical model to data. Once you have this problem, one could ask Mr. Google for a solution, after a web search you will quickly realize that there are numerous ways of achieving what you want. By educating yourself within the most basic numerical methods, presented in this course, you will be able to judge for yourself which method to use in a specific case. If you choose a method suggested on the web, and try it out, it might happen that it works quite fine in many cases. But sooner or later you will encounter a problem that the computer struggles with, and it is very useful to have some skills within numerical analysis which can be helpful in identifying why the numerical method does not find a solution in some cases. If you know the why, it is much easier to find a cure. Another motivation is that development of most of the different numerical methods are *not that difficult*, they usually follow a very similar pattern, but there are some "tricks". It is extremely useful to

learn these tricks, they can be adopted to a range of different problems, many are easily implemented in a spreadsheet. There are some more deeper arguments, and that is that the numerical methods are developed to solve a *general* problem. Most of the time we work with *specific* problems, and we would like to have an algorithm that is optimal for our problem that goes beyond only choosing the right one. Having understood and learned all the cool tricks that was used in the development of the algorithm in the general case, it is an excellent starting point for adopting the algorithm to your specific situation. Secondly development of an algorithm is a concrete case of *Computational Thinking*. Computational thinking is not necessarily related to computers and programming, but it is a way of structuring your work into precise statements that are being executed one at a time in a specific order. By learning about algorithmic development, you will train yourself in the art of computational thinking, which is a useful skill in all kind of problem solving.

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Aksel Hiorth

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The mathematics introduced in this chapter is absolutely essential in order to understand the development of numerical algorithms. We strongly advice you to study it carefully, implement python scripts and investigate the results, reproduce the analytical derivations and compare with the numerical solutions.

1.1 Truncation Errors

The solution to a physical model is usually a function. The function could describe the temperature evolution of the earth, it could be growth of cancer cells, the water pressure in an oil reservoir, the list is endless. If we can solve the model analytically, the answer is given in terms of a continuous function. Most of the models cannot be solved analytically, then we have to rely on computers to help us. The computer does not have any concept of continuous functions, a function is always evaluated at some point in space and/or time. Assume for simplicity that the solution to our problem is $f(x) = \sin x$, and we would like to visualize the solution. How many points do we need in our plot to approximate the true function? In figure 1.1, there is a plot of $\sin x$ on the interval $[-\pi, \pi]$.

From the figure we see that in some areas only a couple of points are needed in order to represent the function well, and in some areas more points are needed. To state it more clearly; between $[-1, 1]$ a linear

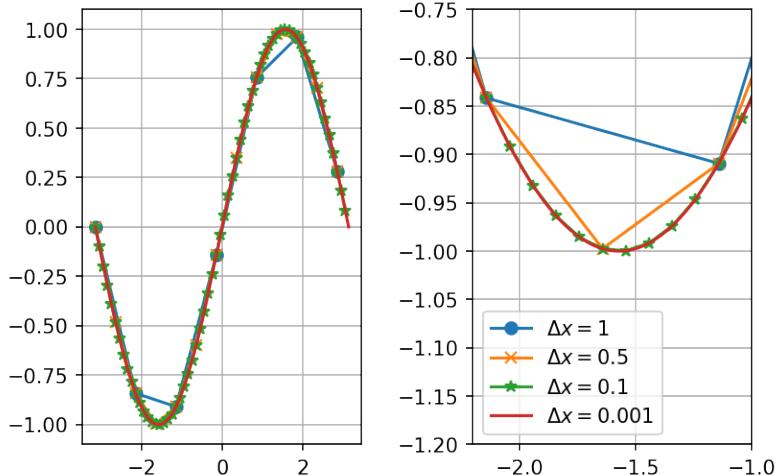


Fig. 1.1 A plot of $\sin x$ for different spacing of the x -values.

function (few points) approximate $\sin x$ well, whereas in the area where the derivative of the function changes e.g. in $[-2, -1]$, we need the points to be more closely spaced to capture the behavior of the true function.

Discretization and Truncation Error

To represent a function of space and/or time in a computer, the function needs to be discretized. When a function is discretized it leads to discretization errors. The difference between the "true" answer and the answer obtained from a practical (numerical) calculation is called the *truncation error*.

Why do we care about the number of points? In many cases the function we would like to evaluate can take a very long time to evaluate. Sometimes simulation time is not an issue, then we can use a large number of function evaluations. However, in many applications simulation time is *an issue*, and it would be good to know where the points needs to be closely spaced, and where we can manage with only a few points.

What is a *good representation* of the true function? We cannot rely on visual inspection. In the next section we will show how Taylor polynomial representation of a function is a natural starting point to answer this question.

1.2 Taylor Polynomial Approximation

There are many ways of representing a function, but perhaps one of the most widely used is Taylor polynomials. Taylor series are the basis for solving ordinary and differential equations, simply because it makes it possible to evaluate any function with a set of limited operations: *addition, subtraction, and multiplication*. The Taylor polynomial, $P_n(x)$ of degree n of a function $f(x)$ at the point c is defined as:

Taylor polynomial:

$$\begin{aligned} P_n(x) &= f(c) + f'(c)(x - c) + \frac{f''(c)}{2!}(x - c)^2 + \cdots + \frac{f^{(n)}(c)}{n!}(x - c)^n \\ &= \sum_{k=0}^n \frac{f^{(k)}(c)}{k!}(x - c)^k. \end{aligned} \quad (1.1)$$

If the series is around the point $c = 0$, the Taylor polynomial $P_n(x)$ is often called a Maclaurin polynomial, more examples can be found here¹. If the series converge (i.e. that the higher order terms approach zero), then we can represent the function $f(x)$ with its corresponding Taylor series around the point $x = c$:

$$f(x) = f(c) + f'(c)(x - c) + \frac{f''(c)}{2!}(x - c)^2 + \cdots = \sum_{k=0}^{\infty} \frac{f^{(k)}(c)}{k!}(x - c)^k. \quad (1.2)$$

The Maclaurin series of $\sin x$ is:

$$\sin x = x - \frac{x^3}{3!} + \frac{x^5}{5!} - \frac{x^7}{7!} + \cdots = \sum_{k=0}^{\infty} \frac{(-1)^n}{(2n+1)!} x^{2n+1}. \quad (1.3)$$

In figure 1.2, we show the first nine terms in the Maclaurin series for $\sin x$ (all even terms are zero).

Note that we get a decent representation of $\sin x$ on the domain, by *only knowing the function and its derivative in a single point*. The error term in Taylors formula, when we represent a function with a finite number of polynomial elements is given by:

¹ https://en.wikipedia.org/wiki/Taylor_series

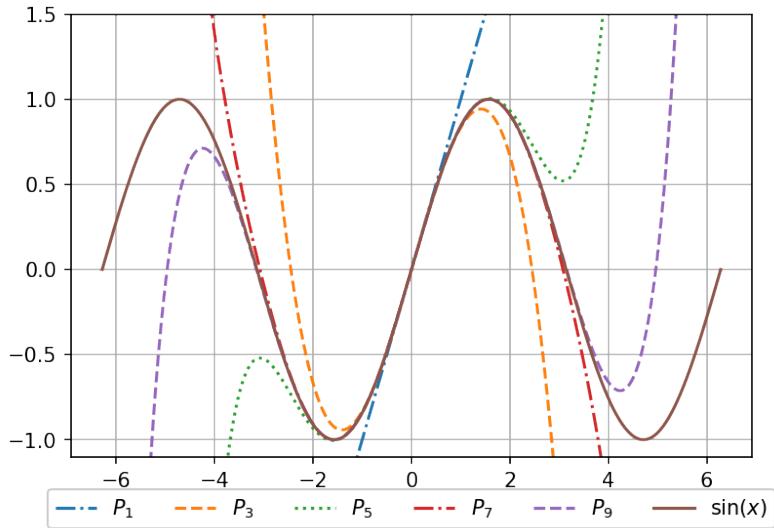


Fig. 1.2 Up to ninth order in the Maclaurin series of $\sin x$.

Error term in Taylors formula:

$$\begin{aligned} R_n(x) &= f(x) - P_n(x) = \frac{f^{(n+1)}(\eta)}{(n+1)!}(x-c)^{n+1} \\ &= \frac{1}{n!} \int_c^x (x-\tau)^n f^{(n+1)}(\tau) d\tau, \end{aligned} \quad (1.4)$$

for some η in the domain $[x, c]$.

If we want to calculate $\sin x$ to a precision lower than a specified value we can do it as follows:

```
import numpy as np

# Sinus implementation using the Maclaurin Serie
# By setting a value for eps this value will be used
# if not provided
def my_sin(x,eps=1e-16):
    f = power = x
    x2 = x*x
    sign = 1
    i=0
    while(power>=eps):
        sign = - sign
        power = power * x2 / (i+1)
        x2 = x2 * x2 / (i+1)
        i=i+1
```

```

power *= x2/(2*i+2)/(2*i+3)
f += sign*power
i += 1
print('No function evaluations: ', i)
return f

x=0.8
eps = 1e-9
print(my_sin(x,eps), 'error = ', np.sin(x)-my_sin(x,eps))

```

This implementation needs some explanation:

- The error term is given in equation (1.4), and it is an even power in x . We do not know which η to use in equation (1.4), thus we use a trick and simply say that the error term is smaller than the highest order term. Thus, we stop the evaluation if the highest order term in the series is lower than the uncertainty. Thus, in practice we add the error term to the function evaluation, our estimate will always be better than the specified accuracy.
- We evaluate the polynomials in the Taylor series by using the previous values too avoid too many multiplications within the loop, we do this by using the following identity:

$$\sin x = \sum_{k=0}^{\infty} (-1)^n t_n, \text{ where: } t_n \equiv \frac{x^{2n+1}}{(2n+1)!}, \text{ hence :}$$

$$t_{n+1} = \frac{x^{2(n+1)+1}}{(2(n+1)+1)!} = \frac{x^{2n+1}x^2}{(2n+1)!(2n+2)(2n+3)}$$

$$= t_n \frac{x^2}{(2n+2)(2n+3)} \quad (1.5)$$

1.2.1 Evaluation of polynomials

How to evaluate a polynomial of the type: $p_n(x) = a_0 + a_1x + a_2x^2 + \dots + a_nx^n$? We already saw a hint in the previous section that it can be done in different ways. One way is simply to do:

```

pol = a[0]
for i in range(1,n+1):
    pol = pol + a[i]*x**i

```

Note that there are n additions, whereas there are $1 + 2 + 3 + \dots + n = n(n+1)/2$ multiplications for all the iterations. Instead of evaluating

the powers all over in each loop, we can use the previous calculation to save the number of multiplications:

```
pol = a[0] + a[1]*x
power = x
for i in range(2,n+1):
    power = power*x
    pol = pol + a[i]*power
```

In this case there are still n additions, but now there are $2n - 1$ multiplications. For $n = 15$, this amounts to 120 for the first, and 29 for the second method. Polynomials can also be evaluated using *nested multiplication*:

$$\begin{aligned} p_1 &= a_0 + a_1 x \\ p_2 &= a_0 + a_1 x + a_2 x^2 = a_0 + x(a_1 + a_2 x) \\ p_3 &= a_0 + a_1 x + a_2 x^2 + a_3 x^3 = a_0 + x(a_1 + x(a_2 + a_3 x)) \\ &\vdots \end{aligned} \tag{1.6}$$

and so on. This can be implemented as:

```
pol = a[n]
for i in range(n-1,1,-1):
    pol = a[i] + pol*x
```

In this case we only have n multiplications. So if you know beforehand exactly how many terms is needed to calculate the series, this method would be the preferred method, and is implemented in NumPy as `polyval`².

1.3 Calculating Numerical Derivatives of Functions

The derivative of a function can be calculated using the definition from calculus:

$$f'(x) = \lim_{h \rightarrow 0} \frac{f(x+h) - f(x)}{h} \simeq \frac{f(x+h) - f(x)}{h}. \tag{1.7}$$

Not that h can be both positive and negative, if h is positive equation (1.7) is termed *forward difference*, because we use the function value on the right ($f(x + |h|)$). If on the other hand h is negative equation (1.7) is termed *backward difference*, because we use the value to the left ($f(x - |h|)$). ($|h|$ is the absolute value of h). In the computer we cannot

²<https://docs.scipy.org/doc/numpy/reference/generated/numpy.polyval.html#r138ee7027ddf-1>

take the limit, $h \rightarrow 0$, a natural question is then: What value to use for h ? In figure 1.3, we have evaluated the numerical derivative of $\sin x$, using the formula in equation (1.7) for different step sizes h .

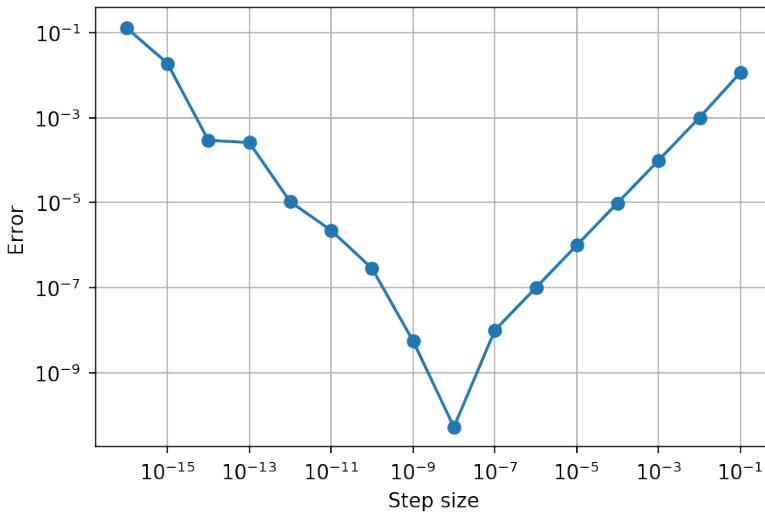


Fig. 1.3 Error in the numerical derivative of $\sin x$ at $x = 0.2$ for different step size.

We clearly see that the error depends on the step size, but there is a minimum; choosing a step size too large give a poor estimate and choosing a too low step size give an even worse estimate. The explanation for this behavior is two competing effects: *mathematical approximation* and *round off errors*. Let us consider approximation or truncation error first. By using the Taylor expansion in equation (1.2) and expand about x and the error formula (1.4), we get:

$$f(x+h) = f(x) + f'(x)h + \frac{h^2}{2}f''(\eta), \text{ hence:}$$

$$f'(x) = \frac{f(x+h) - f(x)}{h} - \frac{h}{2}f''(\eta), \quad (1.8)$$

for some η in $[x, x+h]$. Thus the error to our approximation is $hf''(\eta)/2$, if we reduce the step size by a factor of 10 the error is reduced by a factor of 10. Inspecting the graph, we clearly see that this is correct as the step size decreases from 10^{-1} to 10^{-8} . When the step size decreases more, there is an increase in the error. This is due to round off errors, and can be understood by looking into how numbers are stored in a computer.

1.3.1 Round off Errors

In a computer a floating point number, x , is represented as:

$$x = \pm q2^m. \quad (1.9)$$

This is very similar to our usual scientific notation where we represent large (or small numbers) as $\pm qEm = \pm q10^m$. The processor in a computer handles a chunk of bits at one time, this chunk of bit is usually termed *word*. The number of bits (or byte which almost always means a group of eight bits) in a word is handled as a unit by a processor. Most modern computers use 64-bits (8 bytes) processors. We are not going too much into all the details, the most important message is that the units handled by the processor are *finite*. Thus we cannot store numbers in a computer with infinite accuracy, e.g. $1./3. = 0.3333\dots$ cannot be stored accurately in a computer. In many cases this is not a problem, but in some cases, as with evaluating numerical derivatives, it is. The reason is that we subtract two numbers that are almost equal, and because of this the round off error might dominate the answer. How large is the round off error? This depends on exactly how numbers are stored in the machine. To make the following a bit more understandable, we will recap some binary number basics.

Binary numbers. Binary numbers are used in computers because processors are made of billions of transistors, the end state of a transistor is off or on, representing a 0 or 1 in the binary system. Assume, for simplicity, that we have a processor that uses a word size of 4 bits (instead of 64 bits). How many *unsigned* (positive) integers can we represent in this processor? Let's write down all the possible combinations of ones and zeros and also do the translation from base 2 numerical system to base 10 numerical system:

$$\begin{aligned}
 0\ 0\ 0\ 0 &= 0 \cdot 2^3 + 0 \cdot 2^2 + 0 \cdot 2^1 + 0 \cdot 2^0 = 0 \\
 0\ 0\ 0\ 1 &= 0 \cdot 2^3 + 0 \cdot 2^2 + 0 \cdot 2^1 + 1 \cdot 2^0 = 1 \\
 0\ 0\ 1\ 0 &= 0 \cdot 2^3 + 0 \cdot 2^2 + 1 \cdot 2^1 + 0 \cdot 2^0 = 2 \\
 0\ 0\ 1\ 1 &= 0 \cdot 2^3 + 0 \cdot 2^2 + 1 \cdot 2^1 + 1 \cdot 2^0 = 3 \\
 0\ 1\ 0\ 0 &= 0 \cdot 2^3 + 1 \cdot 2^2 + 0 \cdot 2^1 + 0 \cdot 2^0 = 4 \\
 0\ 1\ 0\ 1 &= 0 \cdot 2^3 + 1 \cdot 2^2 + 0 \cdot 2^1 + 1 \cdot 2^0 = 5 \\
 0\ 1\ 1\ 0 &= 0 \cdot 2^3 + 1 \cdot 2^2 + 1 \cdot 2^1 + 0 \cdot 2^0 = 6 \\
 0\ 1\ 1\ 1 &= 0 \cdot 2^3 + 1 \cdot 2^2 + 1 \cdot 2^1 + 1 \cdot 2^0 = 7 \\
 1\ 0\ 0\ 0 &= 1 \cdot 2^3 + 0 \cdot 2^2 + 0 \cdot 2^1 + 0 \cdot 2^0 = 8 \\
 1\ 0\ 0\ 1 &= 1 \cdot 2^3 + 0 \cdot 2^2 + 0 \cdot 2^1 + 1 \cdot 2^0 = 9 \\
 1\ 0\ 1\ 0 &= 1 \cdot 2^3 + 0 \cdot 2^2 + 1 \cdot 2^1 + 0 \cdot 2^0 = 10 \\
 1\ 0\ 1\ 1 &= 1 \cdot 2^3 + 0 \cdot 2^2 + 1 \cdot 2^1 + 1 \cdot 2^0 = 11 \\
 1\ 1\ 0\ 0 &= 1 \cdot 2^3 + 1 \cdot 2^2 + 0 \cdot 2^1 + 0 \cdot 2^0 = 12 \\
 1\ 1\ 0\ 1 &= 1 \cdot 2^3 + 1 \cdot 2^2 + 0 \cdot 2^1 + 1 \cdot 2^0 = 13 \\
 1\ 1\ 1\ 0 &= 1 \cdot 2^3 + 1 \cdot 2^2 + 1 \cdot 2^1 + 0 \cdot 2^0 = 14 \\
 1\ 1\ 1\ 1 &= 1 \cdot 2^3 + 1 \cdot 2^2 + 1 \cdot 2^1 + 1 \cdot 2^0 = 15
 \end{aligned} \tag{1.10}$$

Hence, with a 4 bits word size, we can represent $2^4 = 16$ integers. The largest number is $2^4 - 1 = 15$, and the smallest is zero. What about negative numbers? If we still keep to a 4 bits word size, there are still $2^4 = 16$ numbers, but we distribute them differently. The common way to do it is to reserve the first bit to be a *sign* bit, a "0" is positive and "1" is negative, i.e. $(-1)^0 = 1$, and $(-1)^1 = -1$. Replacing the first bit with a sign bit in equation (1.10), we get the following sequence of numbers 0,1,2,3,4,5,6,7,-0,-1,-2,-3,-4,-5,-6,-7. The "-0", might seem strange but is used in the computer to extend the real number line $1/0 = \infty$, whereas $1/-0 = -\infty$. In general when there are m bits, we have a total of 2^m numbers. If we include negative numbers, we can choose to have $2^{m-1} - 1$, negative, and $2^{m-1} - 1$ positive numbers, negative zero and positive zero, i.e. $2^{m-1} - 1 + 2^{m-1} - 1 + 1 + 1 = 2^m$.

What about real numbers? As stated earlier we use the scientific notation as in equation (1.9), but still the scientific notation might have a real number in front, e.g. $1.25 \cdot 10^{-3}$. To represent the number 1.25 in binary format we use a decimal separator, just as with base 10. In this case 1.25 is 1.01 in binary format

$$1.01 = 1 \cdot 2^0 + 0 \cdot 2^{-1} + 1 \cdot 2^{-2} = 1 + 0 + 0.25 = 1.25. \tag{1.11}$$

The scientific notation is commonly referred to as *floating point representation*. The term "floating point" is used because the decimal point is not in the same place, in contrast to fixed point where the decimal

point is always in the same place. To store the number $1e-8=0.00000001$ in floating point format, we only need to store 1 and -8 (and possibly the sign), whereas in fixed point format we need to store all 9 numbers. In equation (1.10) we need to spend one bit to store the sign, leaving (in the case of 4 bits word size) three bits to be distributed among the *mantissa*, q , and the exponent, m . It is not given how many bits should be used for the mantissa and the exponent. Thus there are choices to be made, and all modern processors uses the same standard, the IEEE Standard 754-1985³.

Floating point numbers and the IEEE 754-1985 standard. A 64 bits word size is commonly referred to as *double precision*, whereas a 32 bits word size is termed *single precision*. In the following we will consider a 64 bits word size. We would like to know: what is the round off error, what is the largest number that can be represented in the computer, and what is the smallest number? Almost all floating point numbers are represented in *normalized* form. In normalized form the mantissa is written as $M = 1.F$, and it is only F that is stored, F is termed the *fraction*. We will return to the special case of some of the unnormalized numbers later. In the IEEE standard one bit is reserved for the sign, 52 for the fraction (F) and 11 for the exponent (m), see figure 1.4 for an illustration.

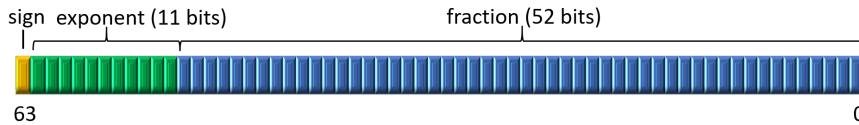


Fig. 1.4 Representation of a 64 bits floating point number according to the IEEE 754-1985 standard. For a 32 bits floating point number, 8, is reserved for the exponent and 23 for the fraction.

The exponent must be positive to represent numbers with absolute value larger than one, and negative to represent numbers with absolute value less than one. To make this more explicit the simple formula in equation (1.9) is rewritten:

$$\pm q2^{E-e}. \quad (1.12)$$

The number e is called the *bias* and has a fixed value, for 64 bits it is $2^{11-1} - 1 = 1023$ (32-bits: $e = 2^{8-1} - 1 = 127$). The number E is

³<https://standards.ieee.org/standard/754-1985.html>

represented by 11 bits and can thus take on values from 0 to $2^{11} - 1 = 2047$. If we have an exponent of e.g. -3, the computer adds 1023 to that number and store the number 1020. Two numbers are special numbers and reserved to represent infinity and zero, $E = 0$ and $E = 2047$. Thus *the largest and smallest possible numerical value of the exponent is: $2046-1023=1023$, and $1-1023=-1022$, respectively.* The fraction of a normalized floating point number takes on values from 1.000...00 to 1.111...11. Thus the lowest normalized number is

$$\begin{aligned} 1.000 + (49 \text{ more zeros}) \cdot 2^{-1022} &= 2^0 \cdot 2^{-1022} \\ &= 2.2250738585072014 \cdot 10^{-308}. \end{aligned} \quad (1.13)$$

It is possible to represent smaller numbers than $2.22 \cdot 10^{-308}$, by allowing *unnormalized* values. If the exponent is -1022, then the mantissa can take on values from 1.000...00 to 0.000...01, but then accuracy is lost. So the smallest possible number is $2^{-52} \cdot 2^{-1022} \simeq 4.94 \cdot 10^{-324}$. The highest normalized number is

$$\begin{aligned} 1.111 + (49 \text{ more ones}) \cdot 2^{1023} &= 2^0 + 2^{-1} + 2^{-2} + \dots + 2^{-52} \\ &= (2 - 2^{-52}) \cdot 2^{1023} = 1.7976931348623157 \cdot 10^{308}. \end{aligned} \quad (1.14)$$

If you enter `print(1.8*10**(308))` in Python, the answer will be `Inf`. If you enter `print(2*10**(308))`, Python will (normally) give an answer. This is because the number $1.8 \cdot 10^{308}$ is floating point number, whereas $2 \cdot 10^{308}$ is an *integer*, and Python does something clever when it comes to representing integers. Python has a third numeric type called long int, which can use the available memory to represent an integer.

There is one more important thing to mention, the round off error. The round off error is related to the machine precision, the machine precision, ϵ_M , is the *smallest possible number that can be added to one, and get a number larger than one*, i.e. $1 + \epsilon_M > 1$. The smallest possible value of the mantissa is $0.000\dots01 = 2^{-52}$, thus the lowest number must be of the form $2^{-52} \cdot 2^m$. If the exponent, m , is lower than 0 then when we add this number to 1, we will only get 1. Thus the machine precision is $\epsilon_M = 2^{-52} = 2.22 \cdot 10^{-16}$ (for 32 bits $2^{-23} = 1.19 \cdot 10^{-7}$). In practical terms this means that e.g. the value of π is 3.14159265358979323846264338..., but in Python it can only be represented by 16 digits: 3.141592653589793. In principle it does not sound so bad to have an answer accurate to 16

digits, and it is much better than most experimental results. So what is the problem? Consider the following example

```
h=1e-16
x = 2.1 + h
y = 2.1 - h
print((x-y)/h)
```

we expect to get the answer 2, but instead we get zero. By changing h to a higher value, the answer will get closer to 2.

Round Off Errors

All numerical floating point operations introduces round off errors at each step in the calculation due to finite word size, these errors accumulate in long simulations and introduce random errors in the final results. After N operations the error is at least $\sqrt{N}\epsilon_M$ (the square root is a random walk estimate, and we assume that the errors are randomly distributed). The round off errors can be much, much higher when numbers of equal magnitude are subtracted. You might be so unlucky that after one operation the answer is completely dominated by round off errors.

Round off error and truncation error in numerical derivatives. Armed with this knowledge of round off errors, we can continue to analyze the result in figure 1.3. The round off error when we represent a floating point number x in the machine will be of the order $x/10^{16}$ (*not* 10^{-16}). In general, when we evaluate a function the error will be of the order $\epsilon|f(x)|$, where $\epsilon \sim 10^{-16}$. Thus equation (1.8) is modified in the following way when we take into account the round off errors:

$$f'(x) = \frac{f(x+h) - f(x)}{h} \pm \frac{2\epsilon|f(x)|}{h} - \frac{h}{2}f''(\eta), \quad (1.15)$$

we do not know the sign of the round off error, so the total error R_2 is:

$$R_2 = \frac{2\epsilon|f(x)|}{h} + \frac{h}{2}|f''(\eta)|. \quad (1.16)$$

We have put absolute values around the function and its derivative to get the maximal error, it might be the case that the round off error cancel part of the truncation error. However, the round off error is random in nature and will change from machine to machine, and each time we run the program. Note that the round off error increases when h decreases,

and the approximation error decreases when h decreases. This is exactly what we see in the figure above. We can find the best step size, by differentiating R_2 and put it equal to zero:

$$\begin{aligned}\frac{dR_2}{dh} &= -\frac{2\epsilon|f(x)|}{h^2} + \frac{1}{2}f''(\eta) = 0 \\ h &= 2\sqrt{\epsilon \left| \frac{f(x)}{f''(\eta)} \right|} \simeq 2 \cdot 10^{-8},\end{aligned}\quad (1.17)$$

In the last equation we have assumed that $f(x)$ and its derivative is 1. This step size corresponds to an error of order $R_2 \sim 10^{-8}$. Inspecting the result in figure 1.3. we see that the minimum is located at $h \sim 10^{-8}$.

1.4 Higher Order Derivatives

There are more ways to calculate the derivative of a function, than the formula given in equation (1.8). Different formulas can be derived by using Taylors formula in (1.2), usually one expands about $x \pm h$:

$$\begin{aligned}f(x+h) &= f(x) + f'(x)h + \frac{h^2}{2}f''(x) + \frac{h^3}{3!}f^{(3)}(x) + \frac{h^4}{4!}f^{(4)}(x) + \dots \\ f(x-h) &= f(x) - f'(x)h + \frac{h^2}{2}f''(x) - \frac{h^3}{3!}f^{(3)}(x) + \frac{h^4}{4!}f^{(3)}(x) - \dots.\end{aligned}\quad (1.18)$$

If we add these two equations, we get an expression for the second derivative, because the first derivative cancels out. But we also observe that if we subtract these two equations we get an expression for the first derivative that is accurate to a higher order than the formula in equation (1.7), hence:

$$f'(x) = \frac{f(x+h) - f(x-h)}{2h} - \frac{h^2}{6}f^{(3)}(\eta), \quad (1.19)$$

$$f''(x) = \frac{f(x+h) + f(x-h) - 2f(x)}{h^2} - \frac{h^2}{12}f^{(4)}(\eta), \quad (1.20)$$

for some η in $[x, x+h]$. In figure 1.5, we have plotted equation (1.8), (1.19), and (1.20) for different step sizes. The derivative in equation (1.19), gives a higher accuracy than equation (1.8) for a larger step size, as can bee seen in figure 1.5.

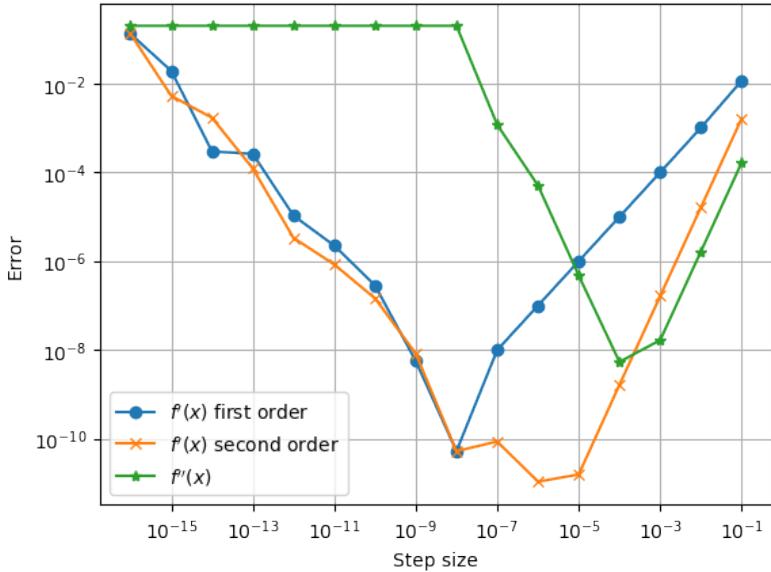


Fig. 1.5 Error in the numerical derivative and second derivative of $\sin x$ at $x = 0.2$ for different step size.

We can perform a similar error analysis as we did before, and then we find for equation (1.19) and (1.20) that the total numerical error is:

$$R_3 = \frac{\epsilon|f(x)|}{h} + \frac{h^2}{6} f^{(3)}(\eta), \quad (1.21)$$

$$R_4 = \frac{4\epsilon|f(x)|}{h^2} + \frac{h^2}{12} f^{(4)}(\eta), \quad (1.22)$$

respectively. Differentiating these two equations with respect to h , and set the equations equal to zero, we find an optimal step size of $h \sim 10^{-5}$ for equation (1.21), which gives an error of $R_2 \sim 10^{-16}/10^{-5} + (10^{-5})^2/6 \simeq 10^{-10}$, and $h \sim 10^{-4}$ for equation (1.22), which gives an error of $R_4 \sim 4 \cdot 10^{-16}/(10^{-4})^2 + (10^{-4})^2/12 \simeq 10^{-8}$. Note that we get the surprising result for the first order derivative in equation (1.19), that a higher step size gives a more accurate result.

Solving systems of equations are one of the most common tasks that we use computers for within modeling. A typical task is that we have a model that contains a set of unknown parameters which we want to determine. To determine these parameters we need to solve a set of equations. In many cases these equations are nonlinear, but often a nonlinear problem is solved *by linearize* the nonlinear equations, and thereby reducing it to a sequence of linear algebra problems. Thus the topic of solving linear systems of equations have been extensively studied, and sophisticated linear equation solving packages have been developed. Python uses functions from the LAPACK¹ library. In this course we will only cover the theory behind numerical linear algebra superficially, and the main purpose is to shed some light on some of the challenges one might encounter solving linear systems. In particular it is important for you to understand when it is stated in the NumPy documentation that the standard linear solver: `solve`² function uses *LU-decomposition* and *partial pivoting*.

2.1 Solving linear equations

There are a number of excellent books covering this topic, see e.g. [3, 7, 5, 6]. In most of the examples covered in this course we will encounter

¹ <https://en.wikipedia.org/wiki/LAPACK>

² <https://docs.scipy.org/doc/numpy/reference/generated/numpy.linalg.solve.html>

problems where we have a set of *linearly independent* equations and one equation for each unknown. For these type of problems there are a number of methods that can be used, and they will find a solution in a finite number of steps. If a solution cannot be found it is usually because the equations are not linearly independent, and our formulation of the physical problem is wrong.

Assume that we would like to solve the following set of equations:

$$2x_0 + x_1 + x_2 + 3x_3 = 1, \quad (2.1)$$

$$x_0 + x_1 + 3x_2 + x_3 = -3, \quad (2.2)$$

$$x_0 + 4x_1 + x_2 + x_3 = 2, \quad (2.3)$$

$$x_0 + x_1 + x_2 + x_3 = 1. \quad (2.4)$$

These equations can be written in matrix form as:

$$\mathbf{A} \cdot \mathbf{x} = \mathbf{b}, \quad (2.5)$$

where:

$$\mathbf{A} \equiv \begin{pmatrix} 2 & 1 & 1 & 3 \\ 1 & 1 & 3 & 1 \\ 1 & 4 & 1 & 1 \\ 1 & 1 & 2 & 2 \end{pmatrix} \quad \mathbf{b} \equiv \begin{pmatrix} 1 \\ -3 \\ 2 \\ 1 \end{pmatrix} \quad \mathbf{x} \equiv \begin{pmatrix} x_0 \\ x_1 \\ x_2 \\ x_3 \end{pmatrix}. \quad (2.6)$$

You can easily verify that $x_0 = -4, x_1 = 1, x_2 = -1, x_3 = 3$ is the solution to the above equations by direct substitution. If we were to replace one of the above equations with a linear combination of any of the other equations, e.g. replace equation (2.4) with $3x_0 + 2x_1 + 4x_2 + 4x_3 = -2$, there would be no unique solution (infinite number of solutions). This can be checked by calculating the determinant of the matrix \mathbf{A} , if $\det \mathbf{A} = 0$, What is the difficulty in solving these equations? Clearly if none of the equations are linearly dependent, and we have N independent linear equations, it should be straight forward to solve them? Two major numerical problems are i) even if the equations are not exact linear combinations of each other, they could be very close, and as the numerical algorithm progresses they could at some stage become linearly dependent due to roundoff errors. ii) roundoff errors may accumulate if the number of equations are large [3].

2.1.1 Gauss-Jordan elimination

Let us continue the discussion by consider Gauss-Jordan elimination, which is a *direct* method. A direct method uses a final set of operations to obtain a solution. According to [3] Gauss-Jordan elimination is the method of choice if we want to find the inverse of \mathbf{A} . However, it is slow when it comes to calculate the solution of equation (2.5). Even if speed and memory use is not an issue, it is also not advised to first find the inverse, \mathbf{A}^{-1} , of \mathbf{A} , then multiply it with \mathbf{b} to obtain the solution, due to roundoff errors (Roundoff errors occur whenever we subtract two numbers that are very close to each other). To simplify our notation, we write equation (2.6) as:

$$\left(\begin{array}{cccc|c} 2 & 1 & 1 & 3 & 1 \\ 1 & 1 & 3 & 1 & -3 \\ 1 & 4 & 1 & 1 & 2 \\ 1 & 1 & 2 & 2 & 1 \end{array} \right). \quad (2.7)$$

The numbers to the left of the vertical dash is the matrix \mathbf{A} , and to the right is the vector \mathbf{b} . The Gauss-Jordan elimination procedure proceeds by doing the same operation on the right and left side of the dash, and the goal is to get only zeros on the lower triangular part of the matrix. This is achieved by multiplying rows with the same (nonzero) number, swapping rows, adding a multiple of a row to another:

$$\left(\begin{array}{cccc|c} 2 & 1 & 1 & 3 & 1 \\ 1 & 1 & 3 & 1 & -3 \\ 1 & 4 & 1 & 1 & 2 \\ 1 & 1 & 2 & 2 & 1 \end{array} \right) \rightarrow \left(\begin{array}{cccc|c} 2 & 1 & 1 & 3 & 1 \\ 0 & 1/2 & 5/2 & -1/2 & -7/2 \\ 0 & 7/2 & 1/2 & -1/2 & 3/2 \\ 0 & 1/2 & 3/2 & 1/2 & 1/2 \end{array} \right) \rightarrow$$

$$\left(\begin{array}{cccc|c} 2 & 1 & 1 & 3 & 1 \\ 0 & 1/2 & 5/2 & -1/2 & -7/2 \\ 0 & 0 & -17 & 3 & 26 \\ 0 & 0 & 1 & -1 & 4 \end{array} \right) \rightarrow \left(\begin{array}{cccc|c} 2 & 1 & 1 & 3 & 1 \\ 0 & 1/2 & 5/2 & -1/2 & -7/2 \\ 0 & 0 & -17 & 3 & 26 \\ 0 & 0 & 0 & 14/17 & 42/17 \end{array} \right)$$
(2.8)

The operations done are: (1 \rightarrow 2) multiply first row with $-1/2$ and add to second, third and the fourth row, (2 \rightarrow 3) multiply second row with -7 , and add to third row, multiply second row with -1 and add to fourth row, (3 \rightarrow 4) multiply third row with $-1/17$ and add to fourth row. These operations can easily be coded into Python:

```
A = np.array([[2, 1, 1, 3],[1, 1, 3, 1],
             [1, 4, 1, 1],[1, 1, 2, 2]],float)
b = np.array([1,-3,2,1],float)
N=4
```

```
# Gauss-Jordan Elimination
for i in range(1,N):
    fact = A[i:,i-1]/A[i-1,i-1]
    A[i:,] -= np.outer(fact,A[i-1,:])
    b[i:] -= b[i-1]*fact
```

Notice that the final matrix has only zeros beyond the diagonal, such a matrix is called *upper triangular*. We still have not found the final solution, but from an upper triangular (or lower triangular) matrix it is trivial to determine the solution. The last row immediately gives us $14/17z = 42/17$ or $z = 3$, now we have the solution for z and the next row gives: $-17y + 3z = 26$ or $y = (26 - 3 \cdot 3)/(-17) = -1$, and so on. In a more general form, we can write our solution of the matrix \mathbf{A} after making it upper triangular as:

$$\begin{pmatrix} a'_{0,0} & a'_{0,1} & a'_{0,2} & a'_{0,3} \\ 0 & a'_{1,1} & a'_{1,2} & a'_{1,3} \\ 0 & 0 & a'_{2,2} & a'_{2,3} \\ 0 & 0 & 0 & a'_{3,3} \end{pmatrix} \cdot \begin{pmatrix} x_0 \\ x_1 \\ x_2 \\ x_3 \end{pmatrix} = \begin{pmatrix} b'_0 \\ b'_1 \\ b'_2 \\ b'_3 \end{pmatrix} \quad (2.9)$$

The back substitution can then be written formally as:

$$x_i = \frac{1}{a'_{ii}} \left[b'_i - \sum_{j=i+1}^{N-1} a'_{ij} x_j \right], \quad i = N-1, N-2, \dots, 0 \quad (2.10)$$

The back substitution can now easily be implemented in Python as:

```
# Back substitution
sol = np.zeros(N,float)
sol[N-1]=b[N-1]/A[N-1,N-1]
for i in range(2,N+1):
    sol[N-i]=(b[N-i]-np.dot(A[(N-i),:],sol))/A[N-i,N-i]
```

Notice that in the Python implementation, we have used vector operations instead of for loops. This makes the code more efficient, but it could also be implemented with for loops:

```
# Back substitution - for loop
sol = np.zeros(N,float)
for i in range(N-1,-1,-1):
    sol[i]= b[i]
    for j in range(i+1,N):
        sol[i] -= A[i][j]*sol[j]
    sol[i] /= A[i][i]
```

There are at least two things to notice with our implementation:

- Matrix and vector notation makes the code more compact and efficient. In order to understand the implementation it is advised to put $i = 1, 2, 3, 4$, and then execute the statements in the Gauss-Jordan elimination and compare with equation (2.8).
- The implementation of the Gauss-Jordan elimination is not robust, in particular one could easily imagine cases where one of the leading coefficients turned out as zero, and the routine would fail when we divide by $A[i-1, i-1]$. By simply changing equation (2.2) to $2x_0 + x_1 + 3x_2 + x_3 = -3$, when doing the first Gauss-Jordan elimination, both x_0 and x_1 would be canceled. In the next iteration we try to divide next equation by the leading coefficient of x_1 , which is zero, and the whole procedure fails.

2.1.2 Pivoting

The solution to the last problem is solved by what is called *pivoting*. The element that we divide on is called the *pivot element*. It actually turns out that even if we do Gauss-Jordan elimination *without* encountering a zero pivot element, the Gauss-Jordan procedure is numerically unstable in the presence of roundoff errors [3]. There are two versions of pivoting, *full pivoting* and *partial pivoting*. In partial pivoting we only interchange rows, while in full pivoting we also interchange rows and columns. Partial pivoting is much easier to implement, and the algorithm is as follows:

1. Find the row in \mathbf{A} with largest absolute value in front of x_0 and change with the first equation, switch corresponding elements in \mathbf{b}
2. Do one Gauss-Jordan elimination, find the row in \mathbf{A} with the largest absolute value in front of x_1 and switch with the second (same for \mathbf{b}), and so on.

For a linear equation we can multiply with a number on each side and the equation would be unchanged, so if we were to multiply one of the equations with a large value, we are almost sure that this equation would be placed first by our algorithm. This seems a bit strange as our mathematical problem is the same. Sometimes the linear algebra routines tries to normalize the equations to find the pivot element that would have been the largest element if all equations were normalized according to some rule, this is called *implicit pivoting*.

2.1.3 LU decomposition

As we have already seen, if the matrix \mathbf{A} is reduced to a triangular form it is trivial to calculate the solution by using back substitution. Thus if it was possible to decompose the matrix \mathbf{A} as follows:

$$\mathbf{A} = \mathbf{L} \cdot \mathbf{U} \quad (2.11)$$

$$\begin{pmatrix} a_{0,0} & a_{0,1} & a_{0,2} & a_{0,3} \\ a_{1,0} & a_{1,1} & a_{1,2} & a_{1,3} \\ a_{2,0} & a_{2,1} & a_{2,2} & a_{2,3} \\ a_{3,0} & a_{3,1} & a_{3,2} & a_{3,3} \end{pmatrix} = \begin{pmatrix} l_{0,0} & 0 & 0 & 0 \\ l_{1,0} & l_{1,1} & 0 & 0 \\ l_{2,0} & l_{2,1} & l_{2,2} & 0 \\ l_{3,0} & l_{3,1} & l_{3,2} & l_{3,3} \end{pmatrix} \cdot \begin{pmatrix} u_{0,0} & u_{0,1} & u_{0,2} & u_{0,3} \\ 0 & u_{1,1} & u_{1,2} & u_{1,3} \\ 0 & 0 & u_{2,2} & u_{2,3} \\ 0 & 0 & 0 & u_{3,3} \end{pmatrix}.$$

The solution procedure would then be to rewrite equation (2.5) as:

$$\mathbf{A} \cdot \mathbf{x} = \mathbf{L} \cdot \mathbf{U} \cdot \mathbf{x} = \mathbf{b}, \quad (2.12)$$

If we define a new vector \mathbf{y} :

$$\mathbf{y} \equiv \mathbf{U} \cdot \mathbf{x}, \quad (2.13)$$

we can first solve for the \mathbf{y} vector:

$$\mathbf{L} \cdot \mathbf{y} = \mathbf{b}, \quad (2.14)$$

and then for \mathbf{x} :

$$\mathbf{U} \cdot \mathbf{x} = \mathbf{y}. \quad (2.15)$$

Note that the solution to equation (2.14) would be done by *forward substitution*:

$$y_i = \frac{1}{l_{ii}} \left[b_i - \sum_{j=0}^{i-1} l_{ij}x_j \right], \quad i = 1, 2, \dots, N-1. \quad (2.16)$$

Why go to all this trouble? First of all it requires (slightly) less operations to calculate the LU decomposition and doing the forward and backward substitution than the Gauss-Jordan procedure discussed earlier. Secondly, and more importantly, is the fact that in many cases one would like to calculate the solution for different values of the \mathbf{b} vector in equation (2.12). If we do the LU decomposition first we can calculate the solution quite fast using backward and forward substitution for any value of the \mathbf{b} vector.

The NumPy function `solve`³, uses LU decomposition and partial pivoting, and we can find the solution to our previous problem simply by the following code:

```
from numpy.linalg import solve
x=solve(A,b)
```

2.2 Iterative methods

The methods described so far are what is called *direct* methods. The direct methods for very large systems might suffer from round off errors. That means that even if the computer has found a solution, the solution is "polluted" by round off errors, or stated more clearly: your solution for \mathbf{x} , when entered into the original equation $\mathbf{Ax} \neq \mathbf{b}$. Below we will describe one trick, and two alternative methods to the direct methods.

2.2.1 Iterative improvement

The first method [4] assumes that we already have solved the matrix equation (2.5), and obtained an *estimate* $\hat{\mathbf{x}}$ of the true solution \mathbf{x} . Assume that $\hat{\mathbf{x}} = \mathbf{x} + \delta\mathbf{x}$, and that

$$\mathbf{A} \cdot \hat{\mathbf{x}} = \mathbf{A} \cdot (\mathbf{x} + \delta\mathbf{x}) = \mathbf{b} + \delta\mathbf{b}, \quad (2.17)$$

subtracting equation (2.5) we get

$$\mathbf{A} \cdot \delta\mathbf{x} = \delta\mathbf{b}. \quad (2.18)$$

Solving equation (2.17) for $\delta\mathbf{b}$ and inserting in the equation above, we get

$$\mathbf{A} \cdot \delta\mathbf{x} = \mathbf{A} \cdot \hat{\mathbf{x}} - \mathbf{b}. \quad (2.19)$$

The usefulness of this method assumes that we have already obtained the LU decomposition of \mathbf{A} , and if possible one should use a higher precision to calculate the right hand side, since there will be a lot of cancellations. Then the whole computational process it is simply to calculate the right hand side and backsubstitute. The improved solution is then obtained by subtracting $\delta\mathbf{x}$ from $\hat{\mathbf{x}}$.

³<https://docs.scipy.org/doc/numpy/reference/generated/numpy.linalg.solve.html>

2.2.2 The Jacobi method

A completely different approach is the Jacobian method, which is simply to decompose the \mathbf{A} matrix in the following way

$$\mathbf{A} = \mathbf{D} + \mathbf{R} \quad (2.20)$$

$$\begin{pmatrix} a_{0,0} & a_{0,1} & a_{0,2} & a_{0,3} \\ a_{1,0} & a_{1,1} & a_{1,2} & a_{1,3} \\ a_{2,0} & a_{2,1} & a_{2,2} & a_{2,3} \\ a_{3,0} & a_{3,1} & a_{3,2} & a_{3,3} \end{pmatrix} = \begin{pmatrix} a_{0,0} & 0 & 0 & 0 \\ 0 & a_{1,1} & 0 & 0 \\ 0 & 0 & a_{2,2} & 0 \\ 0 & 0 & 0 & a_{3,3} \end{pmatrix} + \begin{pmatrix} 0 & a_{0,1} & a_{0,2} & a_{0,3} \\ a_{1,0} & 0 & a_{1,2} & a_{1,3} \\ a_{2,0} & a_{2,1} & 0 & a_{2,3} \\ a_{3,0} & a_{3,1} & 0 & a_{3,3} \end{pmatrix}.$$

We can then write equation (2.5) as

$$\mathbf{D}\mathbf{x} = \mathbf{b} - \mathbf{R} \cdot \mathbf{x}. \quad (2.21)$$

How does this help us? First of all, the matrix \mathbf{D} is easy to invert as it is diagonal, the inverse can be found by simply replace $a_{ii} \rightarrow 1/a_{ii}$. But \mathbf{x} is still present on the right hand side? This is where the *iterations* comes into play, we simply guess at an initial solution \mathbf{x}^k , and then we use equation (2.21) to calculate the next solution \mathbf{x}^{k+1} , and so on

$$\mathbf{x}^{k+1} = \mathbf{D}^{-1}(\mathbf{b} - \mathbf{R} \cdot \mathbf{x}^k). \quad (2.22)$$

Lets write it out on component form for a 4×4 matrix to see what is going on

$$x_0 = \frac{1}{a_{00}}(b_0 - a_{01}x_1^k - a_{02}x_2^k - a_{03}x_3^k), \quad (2.23)$$

$$x_1 = \frac{1}{a_{11}}(b_0 - a_{00}x_0^k - a_{02}x_2^k - a_{03}x_3^k), \quad (2.24)$$

$$x_2 = \frac{1}{a_{22}}(b_0 - a_{00}x_0^k - a_{01}x_1^k - a_{03}x_3^k), \quad (2.25)$$

$$x_3 = \frac{1}{a_{33}}(b_0 - a_{00}x_0^k - a_{01}x_1^k - a_{02}x_2^k). \quad (2.26)$$

Below is a Python implementation

```
def solve_jacobi(A,b,x=np.zeros(len(b)),max_iter=1000,eps=1e-6):
    """
    Solves the linear system Ax=b using the jacobi method, stops if
    solution is not found after max_iter or if solution changes less
    than EPS
    """
    D=np.diag(A)
    R=A-np.diag(D)
```

```

eps=1
x_old=x
iter=0
while(eps>EPS and iter<max_iter):
    iter+=1
    x=(b-np.dot(R,x_old))/D
    eps=np.abs(np.sum(x-x_old))
    x_old=x
print('found solution after ' + str(iter) +' iterations')
return x

```

The iterative method can be appealing if we do not need a high accuracy, we can choose to stop whenever $|\mathbf{x}^{k+1} - \mathbf{x}^k|$ is small enough. For the direct method we have to follow through all the way.

Convergence

The Jacobi method converges if the matrix \mathbf{A} is strictly diagonally dominant. Strictly diagonally dominant means that the absolute value of each entry on the diagonal is greater than the sum of the absolute values of the other entries in the same row, i.e if $|a_{00}| > |a_{01} + a_{02} + \dots|$. In general it can be shown that a iterative scheme $\mathbf{x}^{k+1} = \mathbf{P} \cdot \mathbf{x}^k + \mathbf{q}$ is convergent if and only if every eigenvalue, λ , of \mathbf{P} satisfies $|\lambda| < 1$, i.e. the *spectral radius* $\rho(\mathbf{P}) < 1$.

2.2.3 The Gauss-Seidel method

It is tempting in equation (2.23) to use our estimate of x_0^{k+1} in the next equation, equation (2.24), instead of x_0^k . After all our estimate x_0^{k+1} is an *improved* estimate. This is actually the Gauss-Seidel method. This method also has the advantage that if there are memory issues, one can overwrite the old value of x_i^k . Usually the Gauss-Seidel method converges faster, but not always. A plus for the Jacobi method is that is can be parallelised, as the calculations is only dependent on the old values and do not require information about the new values as for the Gauss Seidel method. Below is a Python implementation of the Gauss-Seidel method

```

def solve_GS(A,b,x=np.zeros(len(b)),max_iter=1000, EPS=1e-6):
    """
    Solves the linear system Ax=b using the Gauss-Seidel method, stops if
    solution is not found after max_iter or if solution changes less
    than EPS
    """
    D=np.diag(A)

```

```
R=A-np.diag(D)
eps=1
iter=0
while(eps>EPS and iter<max_iter):
    iter+=1
    eps=0.
    for i in range(len(x)):
        tmp=x[i]
        x[i]=w*(b[i]- np.dot(R[i,:],x))/D[i]
        eps+=np.abs(tmp-x[i])
print('found solution after ' + str(iter) +' iterations')
return x
```

2.3 Example: Linear regression

In the previous section, we considered a system of N equations and N unknown (x_0, x_1, \dots, x_N). In general we might have more equations than unknowns or more unknowns than equations. An example of the former is linear regression, we might have many data points and we would like to fit a line through the points. How do you fit a single line to more than two points that does not lie on the same line? One way to do it is to minimize the distance from the line to the points, as illustrated in figure 2.1.

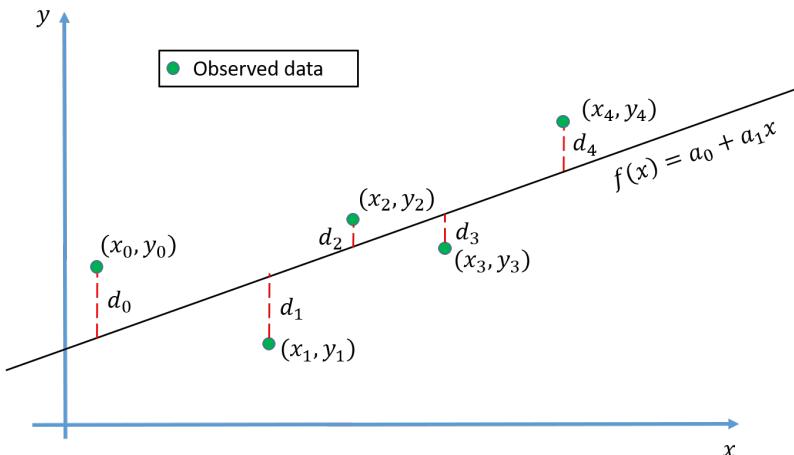


Fig. 2.1 Linear regression by minimizing the total distance to all the points.

Mathematically we can express the distance between a data point (x_i, y_i) and the line $f(x)$ as $y_i - f(x_i)$. Note that this difference can be

negative or positive depending if the data point lies below or above the line. We can then take the absolute value of all the distances, and try to minimize them. When we minimize something we take the derivative of the expression and put it equal to zero. As you might remember from Calculus it is extremely hard to work with the derivative of the absolute value, because it is discontinuous. A much better approach is to square each distance and sum them:

$$S = \sum_{i=0}^{N-1} (y_i - f(x_i))^2 = \sum_{i=0}^{N-1} (y_i - a_0 - a_1 x_i)^2. \quad (2.27)$$

(For the example in figure 2.1, $N = 5$.) This is the idea behind *least square*, and linear regression. One thing you should be aware of is that points lying far from the line will contribute more to equation (2.27). The underlying assumption is that each data point provides equally precise information about the process, this is often not the case. When analyzing experimental data, there may be points deviating from the expected behaviour, it is then important to investigate if these points are more affected by measurements errors than the others. If that is the case one should give them less weight in the least square estimate, by extending the formula above:

$$S = \sum_{i=0}^{N-1} \omega_i (y_i - f(x_i))^2 = \sum_{i=0}^3 \omega_i (y_i - a_0 - a_1 x_i)^2, \quad (2.28)$$

ω_i is a weight factor.

2.3.1 Solving least square, using algebraic equations

Let us continue with equation (2.27), the algebraic solution is to simply find the value of a_0 and a_1 that minimizes S :

$$\frac{\partial S}{\partial a_0} = -2 \sum_{i=0}^{N-1} (y_i - a_0 - a_1 x_i) = 0, \quad (2.29)$$

$$\frac{\partial S}{\partial a_1} = -2 \sum_{i=0}^{N-1} (y_i - a_0 - a_1 x_i) x_i = 0. \quad (2.30)$$

Defining the mean value as $\bar{x} = \sum_i x_i / N$ and $\bar{y} = \sum_i y_i / N$, we can write equation (2.29) and (2.30) as:

$$\sum_{i=0}^{N-1} (y_i - a_0 - a_1 x_i) = N\bar{y} - a_0 N - a_1 N\bar{x} = 0, \quad (2.31)$$

$$\sum_{i=0}^{N-1} (y_i - a_0 - a_1 x_i) x_i = \sum_i y_i x_i - a_0 N\bar{x} - a_1 \sum_i x_i x_i = 0. \quad (2.32)$$

Solving equation (2.31) with respect to a_0 , and inserting the expression into equation (2.32), we find:

$$a_0 = \bar{y} - a_1 \bar{x}, \quad (2.33)$$

$$a_1 = \frac{\sum_i y_i x_i - N\bar{y}\bar{x}}{\sum_i x_i^2 - N\bar{x}^2} = \frac{\sum_i (x_i - \bar{x})(y_i - \bar{y})}{\sum_i (x_i - \bar{x})^2}. \quad (2.34)$$

We leave it as an exercise to show the last expression for a_1 . Clearly the equation (2.34) above will in most cases have a solution. But in addition to a solution, it would be good to have an idea of the goodness of the fit. Intuitively it make sense to add all the distances (residuals) d_i in figure 2.1. This is basically what is done when calculating R^2 (R-squared). However, we would also like to compare the R^2 between different datasets. Therefor we need to normalize the sum of residuals, and therefore the following form of the R^2 is used:

$$R^2 = 1 - \frac{\sum_{i=0}^{N-1} (y_i - f(x_i))^2}{\sum_{i=0}^{N-1} (y_i - \bar{y})^2}. \quad (2.35)$$

In python we can implement equation (2.33), (2.34) and (2.35) as:

```
def OLS(x, y):
    # returns regression coefficients
    # in ordinary least square
    # x: observations
    # y: response
    # R^2: R-squared
    n = np.size(x) # number of data points

    # mean of x and y vector
    m_x, m_y = np.mean(x), np.mean(y)

    # calculating cross-deviation and deviation about x
    SS_xy = np.sum(y*x) - n*m_y*m_x
    SS_xx = np.sum(x*x) - n*m_x*m_x

    # calculating regression coefficients
    b_1 = SS_xy / SS_xx
    b_0 = m_y - b_1*m_x
```

```
#R ~2
y_pred = b_0 + b_1*x
S_yy    = np.sum(y*y) - n*m_y*m_y
y_res   = y-y_pred
S_res   = np.sum(y_res*y_res)

return(b_0, b_1, 1-S_res/S_yy)
```

2.3.2 Least square as a linear algebra problem

It turns out that the least square problem can be formulated as a matrix problem. (Two great explanations see linear regression by matrices⁴, and R^2 -squared⁵.) If we define a matrix \mathbf{X} containing the observations x_i as:

$$\mathbf{X} = \begin{pmatrix} 1 & x_0 \\ 1 & x_1 \\ \vdots & \vdots \\ 1 & x_{N-1} \end{pmatrix}. \quad (2.36)$$

We introduce a vector containing all the response \mathbf{y} , and the regression coefficients $\mathbf{a} = (a_0, a_1)$. Then we can write equation (2.28) as a matrix equation:

$$S = (\mathbf{y} - \mathbf{X} \cdot \mathbf{a})^T (\mathbf{y} - \mathbf{X} \cdot \mathbf{a}). \quad (2.37)$$

Note that this equation can easily be extended to more than one observation variable x_i . By simply differentiating equation (2.37) with respect to \mathbf{a} , we can show that the derivative has a minimum when (see proof below):

$$\mathbf{X}^T \mathbf{X} \mathbf{a} = \mathbf{X}^T \mathbf{y} \quad (2.38)$$

Below is a python implementation of equation (2.38).

```
def OLSM(x, y):
    # returns regression coefficients
    # in ordinary least square using solve function
    # x: observations
    # y: response

    XT = np.array([np.ones(len(x)),x],float)
    X  = np.transpose(XT)
    B  = np.dot(XT,X)
    C  = np.dot(XT,y)
    return solve(B,C)
```

⁴<https://medium.com/@andrew.chamberlain/the-linear-algebra-view-of-least-squares-regression-f67044>

⁵<https://medium.com/@andrew.chamberlain/a-more-elegant-view-of-r-squared-a0a14c177dc3>

2.3.3 Working with matrices on component form

Whenever you want to do some manipulation with matrices, it is very useful to simply write them on component form. If we multiply two matrices \mathbf{A} and \mathbf{B} to form a new matrix \mathbf{C} , the components of the new matrix is simply $C_{ij} = \sum_k A_{ik}B_{kj}$. The strength of doing this is that the elements of a matrix, e.g. A_{ik} are *numbers*, and we can move them around. Proving that e.g. $(\mathbf{AB})^T = \mathbf{B}^T\mathbf{A}^T$ is straight forward using the component form. The transpose of a matrix is simply to exchange columns and rows, hence $\mathbf{C}_{ij}^T = \mathbf{C}_{ji}$

$$\mathbf{C}_{ij}^T = \mathbf{C}_{ji} = \sum_k \mathbf{A}_{jk}\mathbf{B}_{ki} = \sum_k \mathbf{B}_{ik}^T\mathbf{A}_{kj}^T = (\mathbf{B}^T\mathbf{A}^T)_{ij}, \quad (2.39)$$

thus $\mathbf{C}^T = \mathbf{B}^T\mathbf{A}^T$. To derive equation (2.38), we need to take the derivative of equation (2.38) with respect to \mathbf{a} . What we mean by this is that we want to evaluate $\partial S / \partial a_k$ for all the components of \mathbf{a} . A useful rule is $\partial a_i / \partial a_k = \delta_{ik}$, where δ_{ik} is the Kronecker delta, it takes the value of one if $i = k$ and zero otherwise. We can write $S = \mathbf{y}^T\mathbf{y} - \mathbf{y}\mathbf{X} \cdot \mathbf{a} - (\mathbf{X} \cdot \mathbf{a})^T\mathbf{y} - (\mathbf{X} \cdot \mathbf{a})^T\mathbf{X} \cdot \mathbf{a}$. All terms that do not contain \mathbf{a} are zero, thus we only need to evaluate the following terms

$$\begin{aligned} \frac{\partial}{\partial_k} (\mathbf{X} \cdot \mathbf{a})^T \mathbf{y} &= \frac{\partial}{\partial_k} (\mathbf{a}^T \cdot \mathbf{X}^T \mathbf{y}) = \frac{\partial}{\partial_k} \sum_{ij} \mathbf{a}_i^T \mathbf{X}_{ij}^T \mathbf{y}_j = \sum_{ij} \delta_{ik} \mathbf{X}_{ij}^T \mathbf{y}_j \\ &= \sum_j \mathbf{X}_{kj}^T \mathbf{y}_j = \mathbf{X}^T \mathbf{y} \end{aligned} \quad (2.40)$$

$$\begin{aligned} \frac{\partial}{\partial_k} \mathbf{y}^T \mathbf{X} \cdot \mathbf{a} &= \frac{\partial}{\partial_k} \sum_{ij} \mathbf{y}_i^T \mathbf{X}_{ij} \mathbf{a}_j = \sum_{ij} \mathbf{y}_i^T \mathbf{X}_{ij} \delta_{jk} = \sum_j \mathbf{y}_i^T \mathbf{X}_{ik} \\ &= \sum_j \mathbf{y}_i^T \mathbf{X}_{ki}^T = \mathbf{X}^T \mathbf{y} \end{aligned} \quad (2.41)$$

$$\begin{aligned} \frac{\partial}{\partial_k} (\mathbf{X} \cdot \mathbf{a})^T \mathbf{X} \cdot \mathbf{a} &= \frac{\partial}{\partial_k} \sum_{ijl} \mathbf{a}_i^T \mathbf{X}_{ij}^T \mathbf{X}_{jl} \mathbf{a}_l = \sum_{ijl} (\delta_{ik} \mathbf{X}_{ij}^T \mathbf{X}_{jl} \mathbf{a}_l + \mathbf{a}_i^T \mathbf{X}_{ij}^T \mathbf{X}_{jl} \delta_{lk}) \\ &= \sum_{jl} \mathbf{X}_{kj}^T \mathbf{X}_{jl} \mathbf{a}_l + \sum_{ij} \mathbf{a}_i^T \mathbf{X}_{ij}^T \mathbf{X}_{jk} \\ &= \mathbf{X}^T \mathbf{X} \mathbf{a} + \sum_{ij} \mathbf{X}_{kj}^T \mathbf{X}_{ji} \mathbf{a}_i = 2\mathbf{X}^T \mathbf{X} \mathbf{a}. \end{aligned} \quad (2.42)$$

It then follows that $\partial S / \partial \mathbf{a} = 0$ when

$$\mathbf{X}^T \mathbf{X} \mathbf{a} = \mathbf{X}^T \mathbf{y}. \quad (2.43)$$

2.4 Sparse matrices and Thomas algorithm

In many practical examples, such as solving partial differential equations the matrices could be quite large and also contain a lot of zeros. A very important class of such matrices are *banded matrices* this is a type of *sparse matrices* containing a lot of zero elements, and the non-zero elements are confined to diagonal bands. In the following we will focus on one important type of sparse matrix the tridiagonal. In the next section we will show how it enters naturally in solving the heat equation. It turns out that solving banded matrices is quite simple, and can be coded quite efficiently. As with the Gauss-Jordan example, lets consider a concrete example:

$$\left(\begin{array}{ccccc|c} b_0 & c_0 & 0 & 0 & 0 & r_0 \\ a_1 & b_1 & c_1 & 0 & 0 & r_1 \\ 0 & a_2 & b_2 & c_2 & 0 & r_2 \\ 0 & 0 & a_3 & b_3 & c_3 & r_3 \\ 0 & 0 & 0 & a_4 & b_4 & r_4 \end{array} \right) \quad (2.44)$$

The right hand side is represented with r_i . The first Gauss-Jordan step is simply to divide by b_0 , then we multiply with $-a_1$ and add to second row:

$$\rightarrow \left(\begin{array}{ccccc|c} 1 & c'_0 & 0 & 0 & 0 & r'_0 \\ 0 & b_1 - a_1 c'_0 & c_1 & 0 & 0 & r_1 - a_0 r'_0 \\ 0 & a_2 & b_2 & c_2 & 0 & r_2 \\ 0 & 0 & a_3 & b_3 & c_3 & r_3 \\ 0 & 0 & 0 & a_4 & b_4 & r_4 \end{array} \right), \quad (2.45)$$

Note that we have introduced some new symbols to simplify the notation: $c'_0 = c_0/b_0$ and $r'_0 = r_0/b_0$. Then we divide by $b_1 - a_1 c'_0$:

$$\left(\begin{array}{ccccc|c} 1 & c'_0 & 0 & 0 & 0 & r'_0 \\ 0 & 1 & c'_1 & 0 & 0 & r'_1 \\ 0 & a_2 & b_2 & c_2 & 0 & r_2 \\ 0 & 0 & a_3 & b_3 & c_3 & r_3 \\ 0 & 0 & 0 & a_4 & b_4 & r_4 \end{array} \right), \quad (2.46)$$

where $c'_1 = c_1/(b_1 - a_1 c'_0)$ and $r'_1 = (r_1 - a_0 r'_0)/(b_1 - a_1 c'_0)$. If you continue in this manner, you can easily convince yourself that to transform a tridiagonal matrix to the following form:

$$\rightarrow \left(\begin{array}{ccccc|c} 1 & c'_0 & 0 & 0 & 0 & r'_0 \\ 0 & 1 & c'_1 & 0 & 0 & r'_1 \\ 0 & 0 & 1 & c'_2 & 0 & r'_2 \\ 0 & 0 & 0 & 1 & c'_3 & r'_3 \\ 0 & 0 & 0 & 0 & 1 & r'_4 \end{array} \right), \quad (2.47)$$

where:

$$c'_0 = \frac{c_0}{b_0} \quad r'_0 = r_0 b_0 \quad (2.48)$$

$$c'_i = \frac{c_i}{b_i - a_i c'_{i-1}} \quad r'_i = \frac{r_i - a_i r'_{i-1}}{b_i - a_i c'_{i-1}} , \text{ for } i = 1, 2, \dots, N-1 \quad (2.49)$$

Note that we were able to reduce the tridiagonal matrix to an *upper triangular* matrix in only *one* Gauss-Jordan step. This equation can readily be solved using back-substitution, which can also be simplified as there are a lot of zeros in the upper part. Let us denote the unknowns x_i as we did for the Gauss-Jordan case, now we can find the solution as follows:

$$x_{N-1} = r'_{N-1} \quad (2.50)$$

$$x_i = r'_i - x_{i+1} c'_i , \text{ for } i = N-2, N-3, \dots, 0 \quad (2.51)$$

Equation (2.48), (2.49), (2.50) and (2.51) is known as the Thomas algorithm after Llewellyn Thomas.

Notice

Clearly tridiagonal matrices can be solved much more efficiently with the Thomas algorithm than using a standard library, such as LU-decomposition. This is because the solution method takes advantages of the *symmetry* of the problem. We will not show it here, but it can be shown that the Thomas algorithm is stable whenever $|b_i| \geq |a_i| + |c_i|$. If the algorithm fails, an advice is first to use the standard `solve` function in python. If this gives a solution, then *pivoting* combined with the Thomas algorithm might do the trick.

2.5 Example: Solving the heat equation using linear algebra

Exercise 2.1: Conservation Equation or the Continuity Equation

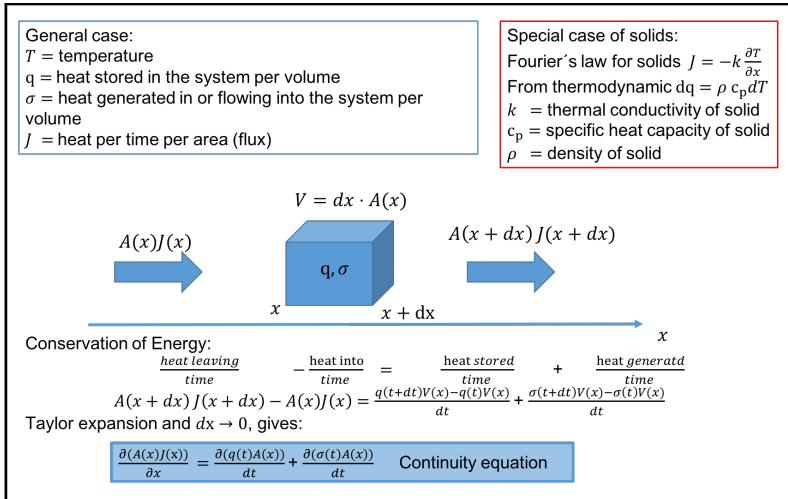


Fig. 2.2 Conservation of energy and the continuity equation.

In figure 2.2, the continuity equation is derived for heat flow. In the case of heat exchange for a solid, we can show that it can be written:

$$\frac{d^2T}{dx^2} + \frac{\dot{\sigma}}{k} = \frac{\rho c_p}{k} \frac{dT}{dt}, \quad (2.52)$$

where $\dot{\sigma}$ is the rate of heat generation in the solid. This equation can be used as a starting point for many interesting models. In this exercise we will investigate the *steady state* solution, *steady state* is just a fancy way of expressing that we want the solution that *does not change with time*. This is achieved by ignoring the derivative with respect to time in equation (2.52). We want to study a system with size L , and is it good practice to introduce a dimensionless variable: $y = x/L$. Equation (2.52) can now be written:

$$\frac{d^2T}{dy^2} + \frac{\dot{\sigma}L^2}{k} = 0 \quad (2.53)$$

Exercise 2.2: Curing of Concrete and Matrix Formulation

Curing of concrete is one particular example that we can investigate with equation (2.53). When concrete is curing, there are a lot of chemical reactions happening, these reactions generate heat. This is a known issue, and if the temperature rises too much compared to the surroundings, the concrete may fracture. In the following we will, for simplicity, assume that the rate of heat generated during curing is constant, $\dot{\sigma} = 100 \text{ W/m}^3$. The left end (at $x = 0$) is insulated, meaning that there is no flow of heat over that boundary, hence $dT/dx = 0$ at $x = 0$. On the right hand side the temperature is kept constant, $x(L) = y(1) = T_1$, assumed to be equal to the ambient temperature of $T_1 = 25^\circ\text{C}$. The concrete thermal conductivity is assumed to be $k = 1.65 \text{ W/m}^\circ\text{C}$.

We leave it as an exercise to show that the analytical solution to equation (2.53) in this case is:

$$T(y) = \frac{\dot{\sigma}L^2}{2k}(1 - y^2) + T_1. \quad (2.54)$$

In order to solve equation (2.53) numerically, we need to discretize it. We replace the second derivative with $dT/dy^2 = (T(y + dy) + T(y - dy) - 2T(y))/dy^2$. Equation (2.52) can now be written:

$$T_{i+1} + T_{i-1} - 2T_i = -h^2\beta, \quad (2.55)$$

where $\beta = \dot{\sigma}L^2/k$.

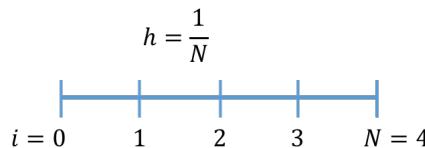


Fig. 2.3 Finite difference grid for $N = 4$.

In figure 2.3, the finite difference grid is shown for $N = 4$. Let us write down equation (2.55) for each grid node to see how the implementation is done in practice:

$$\begin{aligned}
T_{-1} + T_1 - 2T_0 &= -h^2\beta, \\
T_0 + T_2 - 2T_1 &= -h^2\beta, \\
T_1 + T_3 - 2T_2 &= -h^2\beta, \\
T_2 + T_4 - 2T_3 &= -h^2\beta.
\end{aligned} \tag{2.56}$$

The tricky part is now to introduce the boundary conditions. The right hand side is easy, because here the temperature is $T_4 = 25$. However, we see that T_{-1} enters and we have no value for this node. The boundary condition on the left hand side is $dT/dy = 0$, by using the central difference for the derivative allows us to write:

$$\frac{dT}{dy}\Big|_{y=0} = \frac{T_{-1} - T_1}{2h} = 0, \tag{2.57}$$

hence $T_{-1} = T_1$. Thus the final set of equations are:

$$\begin{aligned}
2T_1 - 2T_0 &= -h^2\beta, \\
T_0 + T_2 - 2T_1 &= -h^2\beta, \\
T_1 + T_3 - 2T_2 &= -h^2\beta, \\
T_2 + 25 - 2T_3 &= -h^2\beta,
\end{aligned} \tag{2.58}$$

or in matrix form:

$$\begin{pmatrix} -2 & 2 & 0 & 0 \\ 1 & -2 & 1 & 0 \\ 0 & 1 & -2 & 1 \\ 0 & 0 & 1 & -2 \end{pmatrix} \begin{pmatrix} T_0 \\ T_1 \\ T_2 \\ T_3 \end{pmatrix} = \begin{pmatrix} -h^2\beta \\ -h^2\beta \\ -h^2\beta \\ -h^2\beta - 25 \end{pmatrix}. \tag{2.59}$$

Note that it is now easy to increase N as it is only the boundaries that requires special attention.

- Solve the set of equations using `numpy.linalg.solve`⁶.

The correct solution is $L = 1$ m, and $h = 1/4$, is: $[T_0, T_1, T_2, T_3] = [55.3030303, 53.40909091, 47.72727273, 38.25757576]$.

Solution.

⁶<https://numpy.org/doc/stable/reference/generated/numpy.linalg.solve.html>

Notice

The solution below implements equation (2.2) using sparse matrices, and the standard Numpy `solve` function. You can use the `%timeit` magic command in Ipython and Jupyter notebooks to test the efficiency.

```
#%matplotlib inline
import numpy as np
import scipy as sc
import scipy.sparse.linalg
from numpy.linalg import solve
import matplotlib.pyplot as plt

# Set simulation parameters
h = 0.25          # element size
L = 1.0           # length of domain
n = int(round(L/h)) # number of unknowns
x=np.arange(n+1)*h # includes right bc
T1=25
sigma = 100*L**2/1.65

def tri_diag(a, b, c, k1=-1, k2=0, k3=1):
    """ a,b,c diagonal terms """
    return np.diag(a, k1) + np.diag(b, k2) + np.diag(c, k3)

def analytical(sigma,x):
    return sigma*(1-x*x)/2+T1

#Create matrix for linalg solver
a=np.ones(n-1)
b=-np.ones(n)*2
c=np.ones(n-1)
#Create matrix for sparse solver
diagonals=np.zeros((3,n))
diagonals[0,:]= 1
diagonals[1,:]= -2
diagonals[2,:]= 1

# rhs vector
d=np.repeat(-h*h*sigma,n)

#----boundary conditions -----
#lhs - no flux of heat
diagonals[2,1]= 2
c[0]=2
#rhs - constant temperature
d[n-1]=d[n-1]-T1
#-----
```

```

A=tri_diag(a,b,c)
A_sparse = sc.sparse.spdiags(diagonals, [-1,0,1], n, n,format='csc')
# to view matrix
print(A_sparse.todense())
#Solve linear problems
Ta = solve(A,d,)
Tb = sc.sparse.linalg.spsolve(A_sparse,d)
#Add right boundary node
Ta=np.append(Ta,T1)
Tb=np.append(Tb,T1)
#uncomment to test efficiency
##timeit sc.sparse.linalg.spsolve(A_sparse,d)
##timeit solve(A,d,)

# Plot solutions
plt.plot(x,Ta,x,Tb,'-.',x,analytical(sigma,x),':', lw=3)
plt.xlabel("Dimensionless length")
plt.ylabel(r"Temperature [${}^{\circ}\text{C}$]")
plt.xlim(0,1)
plt.ylim(T1-1)
plt.legend(['sparse','linalg','analytical'])
plt.grid()
plt.show()

```

2.6 CO₂ diffusion into aquifers

The transport of CO₂ into aquifers can be described according to the diffusion equation

$$\frac{\partial C(z,t)}{\partial t} = \frac{\partial}{\partial z} \left(K(z) \frac{\partial C(z,t)}{\partial z} \right), \quad (2.60)$$

where $C(z,t)$ is the concentration of CO₂ as a function of depth (z) and time t , and $K(z)$ is the diffusion constant of CO₂ as a function of depth. This equation can be discretized using standard techniques, to help in that respect consider figure 2.4.

In the following we will assume that there are only four nodes ($i = 0 \dots 3$) in the physical domain, and two ghost nodes $i = -1$, and $i = 4$. There are many ways to attack this problem, but in the following we will borrow ideas from Finite Volume. Finite volume methods is a way of discretizing equations such that we *conserve mass*. The diffusion equation as it is derived in figure 2.2, express that the flux of something (heat, particles, etc) leaving the box surface minus the flux entering the surface of the box is equal to the rate of change of something inside the box. We can formulate this mathematically as:

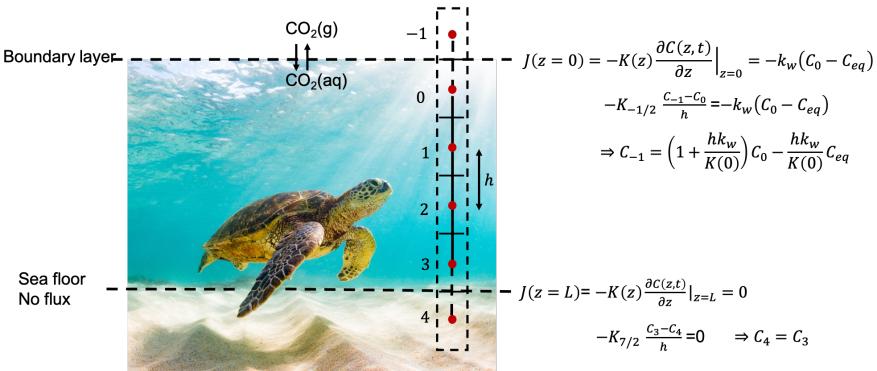


Fig. 2.4 Discretization for diffusion of CO_2 into an aquifer, including boundary conditions.

$$\frac{\partial C(z,t)}{\partial t} \simeq \frac{1}{h} \left[K(z) \frac{\partial C(z,t)}{\partial z} \Big|_{i+1/2} - K(z) \frac{\partial C(z,t)}{\partial z} \Big|_{i-1/2} \right] \quad (2.61)$$

The notation $i \pm 1/2$, means that the flux is to be evaluated *at the surface* of the box (i.e. halfway between the red dots in figure 2.4). $K(z)$ is the diffusion constant, and it is known everywhere, so this is simple to evaluate at the surface. The concentrations are only known at the center of each box, the red dots in figure 2.4. The derivative of the concentration can be evaluated using the central difference formula (remember that the distance between the red dot and edge of the box is $h/2$), hence

$$\frac{C_i^{n+1} - C_i^n}{\Delta t} = \frac{1}{h} \left[K_{i+1/2} \frac{C_{i+1} - C_i}{h} - K_{i-1/2} \frac{C_i - C_{i-1}}{h} \right], \quad (2.62)$$

notice that we have discretized the time derivative, and that we have introduced n to indicate the time step. On the right hand side there are no time indicated, it turns out that we have a choice to put time step n or $n + 1$ on the concentrations on the right hand side. If we put n the scheme is said to be explicit, if we put $n + 1$, the scheme is implicit. Implicit schemes are stable compared to explicit schemes, whereas explicit schemes has slightly higher numerical accuracy **TO DO 1: show this!**. In general we can write

$$\frac{C_i^{n+1} - C_i^n}{\Delta t} = \frac{\theta}{h} \left[K_{i+1/2} \frac{C_{i+1}^n - C_i^n}{h} - K_{i-1/2} \frac{C_i^n - C_{i-1}^n}{h} \right] \quad (2.63)$$

$$+ \frac{1-\theta}{h} \left[K_{i+1/2} \frac{C_{i+1}^{n+1} - C_i^{n+1}}{h} - K_{i-1/2} \frac{C_i^{n+1} - C_{i-1}^{n+1}}{h} \right], \quad (2.64)$$

hence if $\theta = 1$ the scheme is explicit, if $\theta = 0$ the scheme is implicit, and if $\theta = 1/2$, the scheme is called the Crank-Nicolson method. The first and last boundary are special, let us first consider the $i = 0$, this is where the sea is in contact with the CO₂ in the atmosphere, and the flux is $k_w(C_0 - C_{eq})$, hence

$$\frac{C_0^{n+1} - C_0^n}{\Delta t} = \frac{\theta}{h} \left[K_{i+1/2} \frac{C_1^n - C_0^n}{h} - k_w(C_0^n - C_{eq}) \right] \quad (2.65)$$

$$+ \frac{1-\theta}{h} \left[K_{i+1/2} \frac{C_1^{n+1} - C_0^{n+1}}{h} - k_w(C_0^{n+1} - C_{eq}^{n+1}) \right]. \quad (2.66)$$

For the last block the flux is zero towards the seafloor, and equation (2.64) can be written

$$\frac{C_3^{n+1} - C_3^n}{\Delta t} = \frac{\theta}{h} \left[-K_{5/2} \frac{C_3^n - C_2^n}{h} \right] \quad (2.67)$$

$$+ \frac{1-\theta}{h} \left[-K_{5/2} \frac{C_3^{n+1} - C_2^{n+1}}{h} \right]. \quad (2.68)$$

For the blocks $i = 1 \dots 2$, we can collect all terms with $n + 1$ on one side and terms with n on the other side and rewrite equation (2.64)

$$\begin{aligned} & [1 + (1-\theta) \alpha(K_{i+1/2} + K_{i-1/2})] C_i^{n+1} \\ & - (1-\theta) \alpha K_{i+1/2} C_{i+1}^{n+1} - (1-\theta) \alpha K_{i-1/2} C_{i-1}^{n+1} \\ & = [1 - \theta \alpha(K_{i+1/2} + K_{i-1/2})] C_i^n \\ & + \theta \alpha K_{i+1/2} C_{i+1}^n + \theta \alpha K_{i-1/2} C_{i-1}^n, \end{aligned} \quad (2.69)$$

where $\alpha \equiv \Delta t/h^2$. Next, we want to write down the corresponding matrix equations for four grid nodes as indicated in figure 2.4. Notice that we need to use the equations in figure 2.4, for C_{-1} , and C_4 . The left and right hand coefficient matrix \mathbf{L} , and \mathbf{R} are given as

$$\begin{pmatrix} 1 + (1 - \theta)\alpha(K_{1/2} + h k_w) & -(1 - \theta)\alpha K_{1/2} & 0 & 0 \\ -(1 - \theta)\alpha K_{1/2} & 1 + (1 - \theta)\alpha(K_{3/2} + K_{1/2}) & -(1 - \theta)\alpha K_{3/2} & 0 \\ 0 & -(1 - \theta)\alpha K_{3/2} & 1 + (1 - \theta)\alpha(K_{5/2} + K_{3/2}) & -(1 - \theta)\alpha K_{5/2} \\ 0 & 0 & -(1 - \theta)\alpha K_{5/2} & 1 + (1 - \theta)\alpha K_{5/2} \end{pmatrix},$$

$$\begin{pmatrix} 1 - \theta\alpha(K_{1/2} + h k_w) & +\theta\alpha K_{1/2} & 0 & 0 \\ \theta\alpha K_{1/2} & 1 - \theta\alpha(K_{3/2} + K_{1/2}) & \theta\alpha K_{3/2} & 0 \\ 0 & \theta\alpha K_{3/2} & 1 - \theta\alpha(K_{5/2} + K_{3/2}) & \theta\alpha K_{5/2} \\ 0 & 0 & \theta\alpha K_{5/2} & 1 - \theta\alpha K_{5/2} \end{pmatrix},$$

respectively. Introducing $\mathbf{S} = [k_w C_{eq} \Delta t / h, 0, 0, 0]^T$, we can finally write the diffusion equation (2.60) as

$$\mathbf{LC}^{n+1} = \mathbf{RC}^n + \theta\mathbf{S}^n + (1 - \theta)\mathbf{S}^{n+1} \quad (2.70)$$

More stuff to do:

1. Assume zero flux over the air water interface ($k_w=0$), show from the equations above that if we start with a uniform concentration in the sea ($\mathbf{C}^n=\text{constant}$) that \mathbf{C}^{n+1} does not change (as it should).
2. Assume that if the concentration at a specific time n in the sea is equal to C_{eq} then the concentration stays constant at all later times
3. Add chemical reactions

Solving nonlinear equations

3

In this chapter we will cover some theory related to the solution of nonlinear equations, and introduce the most used methods. A nonlinear problem is represented as a single equation or a system of equations, where the response is not changing proportionally to the input. Almost all physical systems are nonlinear, and one frequent use of the methods presented in this chapter is to determine model parameters by matching a nonlinear model to data.

Numerical methods that is guaranteed to find a solution (if it exists) are called *closed methods*, and *open* other vise. In many cases the closed methods requires more iterations for well behaved functions than the open methods. For one dimensional problems we will cover: fixed point iteration, bisection, Newton's method, and the secant method. For multidimensional problems we will cover Newton-Rapson method, which is a direct extension of Newton's method in one dimension, and the steepest decent. The main challenge is that there are (usually) more than one solution, the solution that *you* want for a specific problem is usually dictated by the underlying physics. If computational speed is not an issue, the method of choice is usually the bisection method. It is guaranteed to give an answer, but it might be slow. If speed is an issue, usually Newton's or the secant method will be the fastest (but it depends on the starting point). The secant method is sometimes preferred if the derivative of the function is costly to evaluate. Brents method is a method that combine the secant and bisection method (not covered), and is guaranteed to find a solution if the root is bracketed.

In many practical, engineering, applications one usually implements some of the methods described below directly inside functions. This is because it is usually faster than calling a separate all purpose nonlinear solver, and that one usually has a very good idea of what a good starting point for the nonlinear solver is.

3.1 Nonlinear equations

A nonlinear equation is simply an equation that is not linear. That means that when the variables changes the response is not changing proportional to the values of the variables. Solving a nonlinear equation always proceeds by *iterations*, we start with one or several initial guesses and then search for the solution. In many cases we do not know beforehand if the equation actually has a solution, or multiple solutions. An example of a nonlinear problem is:

$$e^{-x} = x^2. \quad (3.1)$$

Traditionally one collect all the terms on one side, to solve an equation of the form

$$f(x) = x^2 - e^{-x} = 0. \quad (3.2)$$

In figure 3.1, the solution is shown graphically. Note that in one case the solution is when the graph of e^{-x} , and x^2 intersect, whereas in the other case the root is located when $x^2 - e^{-x}$ intersect the x -axis.

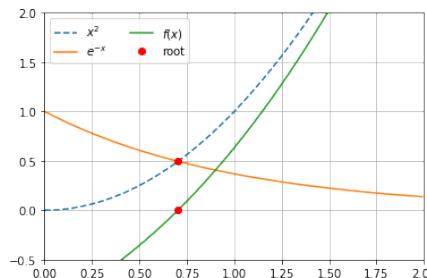


Fig. 3.1 Notice that the root is located at the same place ($x = 0.703467417$)

In the case of more than one unknown, or a set of equations that must be satisfied simultaneously, equation (3.2) is replaced with a vector equation

$$\mathbf{f}(\mathbf{x}) = \mathbf{0}. \quad (3.3)$$

Although this equation looks quite similar to equation (3.2), this equation is *much* harder to solve. The only methods we will cover is the Newton Rapson method, which is a very good method if a good starting point is given. If you have a multidimensional problem, the advice is to try Newton-Raphson, if this method fails you need to try more advanced method, see e.g. [4].

3.2 Example: van der Waals equation of state

Before we begin with the numerical algorithms, let us consider an example: the van der Waals equation of state. The purpose is to illustrate some of the typical challenges. You are probably familiar with the ideal gas law:

$$P\nu = R_g T, \quad (3.4)$$

where $\nu = V/n$ is the molar volume of the gas, P is the pressure, V is the volume, T is the temperature, n is the number of moles of the gas, and R_g is the ideal gas constant. This equation is an example of an *equation of state* (EOS), it relates P , T , and ν . Thus if we know the pressure and temperature of the gas, we can calculate ν . Equation (3.4) assumes that there are no interactions between the molecules in the gas. Clearly, this is too simplistic, and because of this one normally uses an EOS that better reflect the physical properties of the substance. A very famous EOS is the van der Waal EOS, which is a slight modification of equation (3.4):

$$\left(P + \frac{a}{\nu^2} \right) (\nu - b) = R_g T. \quad (3.5)$$

a and b are material constants that needs to be determined experimentally. This equation is *not* used in industrial design, but most equations used in practice are based on equation (3.5). Multiplying equation (3.5) with ν^2 , we get a non linear equation that is cubic in the molar volume. It turns out that cubic EOS are a class of equations that are quite successful in modeling the behavior of real systems [2]. However equation (3.5) is a good starting point for more complex and realistic equations.

It is common practice to rescale EOS with respect to the critical point. At the critical point we have [ref]:

$$\left. \frac{\partial P}{\partial \nu} \right|_{T_c, P_c} = 0 \quad (3.6)$$

$$\left. \frac{\partial^2 P}{\partial \nu^2} \right|_{T_c, P_c} = 0 \quad (3.7)$$

From equation (3.6), (3.7), and (3.5), it follows:

$$\nu_c = 3b \quad , P_c = \frac{a}{27b^2} \quad , R_g T_c = \frac{8a}{27b^2}. \quad (3.8)$$

Inserting these equations into equation (3.5), and defining the *reduced* quantities $\hat{P} = P/P_c$, $\hat{T} = T/T_c$, $\hat{\nu} = \nu/\nu_c$, we get

$$\left(\hat{P} + \frac{3}{\hat{\nu}^2} \right) (3\hat{\nu} - 1) = 8\hat{T}. \quad (3.9)$$

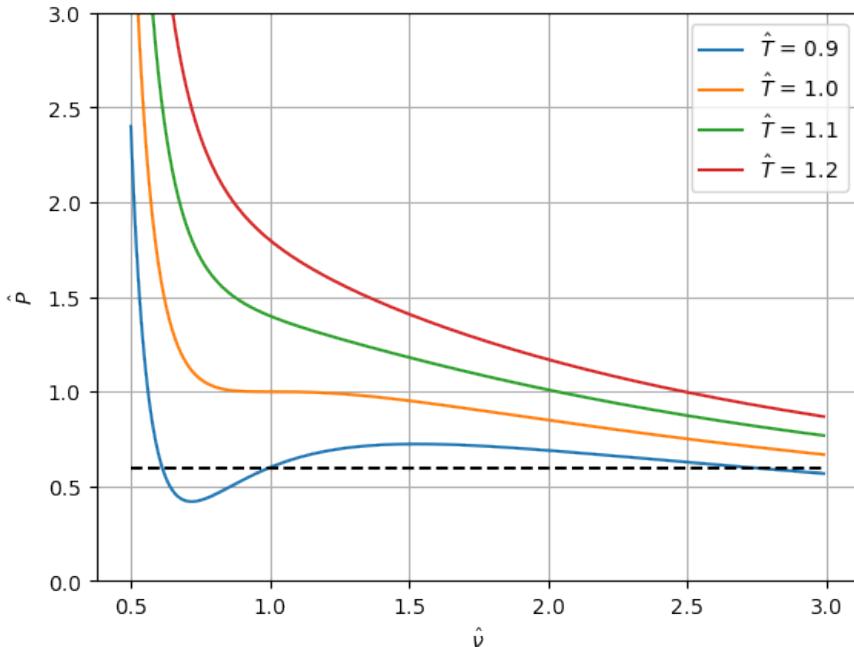


Fig. 3.2 van der Waal isotherms.

In figure 3.2, we have plotted the isotherms. Note that if $\hat{T} < 1$ ($T < T_c$), there might be more than one solution for the molar volume. This is clearly unphysical and additional constraints are needed. For the

curve $\hat{T} = 0.9$, the dashed line shows that for $\hat{P} = 0.7$, there are three solutions. This is a typical behavior of the cubic EOS, and physically it corresponds to the saturated case, where the vapor and liquid phase co-exist. The left root is the liquid state and the right root is the vapor state. The root in the middle represents a meta stable state.

It never hurts to look at your function

The example in figure 3.2 illustrates some important points. Solving a nonlinear problem might be very easy in part of the parameter space (e.g. when $T > T_c$ there are only one solution), but extremely hard in other part of the parameter space (e.g. when $T < T_c$, where there are multiple solutions). However, much of the trick to find a solution is to choose a good starting point. When there are multiple solutions we need to start close to the physical solution.

Exercise 3.1: van der Waal EOS and CO₂

Use equation (3.5), and the parameters for CO₂: $a=3.640 \text{ L}^2\text{bar/mol}$, and $b=0.04267 \text{ L/mol}$, to test the van der Waal EOS in equation (3.5). Use that at 2 MPa and 100 °C, CO₂ has a specific volume of 0.033586 m³/kg.

Solution. The calculation is straight forward, but it is easy to get an error due to units. We will use SI units: $a=0.3640 \text{ m}^6\text{Pa/mol}$, $b=4.267 \cdot 10^{-5} \text{ m}^3/\text{mol}$, $R=8.314 \text{ J/mol K}$. The molar volume is obtained by multiplying by the molar weight of CO₂: $M_w = 44 \text{ g/mol}$, hence $\nu = 1.478 \cdot 10^{-3} \text{ m}^3/\text{mol}$. Using $P = RT/(\nu - b) - a/\nu^2 = 1.993 \text{ MPa}$, or an error of 0.3%.

3.3 Fixed-point iteration

A simple (but not always possible) way of solving a nonlinear equation is to reformulate the problem $f(x) = 0$ to a problem of the form

$$x = g(x). \quad (3.10)$$

The algorithm for solving this equation is to guess at a starting point, x_0 , evaluate $x_1 = g(x_0)$, $x_2 = g(x_1)$, and so on. In some circumstances

we might end up at a stable point, where x does not change. This point is termed a *fixed point*.

Note that the form of $g(x)$ is not uniquely determined. For our function defined in equation (3.1), we can solve for x directly

$$x = e^{-x/2}, \quad (3.11)$$

or we could write:

$$x = x - x^2 + e^{-x}. \quad (3.12)$$

These functions are illustrated in figure 3.3, by visual inspection they look very similar, but as we will show in the next exercise the convergence is quite different.

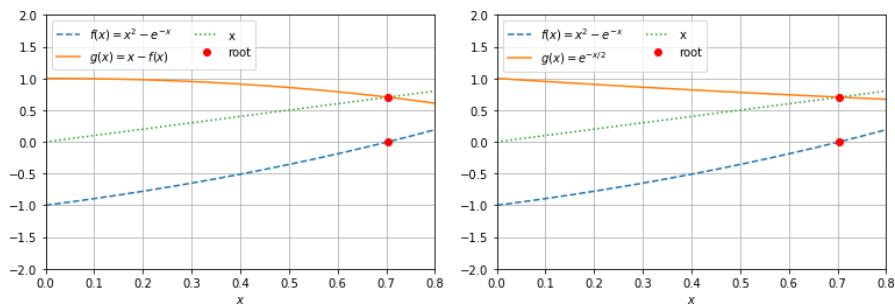


Fig. 3.3 Two examples of iterative functions, that will give the same solution.

Exercise 3.2: Implement the fixed point iteration

Write a Python function that utilizes the fixed point algorithm in the previous section, find the root of $f(x) = x^2 - e^{-x}$. In one case use $g(x) = e^{-x/2}$, and in the other case use $g(x) = x - x^2 + e^{-x}$. How many iterations does it take in each case?

Solution. Below is a straight forward (vanilla) implementation:

```
def iterative(x,g,prec=1e-8, MAXIT=1000):
    '''Approximate solution of x=g(x) by fixed point iterations.
    x : starting point for iterations
    eps : desired precision
    Returns x when x does not change more than prec
    and number of iterations MAXIT are not exceeded
    '''
    eps = 1
    n=0
```

```

while eps>prec and n < MAXIT:
    x_next = g(x)
    eps = np.abs(x-x_next)
    x = x_next
    n += 1
    if(np.isinf(x)):
        print('Quitting .. maybe bad starting point?')
        return x
    if (n<MAXIT):
        print('Found solution: ', x, ' After ', n, 'iterations')
    else:
        print('Max number of iterations exceeded')
return x

```

If we start at $x = 0$, it will take 174 iterations using $x - x^2 + e^{-x}$ ($g(x)$) and only 19 for $e^{-x/2}$ ($h(x)$), the root is $x=0.70346742$.

Exercise 3.3: Finding the molar volume from the van der Waal EOS by fixed point iteration

Extend the code above to take as argument the van der Waal EOS. For simplicity we will use the rescaled EOS in equation (3.9). Show that for the reduced temperature, $\hat{T}=1.2$, and pressure, $\hat{P}=1.5$, the reduced molar volume $\hat{\nu}$ is 1.3522091.

Solution. First we rewrite equation (3.9) in a more useful form

$$\hat{\nu} = \frac{1}{3} \left(1 + \frac{8\hat{T}}{\hat{P} + 3/\hat{\nu}^2} \right) \quad (3.13)$$

The right hand side will play the same role as $g(x)$ above, where x now is the reduced molar volume, and can be implemented in Python as:

```

def dvdwEOS(nu,t,p):
    return (1+8*t/(p+3/nu**2))/3

```

Note that this function requires the values of \hat{P} and \hat{T} , in addition to $\hat{\nu}$ to return a value. Thus in order to use the fixed point iteration method implemented above, we need to pass arguments to our function. This can easily be achieved by taking advantage of Pythons `*args` functionality. By simply rewriting our implementation slightly:

```

def iterative(x,g,*args,prec=1e-8):
    MAX_ITER=1000
    eps = 1
    n=0
    while eps>prec and n < MAX_ITER:

```

```

x_next = g(x,*args)
eps = np.abs(x-x_next)
x = x_next
n += 1
print('Number of iterations: ', n)
return x

```

We can find the root by calling the function as:

```
iterative(1,dvdwEOS,1.2,1.5)
```

The program returns the correct solution after 71 iterations.

3.3.1 When do the fixed point method fail?

If we replace e^{-x} with e^{1-x^2} in equation (3.12), our method will not give a solution. You can easily verify that the $x = 1$ is a solution, so why does our method fail? To investigate this in a bit more detail, we turn to Taylors formula (once again). Assume that the root is located at x^* , and our guess is x_k , then the next x -value will be

$$x_{k+1} = g(x_0) = g(x^*) + g'(x^*)(x_k - x^*) + \dots \quad (3.14)$$

The true solution is x^* , hence $x^* = f(x^*)$, and we can write

$$x_{k+1} - x^* = g'(x^*)(x_k - x^*), \quad (3.15)$$

where we have neglected higher order terms. The point is: at each iteration we want the distance $x_1 - x^*$ to decrease, i.e. to be smaller than $x_0 - x^*$. This can only be achieved if

$$|g'(x^*)| < 1. \quad (3.16)$$

In our example above we saw that if $g(x) = x - x^2 + e^{-x}$, we used 172 iterations and only 19 iterations if we replaced $g(x)$ with $h(x) = e^{-x/2}$ to converge to the *same* root $x=0.70346742$. We can now understand this, because $g'(x) = 1 - 2x - e^{-x}$ and $g(x^*) \simeq -0.90$, whereas $h'(x) = -e^{-x/2}/2$, and $h'(x^*) \simeq 0.35$. We expect the number of iterations, n , needed to reach a certain precision, ε , to scale as

$$|g'(x^*)|^n = \varepsilon. \quad (3.17)$$

We expect to use $\log |h'(x^*)| / \log |g'(x^*)| \simeq 10$ more iterations using $g(x)$ compared to $h(x)$, which is close to the observed value of $172/19 \simeq 9$.

3.3.2 What to do when the fixed point method fail

As discussed in [1], there might be an elegant solution whenever $|g'(x^*)| > 1$. If it is possible to invert the $g(x)$, we can show that the derivative of the inverse function $g'^{-1}(x^*) = 1/g'(x^*)$. Why is this useful? Because if $x^* = g(x^*)$ is the solution we are searching for, then this is equivalent to $x^* = g^{-1}(x^*)$ if and only if we can invert $g(x)$. Note that in many cases it is not possible to invert $g(x)$. Let us first show that $g'^{-1}(x^*) = 1/g'(x^*)$. For simplicity write

$$y = g(x) \Leftrightarrow x = g^{-1}(y), \quad (3.18)$$

taking the derivative with respect to x gives

$$\frac{d}{dx}g^{-1}(y) = \frac{dx}{dy} = 1, \quad (3.19)$$

$$\frac{dg^{-1}(y)}{dy} \frac{dy}{dx} = \frac{dx}{dy} = 1, \quad (3.20)$$

$$\frac{dg^{-1}(y)}{dy} = \frac{1}{\frac{dy}{dx}} = \frac{1}{g'(x)} = \frac{1}{g'(g^{-1}(y))}. \quad (3.21)$$

Going from equation (3.19) to (3.20), we have used the chain rule. Equation (3.21) is general, let us now specify to our fixed point iteration. Then we can use $x^* = g(x^*) = y^*$, and $x^* = g^{-1}(y^*) = g^{-1}(x^*)$ hence we can write the last equation as

$$\frac{d}{dx}g^{-1}(x^*) = \frac{1}{g'(x^*)}. \quad (3.22)$$

Exercise 3.4: Solve $x = e^{1-x^2}$ using fixed point iteration

The solution to $x = e^{1-x^2}$ is clearly $x = 1$.

- First try the fixed point method using $g(x) = e^{1-x^2}$ to find the root $x = 1$. Try to start very close to the true solution $x = 1$. What is the value of $g'(x^*)$?
- Next, invert $g(x)$, what is the derivative of $g^{-1}(x^*)$? Try the fixed point method using $g^{-1}(x^*)$

Solution. First, we calculate the derivative of $g(x)$, $g'(x) = -2xe^{1-x^2}$, hence $g'(x^*) = -2$ and $|g'(x^*)| > 1$. This is an unstable fixed point, and if we start a little bit off from this point we will spiral away from it.

Inverting $y = g(x)$ gives us $g^{-1}(y) = \sqrt{1 - \ln y}$. Note that $y^* = x^* = 1$ is a solution to this equation as it should be. The derivative is

$$g^{-1}'(y) = -\frac{1}{2\sqrt{1 - \ln y}}, \quad (3.23)$$

and $g^{-1}'(y^*) = -1/2$. It takes about 30 iterations to reach the correct solution $y^* = 1$, when the starting point is $y = 0$.

3.4 Rate of convergence

The rate of convergence is the speed at which a *convergent* sequence approach the limit. Assume that our sequence x_k converges to the number x^* , the sequence is said to *converge linearly* to x^* if there exists a number $\mu \in \langle 0, 1 \rangle$, such that

$$\lim_{k \rightarrow \infty} \frac{|x_{k+1} - x^*|}{|x_k - x^*|} = \mu \quad (3.24)$$

Inserting equation (3.15) in equation (3.24), we get:

$$\lim_{k \rightarrow \infty} \frac{|x_{k+1} - x_k|}{|x_k - x^*|} = \frac{|g'(x^*)(x_k - x^*)|}{|x_k - x^*|} = |g'(x^*)|. \quad (3.25)$$

Hence the fixed point iteration is expected to converge *linearly* to the correct solution. The definition in equation (3.24), can be extended to include the definition of quadratic, cubic, etc. convergence:

$$\lim_{k \rightarrow \infty} \frac{|x_{k+1} - x^*|}{|x_k - x^*|^q} = \mu. \quad (3.26)$$

If $q = 2$ the convergence is said to be quadratic and so on.

3.5 The bisection method

The idea behind bisection is that the root is bracketed, i.e. that there exists two points a and b , such that $f(a) \cdot f(b) < 0$. In practice it might be a challenge to find these two points. However, if you know that the function has a only root between two values, and that speed is not a big issue this method guarantees that the root will be found within a

finite number of steps. The basic idea behind the method is to divide the interval into two (i.e. bisecting the interval). The method only works if the function is continuous on the interval.

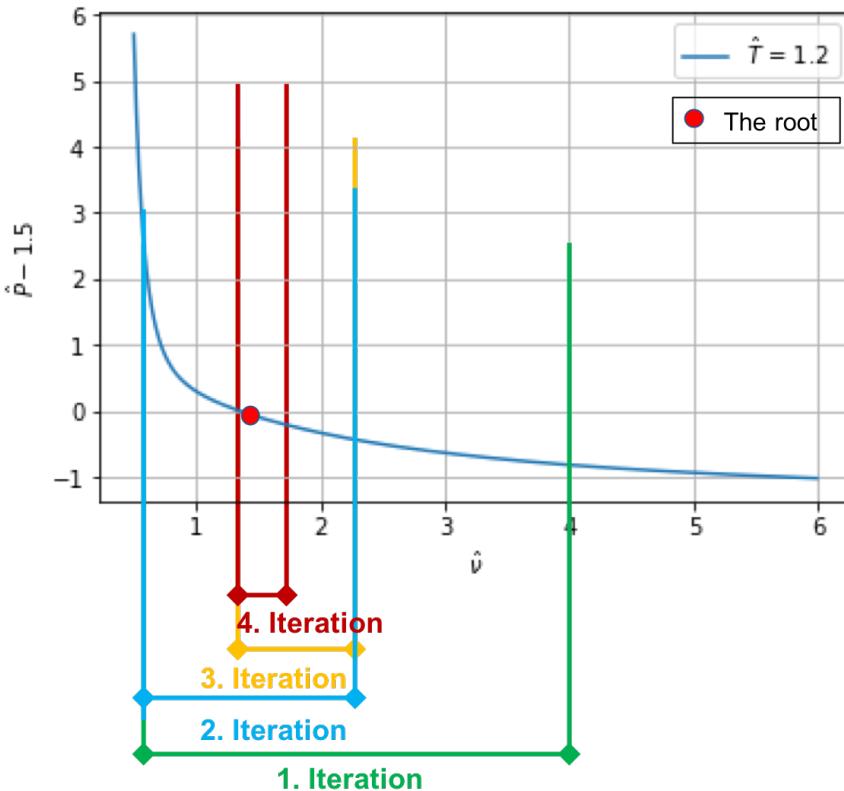


Fig. 3.4 Illustration of the bisection method for the van der Waal EOS.

The algorithm is as follows:

- Test if $f(a) \cdot f(b) < 0$, if not return an error message
- Calculate the midpoint $c = (a + b)/2$. If $f(a) \cdot f(c) < 0$ the root is in the interval $[a, c]$, else the root is in the interval $[c, b]$
- Half the interval, and test in which interval the root lies, and continue until a convergence criterion.

In figure 3.4, there is a graphical illustration. Below is an implementation of the bisection method.

```
def bisection(f,a,b,prec=1e-8,MAXIT=100):
    '''Approximate solution of f(x)=0 on interval [a,b] by bisection.'''

```

```

f      : f(x)=0.
a,b   : brackets the root f(a)*f(b) has to be negative
eps   : desired precision

Returns the midpoint when it is closer than eps to the root,
unless MAXIT are not exceeded
''

if f(a)*f(b) >= 0:
    print('You need to bracket the root, f(a)*f(b) >= 0')
    return None

an = a
bn = b
cn = 0.5*(an + bn)
c_old = cn - 10*prec
n=0
while np.abs(cn-c_old)>=prec and n<MAXIT:
    c_old = cn
    f_cn = f(cn)
    if f(an)*f_cn < 0:
        bn = cn
    elif f(bn)*f_cn < 0:
        an = cn
    elif f_cn == 0:
        print('Found exact solution ', cn,
              ' after ', n, 'iterations')
        return cn
    else:
        print('Bisection method fails.')
        return None
    cn = 0.5*(an+bn)
    n += 1
if n<MAXIT-1:
    print('Found solution ', cn, ' after ', n, 'iterations')
    return cn
else:
    print('Max number of iterations: ', MAXIT, ' reached.')
    print('Try to increase MAXIT or decrease prec')
    print('Returning best guess, value of function is: ', f_cn)
return None

```

Warnings

Note that the implementation of the bisection algorithm is only a few lines of code, and most of the code is to give warnings to the user. In this case it is important to do additional checking, and give the user warnings. If $f(c)=0$, then we must stop and return the exact solution. If we only test if $f(a) \cdot f(c)$ is greater or lower than zero the algorithm would fail.

3.5.1 Rate of convergence

If c_n is the midpoint after n steps, the difference between the solution x^* and c_n is

$$|c_n - x^*| \leq \frac{|b - a|}{2^n} \quad (3.27)$$

Using our previous definition in equation (3.26), we find that

$$\lim_{k \rightarrow \infty} \frac{|c_{k+1} - x^*|}{|c_k - x^*|} \leq \frac{|b - a|/2^{n+1}}{|b - a|/2^n} = \frac{1}{2}, \quad (3.28)$$

hence the bisection method converges linearly.

3.6 Newtons method

Newtons method is one of the most used methods. If it converges, it converges quadratically to the correct solution. The drawback is that contrary to the bisection method it may fail if a bad starting point is given. Newtons method for finding the root of a function $f(x) = 0$ is illustrated in figure 3.5. The main idea is to use more information about the function in the search of the root. In this case we want to find the point where the tangent of the function in x_k intersect the x -axis, and take that as our next point, x_{k+1} .

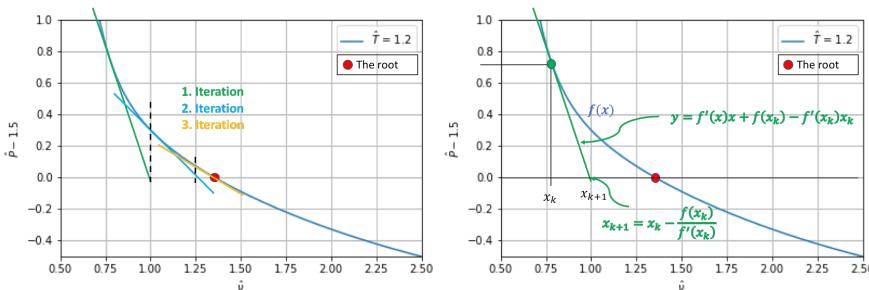


Fig. 3.5 Illustration of Newtons method for the van der Waals EOS.

We can easily derive the algorithm by finding the formula for the tangent line. Using $y = ax + b$ for the tangent line, we immediately know that $a = f'(x_k)$. b can be found as we know that the line intersects $(x_k, f(x_k))$: $f(x_k) = f'(x_k)x_k + b$, hence the equation for the tangent line is $y = f'(x_k)x + f(x_k) - f'(x_k)x_k$. The next point is located where y

crosses the x -axis, hence $0 = f'(x_k)x_{k+1} + f(x_k) - f'(x_k)x_k$. Rearranging this equation, we can write Newtons method in the standard form

$$x_{k+1} = x_k - \frac{f(x_k)}{f'(x_k)}. \quad (3.29)$$

Note that the derivative of $f(x)$ enters in equation (3.29), which means that if our function has a extremal value in our search domain, Newtons method most likely will fail. In particular x_1 , and x_4 in the figure to the right in figure 3.6 are bad starting point for Newtons method.

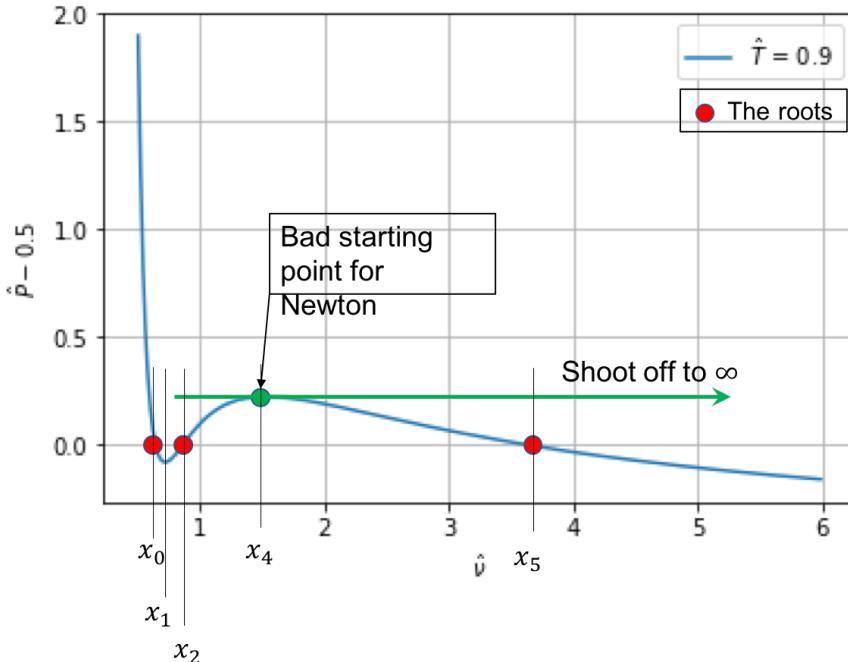


Fig. 3.6 Illustration of some of the possible challenges with Newtons method. Note that if the derivative is zero somewhere in the search interval, Newtons method will fail.

An implementation is shown below.

```
def newton(f, x, prec=1e-8, MAXIT=500):
    '''Approximate solution of f(x)=0 by Newtons method.
    The derivative of the function is calculated numerically
    f    : f(x)=0.
    x    : starting point
    eps : desired precision

    Returns x when it is closer than eps to the root,
```

```

unless MAX_ITERATIONS are not exceeded
,,
MAX_ITERATIONS=MAXIT
x_old = x
h      = 1e-4
for n in range(MAX_ITERATIONS):
    x_new = x_old - 2*h*f(x_old)/(f(x_old+h)-f(x_old-h))
    if(abs(x_new-x_old)<prec):
        print('Found solution:', x_new,
              ', after:', n, 'iterations.')
        return x_new
    x_old=x_new
print('Max number of iterations: ', MAXIT, ' reached.')
print('Try to increase MAXIT or decrease prec')
print('Returning best guess, value of function is: ', f(x_new))
return x_new

```

Comparing figure 3.4 and 3.5, you immediately get the sense that Newtons method converges faster, and indeed it does.

3.6.1 Rate of convergence

Newton's method is similar to the fixed point method, but where we do not use $g(x) = x - f(x)$, but $g(x) = x - \frac{f(x)}{f'(x)}$. We will now analyze Newton's method, using the same approach as in section 3.3.1. First we expand $g(x)$ around the root x^*

$$x_{k+1} = g(x_k) = g(x^*) + g'(x^*)(x_k - x^*) + \frac{1}{2}g''(x^*)(x_k - x^*)^2, \quad (3.30)$$

where we have skipped all higher order terms. You can easily verify that

$$g'(x) = \frac{f''(x)f(x)}{f'(x)^2} \quad (3.31)$$

$$g''(x) = \frac{(f'''(x)f'(x) - 2f''(x)^2f'(x))f(x) + f''(x)f'(x)^2}{f'(x)^4}. \quad (3.32)$$

x^* is a solution, hence $f(x^*) = 0$, we then find from equation (3.31) and (3.32) that $g'(x^*) = 0$, and $g''(x^*) = f''(x^*)/f'(x^*)^2$. Thus from equation (3.30) we get

$$x_{k+1} = x^* + \frac{1}{2} \frac{f''(x^*)}{f'(x^*)^2} (x_k - x^*)^2, \quad (3.33)$$

or equivalently:

$$\frac{x_{k+1} - x^*}{(x - x^*)^2} = \frac{1}{2} \frac{f''(x^*)}{f'(x^*)^2}. \quad (3.34)$$

The denominator has a power of two, and hence Newtons method is *quadratic* convergent (assuming that the sequence x_{k+1} is a convergent sequence). Note that it also follows from the analyses above that Newtons method will fail if the derivative at the root, $f'(x^*)$, is zero.

Exercise 3.5: Compare Newtons, Bisection and the Fixed Point method

Find the root of $f(x) = x^2 - e^{-x}$ using bisection, fixed point, and Newtons method, start at $x = 0$. How many iterations do you need to use reach a precision of 10^{-8} ? What happens if you widen the search domain or start further away from the root?

Solution. The root is located at $x^* = 0.70346742$.

- Fixed point method: we saw earlier that using $g(x) = x - f(x)$ used 174 iterations, and $g(x) = \sqrt{x^2 - f(x)}$ used 19 iterations. If we start at $x = -100$, $g(x) = x - f(x)$ fails, and $g(x) = \sqrt{x^2 - f(x)}$ uses only 21 iterations, and at $x = 100$ we use 20 iterations.
- Bisection method: it use 25 iterations for $a = 0$, and $b = 1$ (implementation shown earlier in the chapter). Choosing $a = -b = -100$ we use 33 iterations.
- Newtons method: it use only 5 function evaluations (implementation above) starting at $x = 0$. Starting at $x = -100$, it uses 106 iterations. Newtons method is slow in this case because the function is very steep around the starting point, see figure 3.7. Starting at $x = 100$, we only use 10 iterations.

A good starting point is crucial

Note that it is not given which method is best, but if we are "close" to the root Newtons method is usually superior. If we are far away, other methods might work better. In many cases one uses a more stable method far away from the root, and then "polish up" the root by a couple of Newton iterations [4]. See also Brents method which combines bisection and linear interpolation (secant method) [4].

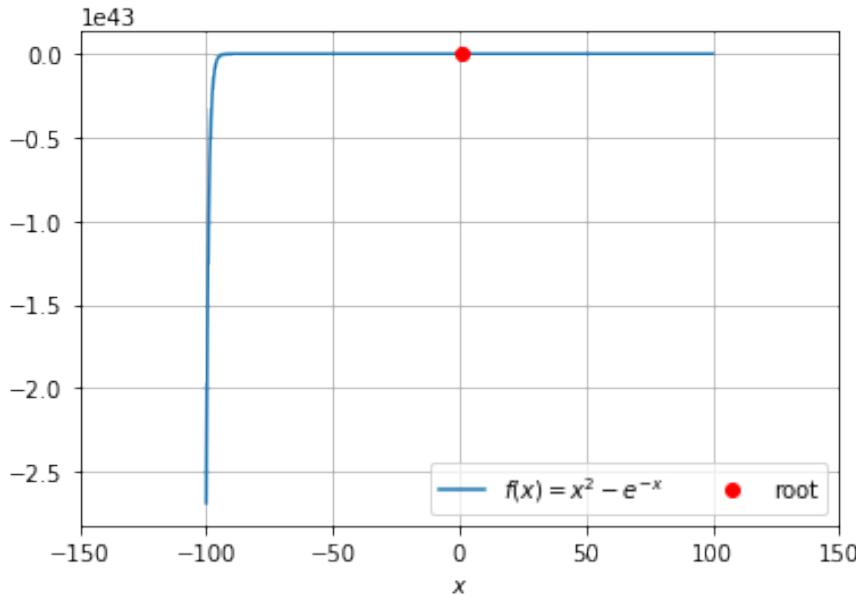


Fig. 3.7 Newtons method performs poorly far away due to the shape of the function close to $x = -100$, bisection performs much better while the fixed point method fails.

3.7 Secant method

The Newtons method is very good if you can choose a good starting point, and you can give in an analytical formula for the derivative. In some cases it is not possible to calculate the derivative analytically, then a very good method of choice is the secant method. It can be derived by simply replacing the derivative in Newtons method by the finite difference approximation

$$f'(x_k) \rightarrow \frac{f(x_k) - f(x_{k-1})}{x_k - x_{k-1}}. \quad (3.35)$$

Inserting this equation into equation (3.29), we get

$$\begin{aligned} x_{k+1} &= x_k - f(x_k) \frac{x_k - x_{k-1}}{f(x_k) - f(x_{k-1})} \\ &= \frac{x_{k-1}f(x_k) - x_k f(x_{k-1})}{f(x_k) - f(x_{k-1})}. \end{aligned} \quad (3.36)$$

For a graphical illustration see figure 3.8

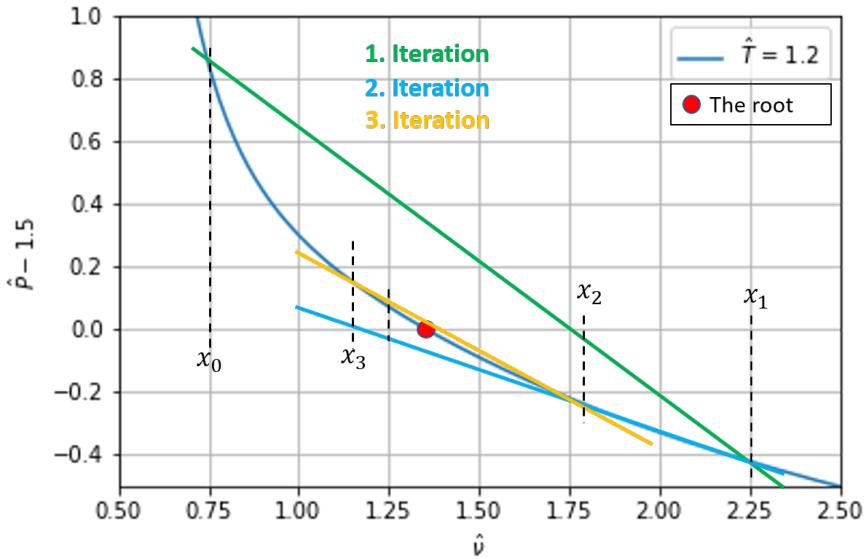


Fig. 3.8 A graphical illustration of the secant method. Note that the starting points x_0 and x_1 do not need to be close. The next point is where the (secant) line crosses the x -axis.

3.7.1 Rate of convergence

The derivation of the rate of convergence for the secant method is a bit more involved. To simplify the notation we introduce the notation $\varepsilon_k \equiv x_k - x^*$, where x^* is the exact solution. Subtracting x^* from each side of equation (3.36) we get

$$\begin{aligned}\varepsilon_{k+1} &= x_{k+1} - x^* = \frac{x_{k-1}f(x_k) - x_kf(x_{k-1})}{f(x_k) - f(x_{k-1})} - x^*, \\ \varepsilon_{k+1} &= \frac{\varepsilon_{k-1}f(x_k) - \varepsilon_kf(x_{k-1})}{f(x_k) - f(x_{k-1})},\end{aligned}\tag{3.37}$$

we now make a Taylor expansion of $f(x_k)$ and $f(x_{k-1})$ about the root x^*

$$\begin{aligned} f(x_k) &= f(x^*) + f'(x^*)(x_k - x^*) + \frac{1}{2}f''(x^*)(x_k - x^*)^2 + \dots, \\ &= f'(x^*)\varepsilon_k + \frac{1}{2}f''(x^*)\varepsilon_k^2 + \dots. \end{aligned} \quad (3.38)$$

$$\begin{aligned} f(x_{k-1}) &= f(x^*) + f'(x^*)(x_{k-1} - x^*) + \frac{1}{2}f''(x^*)(x_{k-1} - x^*)^2 + \dots, \\ &= f'(x^*)\varepsilon_{k-1} + \frac{1}{2}f''(x^*)\varepsilon_{k-1}^2 + \dots, \end{aligned} \quad (3.39)$$

where we have used the fact that $f(x^*) = 0$. Inserting these equations into equation (3.37) and neglecting terms of order ε_k^3 we get

$$\begin{aligned} \varepsilon_{k+1} &= \frac{\varepsilon_{k-1} [f'(x^*)\varepsilon_k + \frac{1}{2}f''(x^*)\varepsilon_k^2] - \varepsilon_k [f'(x^*)\varepsilon_{k-1} + \frac{1}{2}f''(x^*)\varepsilon_{k-1}^2]}{f'(x^*)\varepsilon_k + \frac{1}{2}f''(x^*)\varepsilon_k^2 - [f'(x^*)\varepsilon_{k-1} + \frac{1}{2}f''(x^*)\varepsilon_{k-1}^2]}, \\ &= \frac{\varepsilon_k \varepsilon_{k-1} [\varepsilon_k - \varepsilon_{k-1}]}{[f'(x^*) + \frac{1}{2}f''(x^*)(\varepsilon_k + \varepsilon_{k-1})](\varepsilon_k - \varepsilon_{k-1})}, \\ &= \frac{f''(x^*)}{2f'(x^*)}\varepsilon_k\varepsilon_{k-1}, \end{aligned} \quad (3.40)$$

where we have neglected higher powers of ε . We are searching for a solution of the form $\varepsilon_{k+1} = K\varepsilon_k^q$, q is the rate of convergence. We can invert this equation to get $\varepsilon_k = K^{-1/q}\varepsilon_{k+1}^{1/q}$, or alternatively $\varepsilon_{k-1} = K^{-1/q}\varepsilon_k^{1/q}$ (just set $k \rightarrow k-1$). Inserting these equations into equation (3.40)

$$\varepsilon_k^q = \frac{f''(x^*)}{2f'(x^*)}\varepsilon_k K^{-1/q}\varepsilon_k^{1/q}. \quad (3.41)$$

Clearly, if this equation is to have a solution we must have

$$\begin{aligned} \frac{f''(x^*)}{2f'(x^*)}K^{-1/q} &= 1 \\ \varepsilon_k^q &= \varepsilon_k \varepsilon_k^{1/q} = \varepsilon_k^{1+1/q}, \end{aligned} \quad (3.42)$$

or $q = 1 + 1/q$. Solving this equation we get $q = (1 \pm \sqrt{5})/2$, neglecting the negative solution, we find the rate of convergence for the secant method $q = (1 + \sqrt{5})/2 \simeq 1.618$.

3.8 Newton Rapson method

The derivation of Newtons method, equation (3.29), done in the previous section was based on figure 3.5. We will now derive it using a slightly different approach, but which lends itself easier to extend Newtons method to higher dimensions. The starting point is to expand the function around x_k , using Taylors formula

$$f(x) = f(x_k) + f'(x_k)(x - x_k) + \dots . \quad (3.43)$$

Equation (3.29) can be derived from equation (3.43) by simply demanding that we keep the linear terms, and that the next point x_{k+1} is located where the linear approximation intersects the x -axis, i.e. simply set $f(x) = 0$, and $x = x_{k+1}$ in equation (3.43).

In higher order dimensions, we solve equation (3.3), and equation (3.43) is

$$\mathbf{f}(\mathbf{x}) = \mathbf{f}(\mathbf{x}_k) + \mathbf{J}(\mathbf{x}_k)(\mathbf{x} - \mathbf{x}_k) + \dots . \quad (3.44)$$

$\mathbf{J}(\mathbf{x}_k)$ is the Jacobian. As before, we simply set $\mathbf{f}(\mathbf{x}) = \mathbf{0}$, $\mathbf{x} = \mathbf{x}_{k+1}$, and keep the linear terms, hence

$$\mathbf{x}_{k+1} = \mathbf{x}_k - \mathbf{J}^{-1}(\mathbf{x}_k)\mathbf{f}(\mathbf{x}_k). \quad (3.45)$$

To make the mathematics a bit more clear, let us specify to 2D. Assume that $\mathbf{f}(\mathbf{x}) = [f_x(x, y), f_y(x, y)]$, then the Jacobian is

$$\mathbf{J}(\mathbf{x}_k) = \begin{pmatrix} \frac{\partial f_x}{\partial x} & \frac{\partial f_x}{\partial y} \\ \frac{\partial f_y}{\partial x} & \frac{\partial f_y}{\partial y} \end{pmatrix}. \quad (3.46)$$

3.9 Gradient Descent

This method used is to minimize functions (does not work for root finding). In many nonlinear problems, we would like to minimize (or maximize) a function. An ideal 2D example is shown in figure 3.9. The algorithm moves in the direction of steepest descent. Note that the step size might change towards the search.

Assume that we have a function $\mathbf{f}(\mathbf{x})$, that we would like to minimize. The gradient descent algorithm is simply to update parameters according to the derivative (gradient) of \mathbf{f}

$$\mathbf{x}_{k+1} = \mathbf{x}_k - \gamma \nabla \mathbf{f}. \quad (3.47)$$

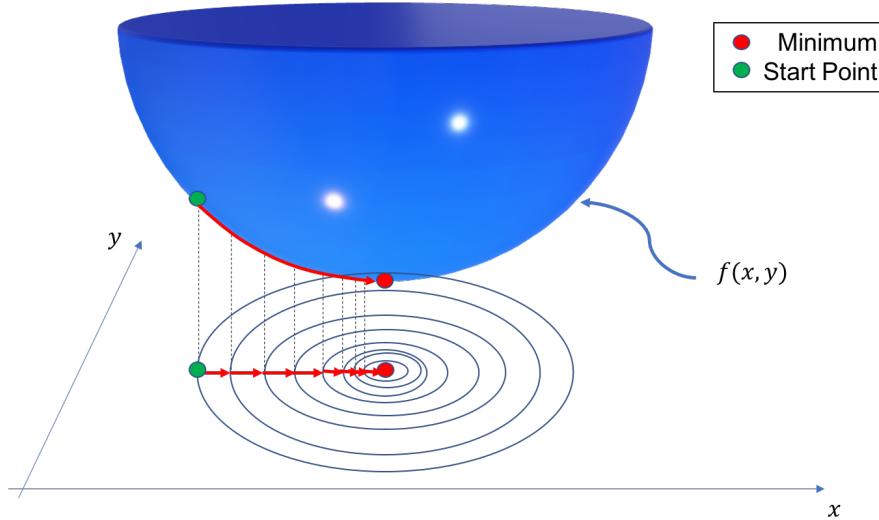


Fig. 3.9 A very simple example of the gradient descent method.

γ is the learning rate, and a good choice of γ is important. γ might also change from one iteration to the other, and does not have to be constant.

Exercise 3.6: Gradient descent solution of linear regression

A very typical example is if we have a model and we would like to fit some parameters of the model to a data set (e.g. linear regression). Assume that we have observations (x_i, y_i) and model predictions $f(x_i, \beta)$, the model parameters are contained in the vector β . The *least square*, S , is the square of the sum of all the *residuals*, i.e. the difference between the observations and model predictions

$$S = \sum_i (y_i - f(x_i, \beta))^2. \quad (3.48)$$

Specializing to linear regression, we choose the model to be linear

$$f(x_i, \beta) = b_0 + b_1 x_i. \quad (3.49)$$

Equation (3.48) now takes the form

$$S = \sum_i (y_i - b_0 + b_1 x_i)^2. \quad (3.50)$$

The gradients are:

$$\frac{\partial S}{\partial b_0} = -2 \sum_i (y_i - b_0 + b_1 x_i),$$

$$\frac{\partial S}{\partial b_1} = -2 \sum_i (y_i - b_0 + b_1 x_i) x_i. \quad (3.51)$$

- Implement the gradient descent method using a constant learning rate of 10^{-3} , to minimize the least square function
- Test the linear regression on the data set $x_i = [0, 1, 2, 3, 4, 5, 6, 7, 8, 9]$, and $y = [1, 3, 2, 5, 7, 8, 8, 9, 10, 12]$, choose a starting value $(b_0, b_1) = (0, 0)$. What happens if you increase the learning rate?

Solution. Below is an implementation of the gradient descent method with a constant learning rate

```
def gradient_descent(f,x,df, g=.001, prec=1e-8,MAXIT=10000):
    '''Minimize f(x) by gradient descent.
    f   : min(f(x))
    x   : starting point
    df  : derivative of f(x)
    g   : learning rate
    prec: desired precision

    Returns x when it is closer than eps to the root,
    unless MAXIT are not exceeded
    '''
    x_old = x
    for n in range(MAXIT):
        x_new = x_old - g*df(x_old)
        if(abs(np.max(x_new-x_old))<prec):
            print('Found solution:', x_new,
                  ', after:', n, 'iterations.')
            return x_new
        x_old=x_new
    print('Max number of iterations: ', MAXIT, ' reached.')
    print('Try to increase MAXIT or decrease prec')
    print('Returning best guess, value of function is: ', f(x_new))
    return x_new
```

The linear regression is implemented as below

```
x_obs_ = np.array([0, 1, 2, 3, 4, 5, 6, 7, 8, 9])
y_obs_ = np.array([1, 3, 2, 5, 7, 8, 8, 9, 10, 12])
def plot_regression_line(b,x=x_obs_, y=y_obs_):
    global N_
    # plotting the actual points as scatter plot
    plt.scatter(x, y, color = "m",
                marker = "o", s = 30,label="data")
```

```

# predicted response vector
y_pred = b[0] + b[1]*x

# plotting the regression line
if(len(b)>1):
    plt.plot(x, y_pred, color = "g", label = "R-squared = {0:.3f}".format(b[2]))
    plt.plot(x, y_pred, color = "g", label = "iteration:" + str(N_) +", (b[0],b[1])= ({0:.3f}")
    plt.legend()
else:
    plt.plot(x, y_pred, color = "g")

# putting labels
plt.xlabel('x')
plt.ylabel('y')
plt.grid()
plt.legend()
# plt.savefig('../fig-nlin/stdec'+str(N_)+'.png', bbox_inches='tight', transparent=True)
N_=N_+1
# function to show plot
plt.show()

def gradient_descent(f,x,df, g=.001, prec=1e-8,MAXIT=10000):
    '''Minimize f(x) by gradient descent.
    f   : min(f(x))
    x   : starting point
    df  : derivative of f(x)
    g   : learning rate
    prec: desired precision

    Returns x when it is closer than eps to the root,
    unless MAXIT are not exceeded
    '''
    x_old = x
    for n in range(MAXIT):
        x_new = x_old - g*df(x_old)
        if(abs(np.max(x_new-x_old))<prec):
            print('Found solution:', x_new,
                  ', after:', n, 'iterations.')
            return x_new
        x_old=x_new
    print('Max number of iterations: ', MAXIT, ' reached.')
    print('Try to increase MAXIT or decrease prec')
    print('Returning best guess, value of function is: ', f(x_new))
    return x_new
#end

def S(b,x=x_obs_,y=y_obs_):
    return np.sum((y-b[0]-b[1]*x)**2)

def dS(b,x=x_obs_,y=y_obs_):
    return np.array([-2*np.sum(y-b[0]-b[1]*x),
                    -2*np.sum((y-b[0]-b[1]*x)*x)])

```

```
b=np.array([0,0])
```

The first four iterations are shown in figure 3.10. If we choose a learning rate that is too high, we will move past the minimum, and the solution will oscillate. This can be avoided by lowering the learning rate as we iterate, by e.g. replacing g with $g/(n+1)$ in the implementation above.

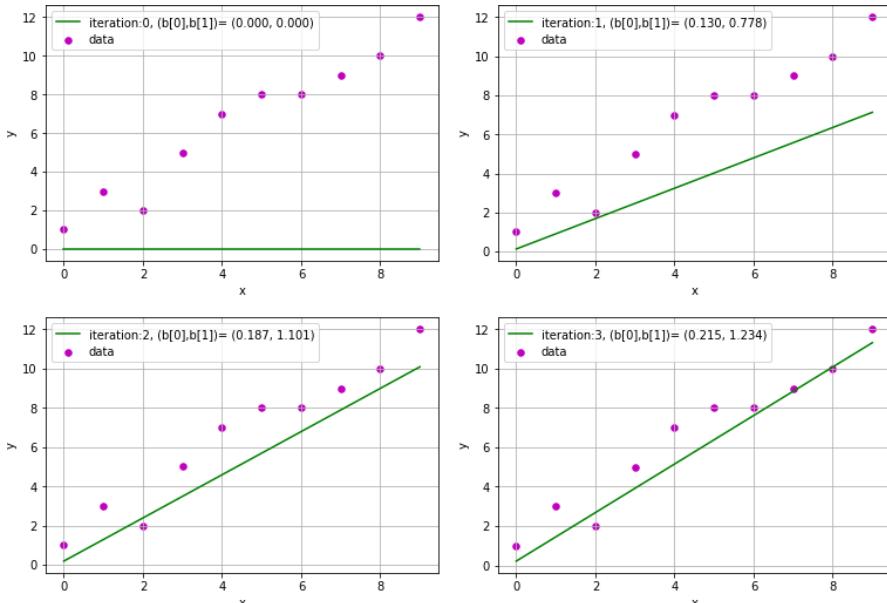


Fig. 3.10 First four iterations of the gradient descent solution of linear regression.

3.10 Other Useful Methods

In this chapter we have covered the *basic*, but you should now be well equipped to dive into other methods. We highly recommend [4] as a starting point, although the code examples are written in C++, the theory is presented in a very accurate, but informal way.

- Brents method: uses root bracketing, bisection, and inverse quadratic interpolation. The 1D method of choice if the function and not its derivative is known

4.1 Numerical Integration

Before diving into the details of this section, it is worth pointing out that the derivation of the algorithms in this section follows a general pattern:

1. We start with a mathematical model (in this case an integral)
2. The mathematical model is formulated in discrete form
3. Then we design an algorithm to solve the model
4. The numerical solution for a test case is compared with the true solution (could be an analytical solution or data)
5. Error analysis: we investigate the accuracy of the algorithm by changing the number of iterations and/or make changes to the implementation or algorithm

In many cases you would not use your own implementation to calculate an integral, but in order to understand which method to use in a specific case, it is important to understand the limitation and advantages of the different algorithms. The only way to achieve this is to have a basic understanding of the development. There might also be some cases where you would like to adapt an integration scheme to your specific needs.

4.1.1 The Midpoint Rule

Numerical integration is encountered in numerous applications in physics and engineering sciences. Let us first consider the most simple case, a

function $f(x)$, which is a function of one variable, x . The most straight forward way of calculating the area $\int_a^b f(x)dx$ is simply to divide the area under the function into N equal rectangular slices with size $h = (b-a)/N$, as illustrated in figure 4.1. The area of one box is:

$$M(x_k, x_k + h) = f(x_k + \frac{h}{2})h, \quad (4.1)$$

and the area of all the boxes is:

$$\begin{aligned} I(a, b) &= \int_a^b f(x)dx \simeq \sum_{k=0}^{N-1} M(x_k, x_k + h) \\ &= h \sum_{k=0}^{N-1} f(x_k + \frac{h}{2}) = h \sum_{k=0}^{N-1} f(a + (k + \frac{1}{2})h). \end{aligned} \quad (4.2)$$

Note that the sum goes from $k = 0, 1, \dots, N - 1$, a total of N elements. We could have chosen to let the sum go from $k = 1, 2, \dots, N$. In Python, C, C++ and many other programming languages the arrays start by indexing the elements from $0, 1, \dots$ to $N - 1$, therefore we choose the convention of having the first element to start at $k = 0$.

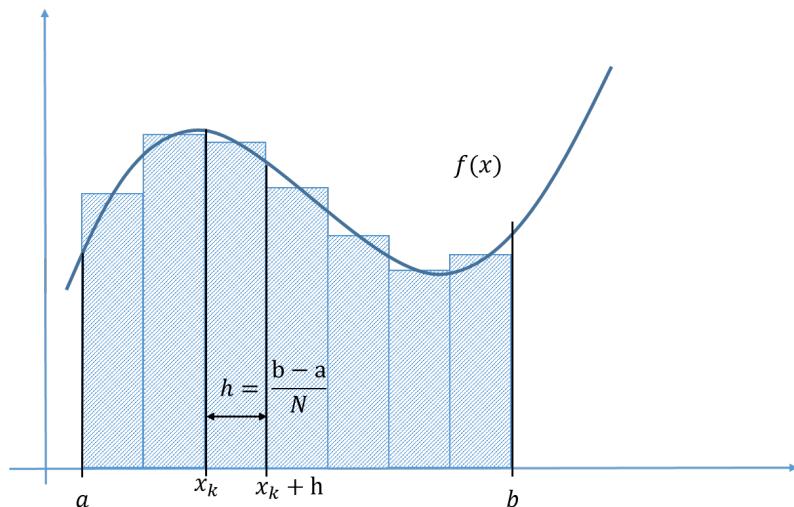


Fig. 4.1 Integrating a function with the midpoint rule.

Below is a Python code, where this algorithm is implemented for $\int_0^\pi \sin(x)dx$

```

import numpy as np
# Function to be integrated
def f(x):
    return np.sin(x)

def int_midpoint(lower_limit, upper_limit, func, N):
    """ calculates the area of func over the domain lower_limit
        to upper limit using N integration points """
    h      = (upper_limit-lower_limit)/N
    area  = 0.
    for k in range(0,N): # loop over k=0,1,...,N-1
        val = lower_limit+(k+0.5)*h # midpoint value
        area += func(val)*h
    return area

N
a=0
b=np.pi
Area = int_midpoint(a,b,f,N)
print('Numerical value= ', Area)
print('Error= ', (2-Area)/2) # Analytical result is 2

```

Notice

There are many ways to calculate loops in a programming language. If you were coding in a lower level programming language like Fortran, C or C++, you would probably implement the loop like (in Python syntax):

```

for k in range(0,N): # loop over k=0,1,...,N-1
    val = lower_limit+(k+0.5)*h # midpoint value
    area += func(val)
return area*h

```

However, in Python, you would always try to avoid loops because they are generally slow. A more efficient way of implementing the above rule would be to replace the loop with list comprehension

```

val  = [lower_limit+(k+0.5)*h for k in range(N)]
ff   = func(val)
area = np.sum(ff)
return area*h

```

or even faster only using numpy

```

val  = np.arange(lower_limit+0.5*h,upper_limit,h)
ff   = func(val)
area = np.sum(ff)
return area*h

```

4.1.2 The Trapezoidal Rule

The numerical error in the above example is quite low, only about 2% for $N = 5$. However, by just looking at the graph above it seems likely that we can develop a better algorithm by using trapezoids instead of rectangles, see figure 4.2.

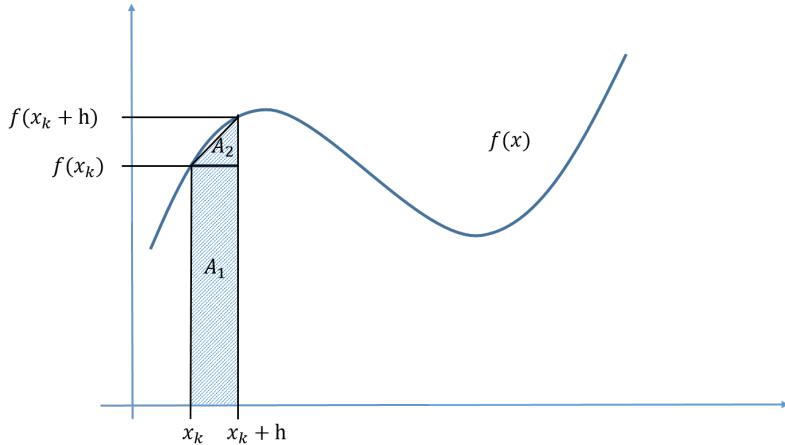


Fig. 4.2 Integrating a function with the trapezoidal rule.

Earlier we approximated the area using the midpoint value: $f(x_k + h/2) \cdot h$. Now we use $A = A_1 + A_2$, where $A_1 = f(x_k) \cdot h$ and $A_2 = (f(x_k + h) - f(x_k)) \cdot h/2$, hence the area of one trapezoid is:

$$A \equiv T(x_k, x_k + h) = (f(x_k + h) + f(x_k))h/2. \quad (4.3)$$

This is the trapezoidal rule, and for the whole interval we get:

$$\begin{aligned} I(a, b) &= \int_a^b f(x)dx \simeq \frac{1}{2}h \sum_{k=0}^{N-1} [f(x_k + h) + f(x_k)] \\ &= h \left[\frac{1}{2}f(a) + f(a + h) + f(a + 2h) + \dots + f(a + (N-2)h) + \frac{1}{2}f(b) \right] \\ &= h \left[\frac{1}{2}f(a) + \frac{1}{2}f(b) + \sum_{k=1}^{N-2} f(a + kh) \right]. \end{aligned} \quad (4.4)$$

Note that this formula was bit more involved to derive, but it requires only one more function evaluations compared to the midpoint rule. Below is a python implementation:

```
def int_trapez(lower_limit, upper_limit, func, N):
    """ calculates the area of func over the domain lower_limit
        to upper limit using N integration points """
    h      = (upper_limit - lower_limit) / N
    area   = func(lower_limit) + func(upper_limit)
    area *= 0.5
    val    = np.arange(lower_limit + h, upper_limit, h)
    area += np.sum(func(val))
    return area * h #notice: multiply with h after the sum
```

In the table below, we have calculated the numerical error for various values of N .

N	h	Error Midpoint	Error Trapezoidal
1	3.14	-57%	100%
5	0.628	-1.66%	3.31%
10	0.314	-0.412%	0.824%
100	0.031	-4.11E-3%	8.22E-3%

Note that we get the surprising result that this algorithm performs poorer, a factor of 2 than the midpoint rule. How can this be explained? By just looking at figure 4.1, we see that the midpoint rule actually over predicts the area from $[x_k, x_k + h/2]$ and under predicts in the interval $[x_k + h/2, x_{k+1}]$ or vice versa. The net effect is that for many cases the midpoint rule give a slightly better performance than the trapezoidal rule. In the next section we will investigate this more formally.

4.1.3 Numerical Errors on Integrals

It is important to know the accuracy of the methods we are using, otherwise we do not know if the computer produce correct results. In the previous examples we were able to estimate the error because we knew the analytical result. However, if we know the analytical result there is no reason to use the computer to calculate the result(!). Thus, we need a general method to estimate the error, and let the computer run until a desired accuracy is reached.

In order to analyze the midpoint rule in more detail we approximate the function by a Taylor series at the midpoint between x_k and $x_k + h$:

$$\begin{aligned} f(x) &= f(x_k + h/2) + f'(x_k + h/2)(x - (x_k + h/2)) \\ &\quad + \frac{1}{2!} f''(x_k + h/2)(x - (x_k + h/2))^2 + \mathcal{O}(h^3) \end{aligned} \quad (4.5)$$

Since $f(x_k + h/2)$ and its derivatives are constants it is straight forward to integrate $f(x)$:

$$\begin{aligned} I(x_k, x_k + h) &= \int_{x_k}^{x_k+h} [f(x_k + h/2) + f'(x_k + h/2)(x - (x_k + h/2)) \\ &\quad + \frac{1}{2!} f''(x_k + h/2)(x - (x_k + h/2))^2 + \mathcal{O}(h^3)] dx \end{aligned} \quad (4.6)$$

The first term is simply the midpoint rule, to evaluate the two other terms we make the substitution: $u = x - x_k$:

$$\begin{aligned} I(x_k, x_k + h) &= f(x_k + h/2) \cdot h + f'(x_k + h/2) \int_0^h (u - h/2) du \\ &\quad + \frac{1}{2} f''(x_k + h/2) \int_0^h (u - h/2)^2 du + \mathcal{O}(h^4) \\ &= f(x_k + h/2) \cdot h - \frac{h^3}{24} f''(x_k + h/2) + \mathcal{O}(h^4). \end{aligned} \quad (4.7)$$

Note that all the odd terms cancels out, i.e. $\int_0^h (u - h/2)^m = 0$ for $m = 1, 3, 5, \dots$. Thus the error for the midpoint rule, $E_{M,k}$, on this particular interval is:

$$E_{M,k} = I(x_k, x_k + h) - f(x_k + h/2) \cdot h = -\frac{h^3}{24} f''(x_k + h/2), \quad (4.8)$$

where we have ignored higher order terms. We can easily sum up the error on all the intervals, but clearly $f''(x_k + h/2)$ will not, in general, have the same value on all intervals. However, an upper bound for the error can be found by replacing $f''(x_k + h/2)$ with the maximal value on the interval $[a, b]$, $f''(\eta)$:

$$E_M = \sum_{k=0}^{N-1} E_{M,k} = -\frac{h^3}{24} \sum_{k=0}^{N-1} f''(x_k + h/2) \leq -\frac{Nh^3}{24} f''(\eta), \quad (4.9)$$

$$E_M \leq -\frac{(b-a)^3}{24N^2} f''(\eta), \quad (4.10)$$

where we have used $h = (b-a)/N$. We can do the exact same analysis for the trapezoidal rule, but then we expand the function around $x_k - h$

instead of the midpoint. The error term is then:

$$E_T = \frac{(b-a)^3}{12N^2} f''(\bar{\eta}). \quad (4.11)$$

At the first glance it might look like the midpoint rule always is better than the trapezoidal rule, but note that the second derivative is evaluated in different points (η and $\bar{\eta}$). Thus it is possible to construct examples where the midpoint rule performs poorer than the trapezoidal rule.

Before we end this section we will rewrite the error terms in a more useful form as it is not so easy to evaluate $f''(\eta)$ (since we do not know which value of η to use). By taking a closer look at equation (4.9), we see that it is closely related to the midpoint rule for $\int_a^b f''(x)dx$, hence:

$$E_M = -\frac{h^2}{24} h \sum_{k=0}^{N-1} f''(x_k + h/2) \simeq -\frac{h^2}{24} \int_a^b f''(x)dx \quad (4.12)$$

$$E_M \simeq \frac{h^2}{24} [f'(b) - f'(a)] = -\frac{(b-a)^2}{24N^2} [f'(b) - f'(a)] \quad (4.13)$$

The corresponding formula for the trapezoid formula is:

$$E_T \simeq \frac{h^2}{12} [f'(b) - f'(a)] = \frac{(b-a)^2}{12N^2} [f'(b) - f'(a)] \quad (4.14)$$

Now, we can make an algorithm that automatically choose the number of steps to reach (at least) a predefined accuracy:

```
import numpy as np
# Function to be integrated
def f(x):
    return np.sin(x)
#Numerical derivative of function
def df(x,func):
    dh=1e-5 # some low step size
    return (func(x+dh)-func(x))/dh

#Adaptive midpoint rule, "adaptive" because the number of
#function evaluations depends on the integrand
def int_adaptive_midpoint(lower_limit, upper_limit,func,tol):
    dfa = df(lower_limit,func) # derivative in point a
    dfb = df(upper_limit,func) # derivative in point b
    N = abs((upper_limit-lower_limit)**2*(dfb-dfa)/24/tol)
    N = int(np.sqrt(N)) + 1 # +1 as int rounds down
    h = (upper_limit-lower_limit)/N
    area = 0.
    print('Number of intervals = ', N)
    for k in range(0,N): # loop over k=0,1,...,N-1
```

```

    val = lower_limit+(k+0.5)*h # midpoint value
    area += func(val)
    return area*h

prec=1e-4
a=0
b=np.pi
Area = int_adaptive_midpoint(a,b,f,prec)
print('Numerical value = ', Area)
print('Error           = ', (2-Area)) # Analytical result is 2

```

Notice

In Python it is sometimes convenient to enter default values for the arguments in a function. In the above example, we could also have written the function definition as

```
def int_adaptive_midpoint(func, lower_limit, upper_limit,
tol=1e-8):
```

If the `tol` parameter is not given the code will assume an accuracy of 10^{-8} .

4.1.4 Practical Estimation of Errors on Integrals (Richardson Extrapolation)

From the example above we were able to estimate the number of steps needed to reach (at least) a certain precision. In many practical cases we do not deal with functions, but with data and it can be difficult to evaluate the derivative. We also saw from the example above that the algorithm gives a higher precision than what we asked for. How can we avoid doing too many iterations? A very simple solution to this question is to double the number of intervals until a desired accuracy is reached. The following analysis holds for both the trapezoid and midpoint method, because in both cases the (global) error scale as h^{21} .

Assume that we have evaluated the integral with a step size h_1 , and the computed result is I_1 . Then we know that the true integral is $I = I_1 + ch_1^2$, where c is a constant that is unknown. If we now half the step size: $h_2 = h_1/2$, then we get a new (better) estimate of the integral, I_2 , which is related to the true integral I as: $I = I_2 + ch_2^2$. Taking the difference between I_2 and I_1 give us an estimation of the error:

¹ You can do the following analysis by assuming that the local error is h^3 , but then you need to take into account that you need to take twice as many steps, which will give the same result.

$$I_2 - I_1 = I - ch_2^2 - (I - ch_1^2) = 3ch_2^2, \quad (4.15)$$

where we have used the fact that $h_1 = 2h_2$. Thus the error term is:

$$E(a, b) = ch_2^2 = \frac{1}{3}(I_2 - I_1). \quad (4.16)$$

This might seem like we need to evaluate the integral twice as many times as needed. This is not the case, by choosing to exactly half the spacing we only need to evaluate for the values that lies halfway between the original points. We will demonstrate how to do this by using the trapezoidal rule, because it operates directly on the x_k values and not the midpoint values. The trapezoidal rule can now be written as:

$$I_2(a, b) = h_2 \left[\frac{1}{2}f(a) + \frac{1}{2}f(b) + \sum_{k=1}^{N_2-1} f(a + kh_2) \right], \quad (4.17)$$

$$\begin{aligned} &= h_2 \left[\frac{1}{2}f(a) + \frac{1}{2}f(b) + \sum_{k=\text{even values}}^{N_2-1} f(a + kh_2) \right. \\ &\quad \left. + \sum_{k=\text{odd values}}^{N_2-1} f(a + kh_2) \right], \end{aligned} \quad (4.18)$$

in the last equation we have split the sum into odd an even values. The sum over the even values can be rewritten:

$$\sum_{k=\text{even values}}^{N_2-1} f(a + kh_2) = \sum_{k=0}^{N_1-1} f(a + 2kh_2) = \sum_{k=0}^{N_1-1} f(a + kh_1), \quad (4.19)$$

note that N_2 is replaced with $N_1 = N_2/2$, we can now rewrite I_2 as:

$$\begin{aligned} I_2(a, b) &= h_2 \left[\frac{1}{2}f(a) + \frac{1}{2}f(b) + \sum_{k=0}^{N_1-1} f(a + kh_1) \right. \\ &\quad \left. + \sum_{k=\text{odd values}}^{N_2-1} f(a + kh_2) \right] \end{aligned} \quad (4.20)$$

Note that the first terms are actually the trapezoidal rule for I_1 , hence:

$$I_2(a, b) = \frac{1}{2}I_1(a, b) + h_2 \sum_{k=\text{odd values}}^{N_2-1} f(a + kh_2). \quad (4.21)$$

The factor $1/2$ in front of $I_1(a, b)$, appears because $h_2 = h_1/2$. A possible algorithm is then:

1. Choose a low number of steps to evaluate the integral, I_0 , the first time, e.g. $N_0 = 1$
2. Double the number of steps, $N_1 = 2N_0$
3. Calculate the missing values by summing over the odd number of steps $\sum_{k=\text{odd}}^{N_1-1}$ values $f(a + kh_1)$
4. Check if $E_1(a, b) = \frac{1}{3}(I_1 - I_0)$ is lower than a specific tolerance
5. If yes quit, if not, return to 2, and continue until $E_i(a, b) = \frac{1}{3}(I_{i+1} - I_i)$ is lower than the tolerance

Below is a Python implementation:

```
def int_adaptive_trapez(lower_limit, upper_limit, func, tol):
    """
    adaptive quadrature, integrate a function from lower_limit
    to upper_limit within tol*(upper_limit-lower_limit)
    """
    NO=1
    h      = (upper_limit-lower_limit)/NO
    area   = (func(lower_limit)+func(upper_limit))*0.5*h
    calc_tol = 2*tol + 1 # just larger than tol to enter the while loop
    TOL= tol*np.abs(h)  # note NO=1
    iterations=0
    while(calc_tol>TOL):
        iterations+=1
        N = NO*2
        h = (upper_limit-lower_limit)/N
        odd_terms=0
        for k in range (1,N,2): # 1, 3, 5, ... , N-1
            val = lower_limit + k*h
            odd_terms += func(val)
        new_area = 0.5*area + h*odd_terms
        calc_tol = abs(new_area-area)/3
        area     = new_area # store new values for next iteration
        NO      = N         # update number of slices
    print('Number of intervals = ', N, ' iterations: ',iterations)
    return area #while loop ended and we can return the area
```

If you compare the number of terms used in the adaptive trapezoidal rule, which was developed by halving the step size, and the adaptive midpoint rule that was derived on the basis of the theoretical error term, you will find the adaptive midpoint rule is more efficient. So why go through all this trouble? In the next section we will see that the development we did for the adaptive trapezoidal rule is closely related to Romberg integration, which is *much* more effective.

4.2 Romberg Integration

The adaptive algorithm for the trapezoidal rule in the previous section can be easily improved by remembering that the true integral was given by² : $I = I_i + ch_i^2 + \mathcal{O}(h^4)$. The error term was in the previous example only used to check if the desired tolerance was achieved, but we could also have added it to our estimate of the integral to reach an accuracy to fourth order:

$$I = I_{i+1} + ch^2 + \mathcal{O}(h^4) = I_{i+1} + \frac{1}{3} [I_{i+1} - I_i] + \mathcal{O}(h^4). \quad (4.22)$$

As before the error term $\mathcal{O}(h^4)$, can be written as: ch^4 . Now we can proceed as in the previous section: First we estimate the integral by one step size $I_i = I + ch_i^4$, next we half the step size $I_{i+1} = I + ch_{i+1}^4$ and use these two estimates to calculate the error term:

$$\begin{aligned} I_{i+1} - I_i &= I - ch_{i+1}^4 - (I - ch_i^4) = -ch_{i+1}^4 + c(2h_{i+1})^4 = 15ch_{i+1}^4, \\ ch_{i+1}^4 &= \frac{1}{15} [I_{i+1} - I_i] + \mathcal{O}(h^6). \end{aligned} \quad (4.23)$$

but now we are in the exact situation as before, we have not only the error term but the correction up to order h^4 for this integral:

$$I = I_{i+1} + \frac{1}{15} [I_{i+1} - I_i] + \mathcal{O}(h^6). \quad (4.24)$$

Each time we half the step size we also gain a higher order accuracy in our numerical algorithm. Thus, there are two iterations going on at the same time; one is the iteration that half the step size (i), and the other one is the increasing number of higher order terms added (which we will denote m). We need to improve our notation, and replace the approximation of the integral (I_i) with $R_{i,m}$. Equation (4.24), can now be written:

$$I = R_{i+1,2} + \frac{1}{15} [R_{i+1,2} - R_{i,2}] + \mathcal{O}(h^6). \quad (4.25)$$

A general formula valid for any m can be found by realizing:

²Note that all odd powers of h is equal to zero, thus the corrections are always in even powers.

$$I = R_{i+1,m+1} + c_m h_i^{2m+2} + \mathcal{O}(h_i^{2m+4}) \quad (4.26)$$

$$\begin{aligned} I &= R_{i,m+1} + c_m h_{i-1}^{2m+2} + \mathcal{O}(h_{i-1}^{2m+4}) \\ &= R_{i,m+1} + 2^{2m+2} c_m h_i^{2m+2} + \mathcal{O}(h_{i-1}^{2m+4}), \end{aligned} \quad (4.27)$$

where, as before $h_{i-1} = 2h_i$. Subtracting equation (4.26) and (4.27), we find an expression for the error term:

$$c_m h_i^{2m+2} = \frac{1}{4^{m+1} - 1} (R_{i,m} - R_{i-1,m}) \quad (4.28)$$

Then the estimate for the integral in equation (4.27) is:

$$I = R_{i,m+1} + \mathcal{O}(h_i^{2m+2}) \quad (4.29)$$

$$R_{i,m+1} = R_{i,m} + \frac{1}{4^{m+1} - 1} (R_{i+1,m} - R_{i,m}). \quad (4.30)$$

A possible algorithm is then:

1. Evaluate $R_{0,0} = \frac{1}{2} [f(a) + f(b)] (b - a)$ as the first estimate
2. Double the number of steps, $N_{i+1} = 2N_i$ or half the step size $h_{i+1} = h_i/2$
3. Calculate the missing values by summing over the odd number of steps $\sum_{k=\text{odd}}^{N_1-1} f(a + kh_{i+1})$
4. Correct the estimate by adding *all* the higher order error term $R_{i,m+1} = R_{i,m} + \frac{1}{4^{m+1}-1} (R_{i+1,m+1} - R_{i,m+1})$
5. Check if the error term is lower than a specific tolerance $E_{i,m}(a, b) = \frac{1}{4^{m+1}-1} (R_{i,m} - R_{i-1,m})$, if yes quit, if no goto 2, increase i and m by one

The algorithm is illustrated in figure 4.3.

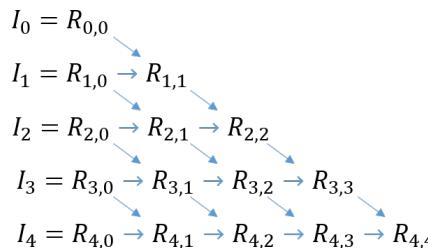


Fig. 4.3 Illustration of the Romberg algorithm. Note that for each new evaluation of the integral $R_{i,0}$, all the correction terms $R_{i,m}$ (for $m > 0$) must be evaluated again.

Note that the tolerance term is not the correct one as it uses the error estimate for the current step, which we also use correct the integral in the current step to reach a higher accuracy. Thus the error on the integral will always be lower than the user specified tolerance. Below is a Python implementation:

```

def int_romberg(func,lower_limit, upper_limit,tol,show=False):
    """ calculates the area of func over the domain lower_limit
        to upper limit for the given tol, if show=True the triangular
        array of intermediate results are printed """
    Nmax = 100
    R = np.empty([Nmax,Nmax]) # storage buffer
    h = (upper_limit-lower_limit) # step size
    R[0,0] = .5*(func(lower_limit)+func(upper_limit))*h
    N = 1
    for i in range(1,Nmax):
        h /= 2
        N *= 2
        odd_terms=0
        for k in range (1,N,2): # 1, 3, 5, ... , N-1
            val = lower_limit + k*h
            odd_terms += func(val)
        # add the odd terms to the previous estimate
        R[i,0] = 0.5*R[i-1,0] + h*odd_terms
        for m in range(0,i): # m = 0, 1, ... , i-1
            # add all higher order terms in h
            R[i,m+1] = R[i,m] + (R[i,m]-R[i-1,m])/(4**((m+1)-1))
        # check tolerance, best guess
        calc_tol = abs(R[i,i]-R[i-1,i-1])
        if(calc_tol<tol):
            break # estimated precision reached
    if(i == Nmax-1):
        print('Romberg routine did not converge after ',
              Nmax, 'iterations!')
    else:
        print('Number of intervals = ', N)

    if(show==True):
        elem = [2**idx for idx in range(i+1)]
        print("Steps StepSize Results")
        for idx in range(i+1):
            print(elem[idx], ',',
                  "{:.6f}".format((upper_limit-lower_limit)/2**idx),end = ' ')
            for l in range(idx+1):
                print("{:.6f}".format(R[idx,l]),end = ' ')
            print('')
    return R[i,i] #return the best estimate

```

Note that the Romberg integration only uses 32 function evaluations to reach a precision of 10^{-8} , whereas the adaptive midpoint and trapezoidal

rule in the previous section uses 20480 and 9069 function evaluations, respectively.

4.2.1 Alternative implementation of adaptive integration

Before we proceed, we will consider an alternative implementation of the adaptive method presented in the previous sections, with the following modification

1. We will use Simpsons rule (see the exercise at the end), which takes the following form $\int_a^b f(x)dx \simeq \frac{h}{6} \left[f(a) + 4f(a + \frac{h}{2}) + 2f(a + h) + 4f(a + 3\frac{h}{2}) + 2f(a + 2h) \right]$
2. We only divide the intervals needed to reach the desired accuracy.

Simpsons rule is accurate up to $\mathcal{O}(h^4)$, and by following the same arguments as above we can estimate the error as $E_i(a, b) = \frac{1}{15}(I_{i+1} - I_i)$. The factor 1/15 (as opposed to 1/3) originates from the higher order accuracy. The integration proceeds as follows

- S is an empty list
- S.append([a,b])
- $I = 0$
- while S not empty do:
 - [a,b]=S.pop(-1)
 - $m = (b + a)/2$
 - $I_1 = \text{simpson_step}(a, b)$
 - $I_2 = \text{simpson_step}(a, m) + \text{simpson_step}(m, b)$
 - if $|I_1 - I_2| < 15|b - a| \cdot tol$
 - $I += I_2$
 - else:
 - S.append([a,m])
 - S.append([m,b])
 - return I

Note the use of the list S, we remove the interval $[a, b]$ from the list and calculates the integral. If the integral is not accurate enough we add to new intervals to the list, and continue until we reach the desired accuracy, then we proceed with the next interval. Since we remove (pop) the element from the list, we know that we will finish the evaluation once the list is empty. This algorithm allows for different sub interval to have

different degrees of subdivisions, contrary to Rombergs algorithm. The full python implementation is shown below

```

def simpson_step(a, b,func):
    m=0.5*(a+b)
    return (b-a)/6*(func(a)+func(b)+4*func(m))

def int_adaptive_simpson(a, b,func,tol):
    """
    adaptive quadrature, integrate a function from a
    to b within tol*(b-a) uses simpsons rule
    """
    S=[]
    S.append([a,b])
    I=0
    iterations=0
    while S:
        iterations +=1
        a,b=S.pop(-1) # last element
        m=(b+a)*0.5 # midpoint
        I1=simpson_step(a,b,func) #simpsons for 1 interval
        I2=simpson_step(a,m,func)+simpson_step(m,b,func) # ...2 intervals
        if(np.abs(I1-I2)<15*np.abs((b-a)*tol)):
            I+=I2 # accuarcy met
        else:
            S.append([a,m]) # half the interval
            S.append([m,b])
    print("Number of iterations: ", iterations)
    return I

```

4.3 Gaussian Quadrature

Many of the methods we have looked into are of the type:

$$\int_a^b f(x)dx = \sum_{k=0}^{N-1} \omega_k f(x_k), \quad (4.31)$$

where the function is evaluated at fixed interval. For the midpoint rule $\omega_k = h$ for all values of k , for the trapezoid rule $\omega_k = h/2$ for the endpoints and h for all the interior points. For the Simpsons rule (see exercise) $\omega_k = h/3, 4h/3, 2h/3, 4h/3, \dots, 4h/3, h/3$. Note that all the methods we have looked at so far samples the function in equal spaced points, $f(a + kh)$, for $k = 0, 1, 2, \dots, N - 1$. If we now allow for the function to be evaluated at unevenly spaced points, we can do a lot better. This realization is the basis for Gaussian Quadrature. We will

explore this in the following, but to make the development easier and less cumbersome, we transform the integral from the domain $[a, b]$ to $[-1, 1]$:

$$\int_a^b f(t)dt = \frac{b-a}{2} \int_{-1}^1 f(x)dx , \text{ where:} \quad (4.32)$$

$$x = \frac{2}{b-a}t - \frac{b+a}{b-a}. \quad (4.33)$$

The factor in front comes from the fact that $dt = (b-a)dx/2$, thus we can develop our algorithms on the domain $[-1, 1]$, and then do the transformation back using: $t = (b-a)x/2 + (b+a)/2$.

Notice

The idea we will explore is as follows: If we can approximate the function to be integrated on the domain $[-1, 1]$ (or on $[a, b]$) as a polynomial of as *large a degree as possible*, then the numerical integral of this polynomial will be very close to the integral of the function we are seeking.

This idea is best understood by a couple of examples. Assume that we want to use $N = 1$ in equation (4.31):

$$\int_{-1}^1 f(x) dx \simeq \omega_0 f(x_0). \quad (4.34)$$

We now choose $f(x)$ to be a polynomial of as large a degree as possible, but with the requirement that the integral is exact. If $f(x) = 1$, we get:

$$\int_{-1}^1 f(x) dx = \int_{-1}^1 1 dx = 2 = \omega_0, \quad (4.35)$$

hence $\omega_0 = 2$. If we choose $f(x) = x$, we get:

$$\int_{-1}^1 f(x) dx = \int_{-1}^1 x dx = 0 = \omega_0 f(x_0) = 2x_0, \quad (4.36)$$

hence $x_0 = 0$.

The Gaussian integration rule for $N = 1$ is:

$$\int_{-1}^1 f(x) dx \simeq 2f(0), \text{ or:}$$

$$\int_a^b f(t) dt \simeq \frac{b-a}{2} 2f\left(\frac{b+a}{2}\right) = (b-a)f\left(\frac{b+a}{2}\right). \quad (4.37)$$

This equation is equal to the midpoint rule, by choosing $b = a + h$ we reproduce equation (4.1). If we choose $N = 2$:

$$\int_{-1}^1 f(x) dx \simeq \omega_0 f(x_0) + \omega_1 f(x_1), \quad (4.38)$$

we can show that now $f(x) = 1$, x , x^2 x^3 can be integrated exact:

$$\int_{-1}^1 1 dx = 2 = \omega_0 f(x_0) + \omega_1 f(x_1) = \omega_0 + \omega_1, \quad (4.39)$$

$$\int_{-1}^1 x dx = 0 = \omega_0 f(x_0) + \omega_1 f(x_1) = \omega_0 x_0 + \omega_1 x_1, \quad (4.40)$$

$$\int_{-1}^1 x^2 dx = \frac{2}{3} = \omega_0 f(x_0) + \omega_1 f(x_1) = \omega_0 x_0^2 + \omega_1 x_1^2, \quad (4.41)$$

$$\int_{-1}^1 x^3 dx = 0 = \omega_0 f(x_0) + \omega_1 f(x_1) = \omega_0 x_0^3 + \omega_1 x_1^3, \quad (4.42)$$

hence there are four unknowns and four equations. The solution is: $\omega_0 = \omega_1 = 1$ and $x_0 = -x_1 = 1/\sqrt{3}$.

The Gaussian integration rule for $N = 2$ is:

$$\int_{-1}^1 f(x) dx \simeq f\left(-\frac{1}{\sqrt{3}}\right) + f\left(\frac{1}{\sqrt{3}}\right), \text{ or:} \quad (4.43)$$

$$\int_a^b f(x) dx \simeq \frac{b-a}{2} \left[f\left(-\frac{b-a}{2}\frac{1}{\sqrt{3}} + \frac{b+a}{2}\right) + f\left(\frac{b-a}{2}\frac{1}{\sqrt{3}} + \frac{b+a}{2}\right) \right]. \quad (4.44)$$

```
def int_gaussquad2(func, lower_limit, upper_limit):
    x    = np.array([-1/np.sqrt(3.), 1/np.sqrt(3)])
    w    = np.array([1, 1])
    xp  = 0.5*(upper_limit-lower_limit)*x
    xp += 0.5*(upper_limit+lower_limit)
    area = np.sum(w*func(xp))
    return area*0.5*(upper_limit-lower_limit)
```

The case N=3. For the case $N = 3$, we find that $f(x) = 1, x, x^2, x^3, x^4, x^5$ can be integrated exactly:

$$\int_{-1}^1 1 dx = 2 = \omega_0 + \omega_1 + \omega_2, \quad (4.45)$$

$$\int_{-1}^1 x dx = 0 = \omega_0 x_0 + \omega_1 x_1 + \omega_2 x_2, \quad (4.46)$$

$$\int_{-1}^1 x^2 dx = \frac{2}{3} = \omega_0 x_0^2 + \omega_1 x_1^2 + \omega_2 x_2^2, \quad (4.47)$$

$$\int_{-1}^1 x^3 dx = 0 = \omega_0 x_0^3 + \omega_1 x_1^3 + \omega_2 x_2^3, \quad (4.48)$$

$$\int_{-1}^1 x^4 dx = \frac{2}{5} = \omega_0 x_0^4 + \omega_1 x_1^4 + \omega_2 x_2^4, \quad (4.49)$$

$$\int_{-1}^1 x^5 dx = 0 = \omega_0 x_0^5 + \omega_1 x_1^5 + \omega_2 x_2^5, \quad (4.50)$$

the solution to these equations are $\omega_{0,1,2} = 5/9, 8/9, 5/9$ and $x_{1,2,3} = -\sqrt{3/5}, 0, \sqrt{3/5}$. Below is a Python implementation:

```
def int_gaussquad3(lower_limit, upper_limit, func):
    x = np.array([-np.sqrt(3./5.), 0., np.sqrt(3./5.)])
    w = np.array([5./9., 8./9., 5./9.])
    xp = 0.5*(upper_limit-lower_limit)*x
    xp += 0.5*(upper_limit+lower_limit)
    area = np.sum(w*func(xp))
    return area*0.5*(upper_limit-lower_limit)
```

Note that the Gaussian quadrature converges very fast. From $N = 2$ to $N = 3$ function evaluation we reduce the error (in this specific case) from 6.5% to 0.1%. Our standard trapezoidal formula needs more than 20 function evaluations to achieve this, the Romberg method uses 4-5 function evaluations. How can this be? If we use the standard Taylor formula for the function to be integrated, we know that for $N = 2$ the Taylor formula must be integrated up to x^3 , so the error term is proportional to $h^4 f^{(4)}(\xi)$ (where ξ is some x-value in $[a, b]$). h is the step size, and we can replace it with $h \sim (b - a)/N$, thus the error scale as c_N/N^4 (where c_N is a constant). Following the same argument, we find for $N = 3$ that the error term is $h^6 f^{(6)}(\xi)$ or that the error term scale as c_N/N^6 . Each time we increase N by a factor of one, the error term reduces by N^2 . Thus if we evaluate the integral for $N = 10$, increasing to $N = 11$ will reduce the error by a factor of $11^2 = 121$.

4.3.1 Error term on Gaussian Integration

The Gaussian integration rule of order N integrates exactly a polynomial of order $2N - 1$. From Taylors error formula, see equation (1.4) in Chapter 1, we can easily see that the error term must be of order $2N$, and be proportional to $f^{(2N)}(\eta)$, see [5] for more details on the derivation of error terms. The drawback with an analytical error term derived from series expansion is that it involves the derivative of the function. As we have already explained, this is very unpractical and it is much more practical to use the methods described in section 4.1.4. Let us consider this in more detail, assume that we evaluate the integral using first a Gaussian integration rule with N points, and then $N + 1$ points. Our estimates of the "exact" integral, I , would then be:

$$I = I_N + ch_N^{2N}, \quad (4.51)$$

$$I = I_{N+1} + ch_{N+1}^{2N+1}. \quad (4.52)$$

In principle $h_{N+1} \neq h_N$, but in the following we will assume that $h_N \simeq h_{N+1}$, and $h \ll 1$. Subtracting equation (4.51) and (4.52) we can show that a reasonable estimate for the error term ch^{2N} would be:

$$ch^N = I_{N+1} - I_N. \quad (4.53)$$

If this estimate is lower than a given tolerance we can be quite confident that the higher order estimate I_{N+1} approximate the true integral within our error estimate. This is the method implemented in SciPy, `integrate.quadrature`³

4.3.2 Common Weight functions for Classical Gaussian Quadratures

4.4 Integrating functions over an infinite range

Integrating a function over an infinite range can be done by the following trick. Assume that we would like to evaluate

$$\int_a^\infty f(x) dx. \quad (4.54)$$

If we introduce the following substitution

³<https://docs.scipy.org/doc/scipy-0.14.0/reference/generated/scipy.integrate.quadrature.html>

$$z = \frac{x - a}{1 + x - a}, \quad (4.55)$$

or equivalently

$$x = a + \frac{z}{1 - z}, \quad (4.56)$$

then if $x = a$, $z = 0$, and if $x \rightarrow \infty$ then $z \rightarrow 1$, hence:

$$\int_a^\infty f(x)dx = \int_0^1 f(a + \frac{z}{1 - z}) \frac{dz}{(1 - z)^2}. \quad (4.57)$$

4.4.1 Which method to use in a specific case? (NOT COMPLETED)

There are no general answers to this question, and one need to decide from case to case. If computational speed is not an issue, and the function to be integrated can be evaluated at any points all the methods above can be used. If the function to be integrated is a set of observations at different times, that might be unevenly spaced, I would use the midpoint rule:

$$I(a, b) = \int_a^b f(x)dx \simeq \sum_{k=0}^{N-1} M(x_k, x_k + h) = \sum_{k=0}^{N-1} h_i f(x_k + \frac{h_i}{2}) \quad (4.58)$$

This is because we do not know anything about the function between the points, only when it is observed, and the formula uses only the information at the observation points. There is a second more subtle reason, and that is the fact that in many cases the observations at different times are the *average* value of the observable quantity and in those cases the midpoint rule would be the exact answer.

Exercise 4.1: Numerical Integration

- a)** Show that for a linear function, $y = a \cdot x + b$ both the trapezoidal rule and the rectangular rule are exact
- b)** Consider $I(a, b) = \int_a^b f(x)dx$ for $f(x) = x^2$. The analytical result is $I(a, b) = \frac{b^3 - a^3}{3}$. Use the Trapezoidal and Midpoint rule to evaluate these integrals and show that the error for the Trapezoidal rule is exactly twice as big as the Midpoint rule.

- c) Use the fact that the error term on the trapezoidal rule is twice as big as the midpoint rule to derive Simpkins formula: $I(a, b) = \sum_{k=0}^{N-1} I(x_k, x_k + h) = \frac{h}{6} \left[f(a) + 4f(a + \frac{h}{2}) + 2f(a + h) + 4f(a + 3\frac{h}{2}) + 2f(a + 2h) + \dots + f(b) \right]$
 Hint: $I(x_k, x_k + h) = M(x_k, x_k + h) + E_M$ (midpoint rule) and $I(x_k, x_k + h) = T(x_k, x_k + h) + E_T = T(x_k, x_k + h) - 2E_M$ (trapezoidal rule).

Solution. Simpkins rule is an improvement over the midpoint and trapezoidal rule. It can be derived in different ways, we will make use of the results in the previous section. If we assume that the second derivative is reasonably well behaved on the interval x_k and $x_k + h$ and fairly constant we can assume that $f''(\eta) \simeq f''(\bar{\eta})$, hence $E_T = -2E_M$.

$$I(x_k, x_k + h) = M(x_k, x_k + h) + E_M \text{ (midpoint rule)} \quad (4.59)$$

$$\begin{aligned} I(x_k, x_k + h) &= T(x_k, x_k + h) + E_T \\ &= T(x_k, x_k + h) - 2E_M \text{ (trapezoidal rule),} \end{aligned} \quad (4.60)$$

we can now cancel out the error term by multiplying the first equation with 2 and adding the equations:

$$3I(x_k, x_k + h) = 2M(x_k, x_k + h) + T(x_k, x_k + h) \quad (4.61)$$

$$= 2f(x_k + \frac{h}{2})h + [f(x_k + h) + f(x_k)] \frac{h}{2} \quad (4.62)$$

$$I(x_k, x_k + h) = \frac{h}{6} \left[f(x_k) + 4f(x_k + \frac{h}{2}) + f(x_k + h) \right]. \quad (4.63)$$

Now we can do as we did in the case of the trapezoidal rule, sum over all the elements:

$$\begin{aligned} I(a, b) &= \sum_{k=0}^{N-1} I(x_k, x_k + h) \\ &= \frac{h}{6} \left[f(a) + 4f(a + \frac{h}{2}) + 2f(a + h) + 4f(a + 3\frac{h}{2}) \right. \\ &\quad \left. + 2f(a + 2h) + \dots + f(b) \right] \end{aligned} \quad (4.64)$$

$$= \frac{h'}{3} \left[f(a) + f(b) + 4 \sum_{k=\text{odd}}^{N-2} f(a + kh') + 2 \sum_{k=\text{even}}^{N-2} f(a + kh') \right], \quad (4.65)$$

note that in the last equation we have changed the step size $h = 2h'$.

d) Show that for $N = 2$ ($f(x) = 1, x, x^3$), the points and Gaussian quadrature rule for $\int_0^1 x^{1/2} f(x) dx$ is $\omega_{0,1} = -\sqrt{70}150+1/3, \sqrt{70}150+1/3$ and $x_{0,1} = -2\sqrt{70}63 + 5/9, 2\sqrt{70}63 + 5/9$

1. Integrate $\int_0^1 x^{1/2} \cos x dx$ using the rule derived in the exercise above and compare with the standard Gaussian quadrature rule for ($N = 2$, and $N = 3$).

e) Make a Python program that uses the Midpoint rule to integrate experimental data that are unevenly spaced and given in the form of two arrays.

5.1 Ordinary Differential Equations

Physical systems evolves in space and time, and very often they are described by a ordinary differential equations (ODE) and/or partial differential equations (PDE). The difference between an ODE and a PDE is that an ODE only describes the changes in one spatial dimension *or* time, whereas a PDE describes a system that evolves in the x -, y -, z -dimension and/or in time. In the following we will spend a significant amount of time to explore one of the simplest algorithm, Eulers method. Sometimes this is exactly the algorithm you would like to use, but with very little extra effort much more sophisticated algorithms can easily be implemented, such as the Runge-Kutta fourth order method. However, all these algorithms, will at some point run into the same kind of troubles if used reckless. Thus we will use the Eulers method as a playground, investigate when the algorithm run into trouble and suggests ways to fix it, these approaches can easily be extended to the higher order methods. Most of the other algorithms boils down to the same idea of extrapolating a function using derivatives multiplied with a small step size.

5.2 A Simple Model for Fluid Flow

Let us consider a simple example from chemical engineering, a continuous stirred tank reactor (CSTR), see figure 5.1. The flow is incompressible

($q_{\text{out}} = q_{\text{in}}$), a fluid is entering on the top and exiting at the bottom, the tank has a fixed volume V . Assume that the tank is filled with saltwater, and that freshwater is pumped into it, how much time does it take before 90% of the saltwater is replaced with freshwater? The tank is *well mixed*, illustrated with the propeller, this means that at every time the concentration is uniform in the tank, i.e. that $C(t) = C_{\text{out}}(t)$.

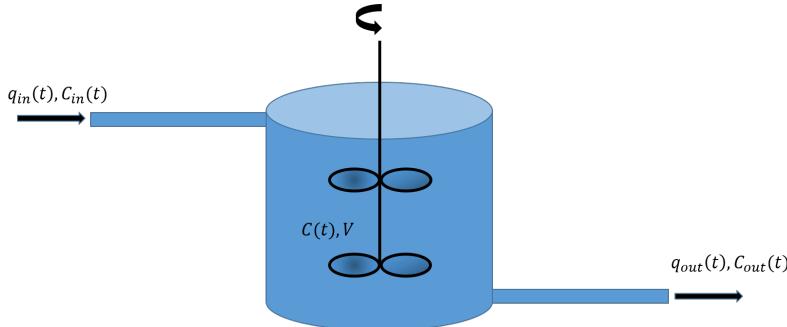


Fig. 5.1 A continuous stirred tank model, $C(t) = C_{\text{out}}(t)$, and $q_{\text{out}} = q_{\text{in}}$.

The concentration C is measured in gram of salt per liter water, and the flow rate q is liter of water per day. The model for the salt balance in this system can be described in words by:

$$\begin{aligned} [\text{accumulation of salt}] &= [\text{salt into the system}] - [\text{salt out of the system}] \\ &\quad + [\text{generation of salt}]. \end{aligned} \quad (5.1)$$

In our case there are no generation of salt within the system so this term is zero. The flow of salt into the system during a time Δt is: $q_{\text{in}}(t) \cdot C_{\text{in}}(t) \cdot \Delta t = q(t) \cdot C_{\text{in}}(t) \cdot \Delta t$, the flow of salt out of the system is: $q_{\text{out}}(t) \cdot C_{\text{out}}(t) \cdot \Delta t = q(t) \cdot C(t) \cdot \Delta t$, and the accumulation during a time step is: $C(t + \Delta t) \cdot V - C(t) \cdot V$, hence:

$$C(t + \Delta t) \cdot V - C(t) \cdot V = q(t) \cdot C_{\text{in}}(t) \cdot \Delta t - q(t) \cdot C(t) \cdot \Delta t. \quad (5.2)$$

Note that it is not a priori apparent, which time the concentrations and flow rates on the right hand side should be evaluated at, we could have chosen to evaluate them at $t + \Delta t$, or at any time $t \in [t, t + \Delta t]$. We will return to this point later in this chapter. Dividing by Δt , and taking the limit $\Delta t \rightarrow 0$, we can write equation (5.2) as:

$$V \frac{dC(t)}{dt} = q(t) [C_{\text{in}}(t) - C(t)]. \quad (5.3)$$

Seawater contains about 35 gram salt/liter fluid, if we assume that the fresh water contains no salt, we have the boundary conditions $C_{\text{in}}(t) = 0$, $C(0) = 35 \text{ gram/l}$. The equation (5.3) the reduces to:

$$V \frac{dC(t)}{dt} = -qC(t), \quad (5.4)$$

this equation can easily be solved, by dividing by C , multiplying by dt and integrating:

$$\begin{aligned} V \int_{C_0}^C \frac{dC}{C} &= -q \int_0^t dt, \\ C(t) &= C_0 e^{-t/\tau}, \text{ where } \tau \equiv \frac{V}{q}. \end{aligned} \quad (5.5)$$

This equation can be inverted to give $t = -\tau \ln[C(t)/C]$. If we assume that the volume of the tank is $1 \text{ m}^3 = 1000 \text{ liters}$, and that the flow rate is 1 liter/min, we find that $\tau = 1000 \text{ min} = 0.69 \text{ days}$ and that it takes about $-0.69 \ln 0.9 \simeq 1.6 \text{ days}$ to reduce the concentration by 90% to 3.5 gram/liter.

The CSTR

You might think that the CSTR is a very simple model, and it is, but this type of model is the basic building blocks in chemical engineering. By putting CSTR tanks in series and/or connecting them with pipes, the efficiency of manufacturing various type of chemicals can be investigated. Although the CSTR is an idealized model for the part of a chemical factory, it is actually a *very good* model for fluid flow in a porous media. By connecting CSTR tanks in series, one can model how chemical tracers propagate in the subsurface. The physical reason for this is that dispersion in porous media will play the role of the propellers and mix the concentration uniformly.

5.3 Eulers Method

If the system gets slightly more complicated, e.g several tanks in series with a varying flow rate or if salt was generated in the tank, there is a good chance that we have to solve the equations numerically to obtain a

solution. Actually, we have already developed a numerical algorithm to solve equation (5.3), before we arrived at equation (5.3) in equation (5.2). This is a special case of Eulers method, which is basically to replace the derivative in equation (5.3), with $(C(t + \Delta t) - C(t))/\Delta t$. By rewriting equation (5.2), so that we keep everything related to the new time step, $t + \Delta t$, on one side, we get:

$$VC(t + \Delta t) = VC(t) + qC_{\text{in}}(t) - qC(t), \quad (5.6)$$

$$C(t + \Delta t) = C(t) + \frac{\Delta t}{\tau} [C_{\text{in}}(t) - C(t)], \quad (5.7)$$

we introduce the short hand notation: $C(t) = C_n$, and $C(t + \Delta t) = C_{n+1}$, hence the algorithm can be written more compact as:

$$C_{n+1} = \left(1 - \frac{\Delta t}{\tau}\right) C_n + \frac{\Delta t}{\tau} C_{\text{in},n}, \quad (5.8)$$

In the script below, we have implemented equation (5.8).

```
def analytical(x):
    return np.exp(-x)

def euler_step(c_old, c_in, tau_inv, dt):
    fact=dt*tau_inv
    return (1-fact)*c_old+fact*c_in

def ode_solv(c_init, t_final, vol, q, dt):
    f=[];t=[]
    tau_inv = q/vol
    c_in   = c_init #freshwater into tank
    c_old  = c_init #seawater present
    ti=0.
    while(ti <= t_final):
        t.append(ti); f.append(c_old)
        c_new = euler_step(c_old,c_in,tau_inv,dt)
        c_old = c_new
        ti   += dt
    return t,f
```

In figure 5.2 the result of the implementation is shown for different values of Δt . Clearly we see that the results are dependent on the step size, as the step increases the numerical solution deviates from the analytical solution. At some point the numerical algorithm fails completely, and produces results that have no meaning.

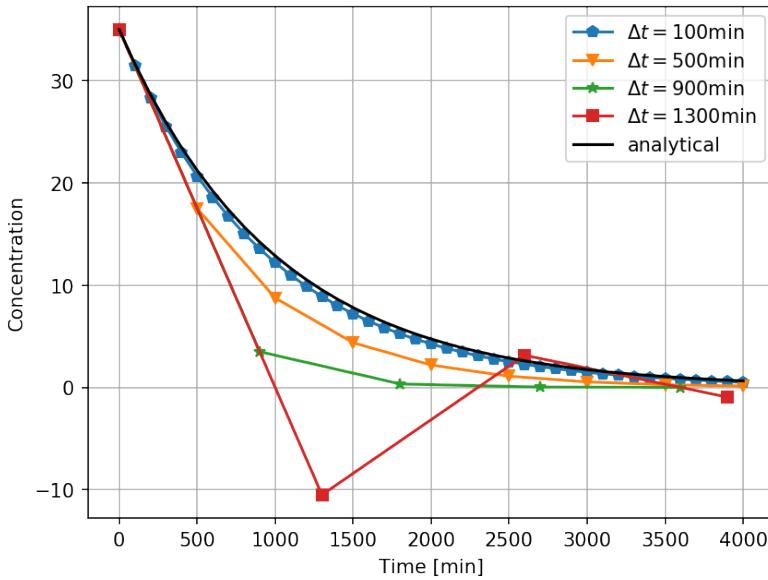


Fig. 5.2 The concentration in the tank for different step size Δt .

5.3.1 Error Analysis - Eulers Method

There are two obvious questions:

1. When does the algorithm produce unphysical results?
2. What is an appropriate step size?

Let us consider the first question, clearly when the concentrations gets negative the solution is unphysical. From equation (5.8), we see that when $\Delta t/\tau > 1$, the concentration become negative. For this specific case (the CSTR), there is a clear physical interpretation of this condition. Inserting $\tau = V/q$, we can rewrite the condition $\Delta t/\tau < 1$ as $q\Delta t < V$. The volume into the tank during one time step is: $q\Delta t$, which means that whenever we *flush more than one tank volume through the tank during one time step, the algorithm fails*. When this happens the new concentration in the tank cannot be predicted from the old one. This makes sense, because we could have switched to a new solution (e.g. seawater) during that time step, then the new solution does not have any relation to the old solution.

The second question, "what is an appropriate step size?", is a bit more difficult to answer. One strategy could be to simply use the results from chapter [Taylor], where we showed that the truncation error had

a minimum value with a step size of 10^{-8} (when using a first order Taylor approximation). How does the value 10^{-8} relate to the step sizes in minutes used in our Euler implementation? In order to see the connection, we need to rewrite equation (5.3) in a dimensionless form, by making the following substitution: $t \rightarrow t/\tau$:

$$\frac{dC(\tau)}{d\tau} = [C_{\text{in}}(\tau) - C(\tau)]. \quad (5.9)$$

As we found earlier $\tau = 1000\text{min}$, thus a step size of e.g. 1 min would correspond to a dimensionless time step of $\Delta t \rightarrow 1\text{min}/1000\text{min} = 10^{-3}$. This number can be directly compared to the value 10^{-8} , which is the lowest value we can choose without getting into trouble with round off errors on the machine.

Dimensionless variables

It is a good idea (necessary) to formulate our equations in terms of dimensionless variables. The algorithms we develop can then be used in the same form regardless of changes in the system size and flow rates. Thus we do not need to rewrite the algorithm each time the physical system changes. This also means that if you use an algorithm developed by someone else (e.g. in Matlab or Python), you should always formulate the ODE system in dimensionless form before using the algorithm.

A second reason is that from a pure modeling point of view, dimensionless variables is a way of getting some understanding of what kind of combination of the physical parameters that describes the behavior of the system. For the case of the CSTR, there is a time scale $\tau = V/q$, which is an intrinsic measure of time in the system. No matter what the flow rate through the tank or the volume of the tank is, it will always take 0.1τ before the concentration in the tank is reduced by 90%.

As already mentioned a step size of 10^{-8} , is probably the smallest we can choose with respect to round off errors, but it is smaller than necessary and would lead to large simulation times. If it takes 1 second to run the simulation with a step size of 10^{-3} , it would take 10^5 seconds or 1 day with a step size of 10^{-8} . To continue the error analyses, we write our ODE for a general system as:

$$\frac{dy}{dt} = f(y, t), \quad (5.10)$$

or in discrete form:

$$\begin{aligned} \frac{y_{n+1} - y_n}{h} - \frac{h}{2} y''(\eta_n) &= f(y, t). \\ y_{n+1} &= y_n + h f(y, t) + \frac{h^2}{2} y''(\eta_n). \end{aligned} \quad (5.11)$$

h is now the (dimensionless) step size, equal to Δt if the derivative is with respect to t or Δx if the derivative is respect to x etc. Note that we have also included the error term related to the numerical derivative, $\eta_n \in [t_n, t_n + h]$. At each step we get an error term, and the distance between the true solution and our estimate, the *local error*, after N steps is:

$$\begin{aligned} \epsilon &= \sum_{n=0}^{N-1} \frac{h^2}{2} y''(\eta_n) = \frac{h^2}{2} \sum_{n=0}^{N-1} f'(y_n, \eta_n) \simeq \frac{h}{2} \int_{t_0}^{t_f} f'(y, \eta) d\eta \\ &= \frac{h}{2} [f(y(t_f), t_f) - f(y(t_0), t_0)]. \end{aligned} \quad (5.12)$$

Note that when we replace the sum with an integral in the equation above, this is only correct if the step size is not too large. From equation (5.12) we see that even if the error term on the numerical derivative is h^2 , the local error is proportional to h (one order lower). This is because we accumulate errors for each step.

In the following we specialize to the CSTR, to see if we can gain some additional insight. First we change variables in equation (5.4): $y = C(t)/C_0$, and $x = t/\tau$, hence:

$$\frac{dy}{dx} = -y. \quad (5.13)$$

The solution to this equation is $y(x) = e^{-x}$, substituting back for the new variables y and x , we reproduce the result in equation (5.5). The local error, equation (5.12), reduces to:

$$\epsilon = \frac{h}{2} [-y(x_f) + y(x_0)] = \frac{h}{2} [1 - e^{-x_f}], \quad (5.14)$$

we have assumed that $x_0 = t_0/\tau = 0$. This gives the estimated local error at time x_f . For $x_f = 0$, the numerical error is zero, this makes sense because at $x = 0$ we know the exact solution because of the initial

conditions. When we move further away from the initial conditions, the numerical error increases, but equation (5.14) ensures us that as long as the step size is low enough we can get as close as possible to the true solution, since the error scales as h (at some point we might run into trouble with round off error in the computer).

Can we prove directly that we get the analytical result? In this case it is fairly simple, if we use Eulers method on equation (5.13), we get:

$$\frac{y_{n+1} - y_n}{h} = -y_n f.$$

$$y_{n+1} = (1 - h)y_n, \quad (5.15)$$

or alternatively:

$$y_1 = (1 - h)y_0,$$

$$y_2 = (1 - h)y_1 = (1 - h)^2 y_0,$$

$$\vdots$$

$$y_{N+1} = (1 - h)^N y_0 = (1 - h)^{x_f/h} y_0. \quad (5.16)$$

In the last equation, we have used the fact the number of steps, N , is equal to the simulation time divided by the step size, hence: $N = x_f/h$. From calculus, the equation above is one of the well known limits for the exponential function: $\lim_{x \rightarrow \infty} (1 + k/x)^{mx} = e^{mk}$, hence:

$$y_n = (1 - h)^{x_f/h} y_0 \rightarrow e^{-x_f}, \quad (5.17)$$

when $h \rightarrow 0$. Below is an implementation of the Euler algorithm in this simple case, we also estimate the local error, and global error after N steps.

```
import matplotlib.pyplot as plt
import numpy as np
def euler(tf,h):
    t=[];f=[]
    ti=0.;fi=1.
    t.append(ti);f.append(fi)
    global_err=0.
    while(ti<= tf):
        ti+=h
        fi=fi*(1-h)
        global_err += abs(np.exp(-ti)-fi)
        t.append(ti);f.append(fi)
    print("error= ", np.exp(-ti)-fi, " est.error=", .5*h*(1-np.exp(-ti)))
    print("global error=",global_err)
```

```

    return t,f
t,f=euler(1,1e-5)

```

By changing the step size h , you can easily verify that the local error systematically increases or decreases proportional to h . Something curious happens with the global error when the step size is changed, it does not change very much. The global error involves a second sum over the local error for each step, which can be approximated as a second integration in equation (5.14):

$$\epsilon_{\text{global}} = \frac{1}{2} \int_0^{x_f} [-y(x) + y(0)] dx = \frac{1}{2} [x_f + e^{-x_f} - 1]. \quad (5.18)$$

Note that the global error does not go to zero when the step size decreases, which can easily be verified by changing the step size. This is strange, but can be understood by the following argument: when the step size decreases the local error scales as $\sim h$, but the number of steps scales as $1/h$, so the global error must scale as $h \times 1/h$ or some constant value. Usually it is much easier to control the local error than the global error, this should be kept in mind if you ever encounter a problem where it is important control the global error. For the higher order methods that we will discuss later in this chapter, the global error will go to zero when h decreases.

The answer to our original question, "What is an appropriate step size?", will depend on what you want to achieve in terms of local or global error. In most practical situations you would specify a local error that is acceptable for the problem under investigation and then choose a step size where the local error always is lower than this value. In the next subsection we will investigate how to achieve this in practice.

5.3.2 Adaptive step size - Eulers Method

We want to be sure that we use a step size that achieves a certain accuracy in our numerical solution, but at the same time that we do not waste simulation time using a too low step size. The following approach is similar to the one we derived for the Romberg integration, and a special case of what is known as Richardson Extrapolation. The method is easily extended to higher order methods.

We know that Eulers algorithm is accurate to second order. Our estimate of the new value, y_1^* (where we have used a * to indicate that

we have used a step size of size h), should then be related to the true solution $y(t_1)$ in the following way:

$$y_1^* = y(t_1) + ch^2. \quad (5.19)$$

The constant c is unknown, but it can be found by taking two smaller steps of size $h/2$. If the steps are not too large, our new estimate of the value y_1 will be related to the true solution as:

$$y_1 = y(t_1) + 2c\left(\frac{h}{2}\right)^2. \quad (5.20)$$

The factor 2 in front of c is because we now need to take two steps, and we accumulate a total error of $2c(h/2)^2 = ch^2/2$. It might not be completely obvious that the constant c should be the same in equation (5.19) and (5.20). If you are not convinced, there is an exercise at the end of the chapter. We define:

$$\Delta \equiv y_1^* - y_1 = c\frac{h^2}{2}. \quad (5.21)$$

The truncation error in equation (5.20) is:

$$\epsilon = y(t_1) - y_1 = 2c\left(\frac{h}{2}\right)^2 = \Delta. \quad (5.22)$$

Now we have everything we need: We want the local error to be smaller than some predefined tolerance, ϵ' , or equivalently that $\epsilon \leq \epsilon'$. To achieve this we need to use an optimal step size, h' , that gives us exactly the desired error:

$$\epsilon' = c\frac{h'^2}{2}. \quad (5.23)$$

Dividing equation (5.23) by equation (5.22), we can estimate the optimal step size:

$$h' = h\sqrt{\left|\frac{\epsilon'}{\epsilon}\right|}, \quad (5.24)$$

where the estimated error, ϵ , is calculated from equation (5.22). Equation (5.24) serves two purposes, if the estimated error ϵ is higher than the tolerance, ϵ' , we have specified it will give us an estimate for the step size we should choose in order to achieve a higher accuracy, if on the other

hand $\epsilon' > \epsilon$, then we get an estimate for the next, larger step. Before the implementation we note, as we did for the Romberg integration, that equation (5.22) also gives us an estimate for the error term in equation (5.20) as an improved estimate of y_1 . This we get for free and will make our Euler algorithm accurate to h^3 , hence the improved Euler step, \hat{y}_1 , is to *subtract* the error term from our previous estimate:

$$\hat{y}_1 = y_1 - \epsilon = 2y_1 - y_1^*. \quad (5.25)$$

Below is an implementation of the adaptive Euler algorithm:

```
def one_step(c_old, c_in,h):
    return (1-h)*c_old+h*c_in

def adaptive_euler(c_init,c_init,t_final,tol=1e-4):
    f=[];t=[]
    c_in      = c_init #freshwater into tank
    c_old     = c_init #seawater present
    ti=0.; h_new=1e-3;
    no_steps=0
    global_err=0.
    while(ti <= t_final):
        t.append(ti); f.append(c_old)
        toli=10.*tol; # a high init tolerance to enter while loop
        while(tol>tol):# first two small steps
            hi=h_new
            k1 = one_step(c_old,c_in,hi*.5)
            k2 = one_step(k1,c_in,hi*.5)
            # ... and one large step
            k3 = one_step(c_old,c_in,hi)
            toli = abs(k3-k2)
            h_new=hi*np.sqrt(tol/toli)
            no_steps+=3
        toli=1.
        c_old=2*k2-k3 # higher order correction
    # normal Euler, uncomment and inspect the global error
    #     c_old = k2
    ti    += hi
    global_err += abs(np.exp(-ti)-c_old)
    print("No steps=", no_steps, "Global Error=", global_err)
    return t,f
```

In figure 5.3 the result of the implementation is shown. Note that the number of steps for an accuracy of 10^{-6} is only about 3000. Without knowing anything about the accuracy, we would have to assume that we needed a step size of the order of h in order to reach a local accuracy of h because of equation (5.12). In the current case, we would have needed 10^7 steps, which would lead to unnecessary long simulation times.

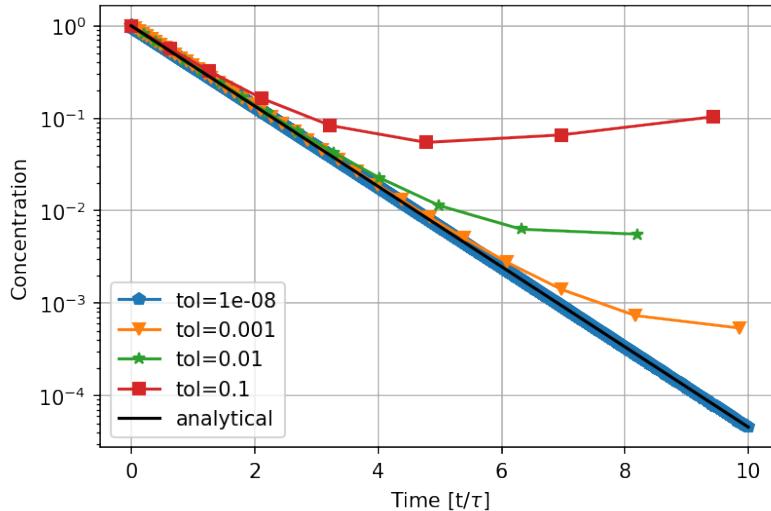


Fig. 5.3 The concentration in the tank using adaptive Euler. Number of Euler steps are: 3006, 117, 48 and 36 for the different step sizes.

Local error and bounds

In the previous example we set an absolute tolerance, and required that our estimate y_n always is within a certain bound of the true solution $y(t_n)$, i.e. $|y(t_n) - y_n| \leq \epsilon'$. This is a very strong demand, and sometimes it makes more sense to require that we also accept a relative tolerance proportional to function value. In some areas the solution might have a very large value, and then another possibility would be to have an ϵ' that varied with the function value: $\epsilon' = atol + |y|rtol$, where 'atol' is the absolute tolerance and 'rtol' is the relative tolerance. A sensible choice would be to set 'atol=rtol' (e.g. $= 10^{-4}$).

5.4 Runge-Kutta Methods

The Euler method only have an accuracy of order h , and a global error that do not go to zero as the step size decrease. The Runge-Kutta methods may be motivated by inspecting the Euler method in figure 5.4. The Euler method uses information from the previous time step to estimate the value at the new time step. The Runge Kutta methods uses

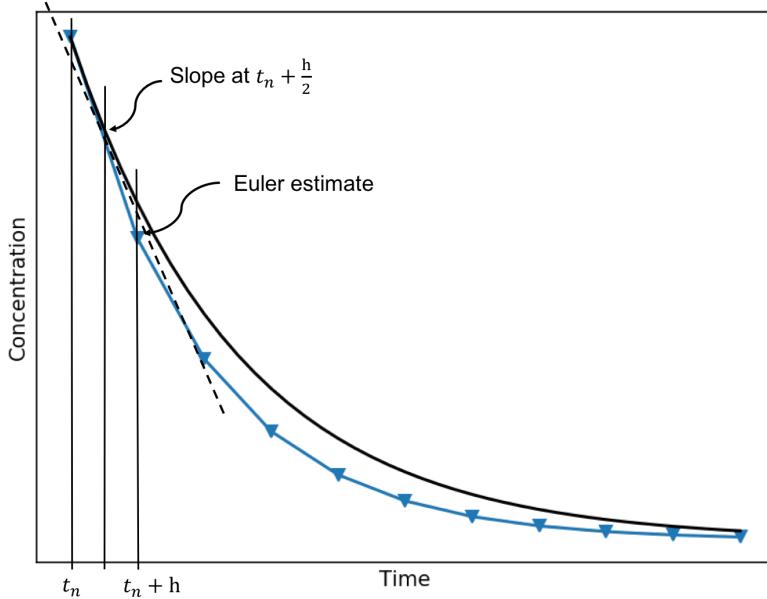


Fig. 5.4 Illustration of the Euler algorithm, and a motivation for using the slope at a distance from the t_n .

the information about the slope between the points t_n and $t_n + h$. By inspecting figure 5.4, we clearly see that by using the slope at $t_n + h/2$ would give us a significant improvement. The 2. order Runge-Kutta method can be derived by Taylor expanding the solution around $t_n + h/2$, we do this by setting $t_n + h = t_n + h/2 + h/2$:

$$y(t_n + h) = y(t_n + \frac{h}{2}) + \frac{h}{2} \left. \frac{dy}{dt} \right|_{t=t_n+h/2} + \frac{h^2}{4} \left. \frac{d^2y}{dt^2} \right|_{t=t_n+h/2} + \mathcal{O}(h^3). \quad (5.26)$$

Similarly we can expand the solution in $y(t_n)$ about $t_n + h/2$, by setting $t_n = t_n + h/2 - h/2$:

$$y(t_n) = y(t_n + \frac{h}{2}) - \frac{h}{2} \left. \frac{dy}{dt} \right|_{t=t_n+h/2} + \frac{h^2}{4} \left. \frac{d^2y}{dt^2} \right|_{t=t_n+h/2} - \mathcal{O}(h^3). \quad (5.27)$$

Subtracting these two equations the term $y(t_n + \frac{h}{2})$, and all even powers in the derivative cancels out:

$$\begin{aligned} y(t_n + h) &= y(t_n) + h \left. \frac{dy}{dt} \right|_{t=t_n+h/2} + \mathcal{O}(h^3), \\ y(t_n + h) &= y(t_n) + h f(y_{n+h/2}, t_n + h/2) + \mathcal{O}(h^3). \end{aligned} \quad (5.28)$$

In the last equation, we have used equation (5.10). Note that we now have an expression that is very similar to Eulers algorithm, but it is accurate to order h^3 . There is one problem, and that is that the function f is to be evaluated at the point $y_{n+1/2} = y(t_n + h/2)$ which we do not know. This can be fixed by using Eulers algorithm: $y_{n+1/2} = y_n + h/2f(y_n, t_n)$. We can do this even if Eulers algorithm has an error term of order h^2 , because the f in equation (5.28) is multiplied by h , and thus our algorithm is still has an error term of order h^3 .

The 2. order Runge-Kutta:

$$\begin{aligned} k_1 &= hf(y_n, t_n) \\ k_2 &= hf(y_n + \frac{1}{2}k_1, t_n + h/2) \\ y_{n+1} &= y_n + k_2 \end{aligned} \quad (5.29)$$

Below is a Python implementation of equation (5.29):

```
def fm(c_old,c_in):
    return c_in-c_old

def rk2_step(c_old, c_in, h):
    k1=h*fm(c_old,c_in)
    k2=h*fm(c_old+0.5*k1,c_in)
    return c_old+k2

def ode_solv(c_into,c_init,t_final,h):
    f=[];t=[]
    c_in = c_into #freshwater into tank
    c_old = c_init #seawater present
    ti=0.
    while(ti <= t_final):
        t.append(ti); f.append(c_old)
        c_new = rk2_step(c_old,c_in,h)
        c_old = c_new
        ti += h
    return t,f
```

In figure 5.5 the result of the implementation is shown. Note that when comparing Runge-Kutta 2. order with Eulers method, see figure 5.5

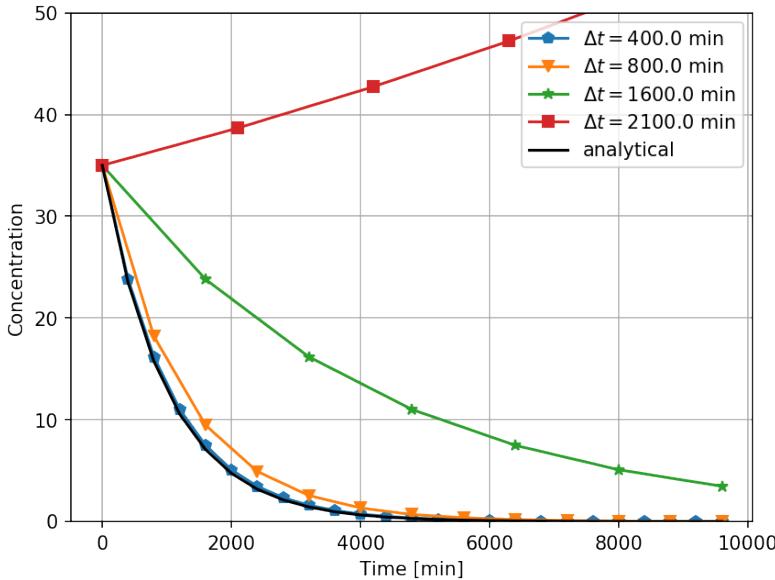


Fig. 5.5 The concentration in the tank for different step size Δt .

and 5.2, we of course have the obvious result that a larger step size can be taken, without loosing numerical accuracy. It is also worth noting that we can take steps that is larger than the tank volume. Eulers method failed whenever the time step was larger than one tank volume ($h = t/\tau > 1$), whereas the Runge-Kutta method finds a physical solution for step sizes lower than twice the tank volume. If the step size is larger, we see that the concentration in the tank increases, which is clearly unphysical.

The Runge-Kutta fourth order method is one of he most used methods, it is accurate to order h^4 , and has an error of order h^5 . The development of the algorithm itself is similar to the 2. order method, but of course more involved. We just quote the result:

The 4. order Runge-Kutta:

$$\begin{aligned}
 k_1 &= h f(y_n, t_n) \\
 k_2 &= h f(y_n + \frac{1}{2}k_1, t_n + h/2) \\
 k_3 &= h f(y_n + \frac{1}{2}k_2, t_n + h/2) \\
 k_4 &= h f(y_n + k_3, t_n + h) \\
 y_{n+1} &= y_n + \frac{1}{6}(k_1 + 2k_2 + 2k_3 + k_4)
 \end{aligned} \tag{5.30}$$

In figure 5.6 the result of the Runge-Kutta fourth order is shown, by comparing it to figure 5.5 it is easy to see that a larger step size can be chosen.

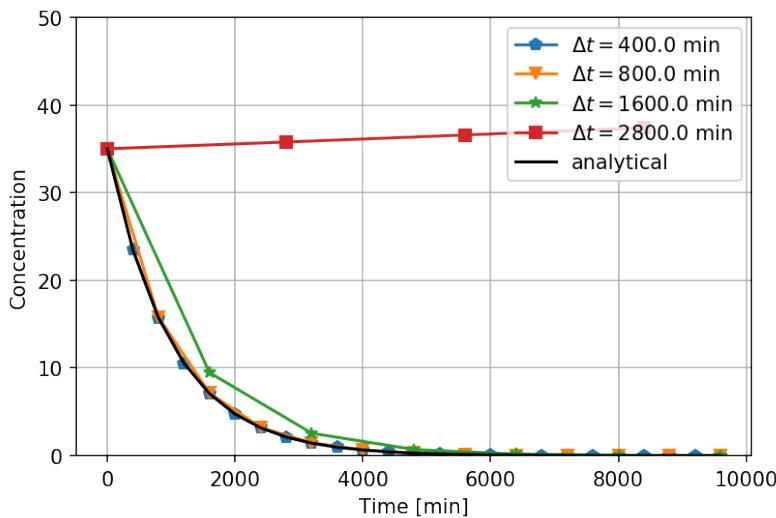


Fig. 5.6 The concentration in the tank for different step size Δt .

5.4.1 Adaptive step size - Runge-Kutta Method

Just as we did with Eulers method, we can implement an adaptive method. The derivation is exactly the same, but this time our method is accurate to fourth order, hence the error term is of order h^5 . We start by taking one large step of size h , our estimate, y_1^* is related to the true solution, $y(t_1)$, in the following way:

$$y_1^* = y(t_1) + ch^5, \quad (5.31)$$

Next, we take two steps of half the size, $h/2$, hence:

$$y_1 = y(t) + 2c \left(\frac{h}{2}\right)^5. \quad (5.32)$$

Subtracting equation (5.31) and (5.32), we find an expression similar to equation (5.21):

$$\Delta \equiv y_1^* - y_1 = c \frac{15}{16} h^5, \quad (5.33)$$

or $c = 16\Delta/(15h^5)$. For the Euler scheme, Δ also happened to be equal to the truncation error, but in this case it is:

$$\epsilon = 2c \left(\frac{h}{2}\right)^5 = \frac{\Delta}{15} \quad (5.34)$$

we want the local error, ϵ , to be smaller than some tolerance, ϵ' . The optimal step size, h' , that gives us exactly the desired error is then:

$$\epsilon' = 2c \left(\frac{h'}{2}\right)^5. \quad (5.35)$$

Dividing equation (5.35) by equation (5.34), we can estimate the optimal step size:

$$h' = h \left| \frac{\epsilon}{\epsilon'} \right|^{1/5}, \quad (5.36)$$

ϵ can be calculated from equation (5.34). In figure 5.7 the result of an implementation is shown (see the exercises).

In general we can use the same procedure any method accurate to order h^p , and you can easily verify that:

Error term and step size for a h^p method:

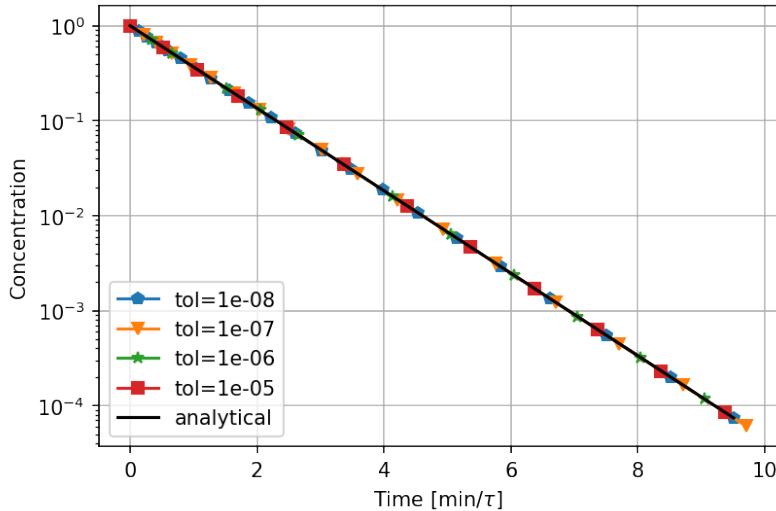


Fig. 5.7 The concentration in the tank for different step size Δt . Number of rk4 steps are: 138, 99, 72 and 66 for the different step sizes and 'rtol=0', for 'rtol=tol' the number of rk4 steps are 81, 72, 63, 63.

$$|\epsilon| = \frac{|\Delta|}{2^p - 1} = \frac{|y_1^* - y_1|}{2^p - 1}, \quad (5.37)$$

$$h' = \beta h \left| \frac{\epsilon}{\epsilon_0} \right|^{\frac{1}{p+1}}, \quad (5.38)$$

$$\hat{y}_1 = y_1 - \epsilon = \frac{2^p y_1 - y_1^*}{2^p - 1}, \quad (5.39)$$

where β is a safety factor $\beta \simeq 0.8, 0.9$, and you should always be careful that the step size do not become too large so that the method breaks down. This can happens when ϵ is very low, which may happen if $y_1^* \simeq y_1$ and/or if $y_1^* \simeq y_1 \simeq 0$.

5.4.2 Conservation of Mass

A mathematical model of a physical system should always be formulated in such a way that it is consistent with the laws of nature. In practical situations this statement is usually equivalent to state that the mathematical model should respect conservation laws. The conservation laws can be conservation of mass, energy, momentum, electrical charge, etc. In our example with the mixing tank, we were able to derive an

expression for the concentration of salt out of the tank, equation (5.5), by *demanding* conservation of mass (see equation (5.2)).

A natural question to ask is then: If our mathematical model respect conservation of mass, are we sure that our solution method respect conservation of mass? We of course expect that when the grid spacing approaches zero our numerical solution will get closer and closer to the analytical solution. Clearly when $\Delta x \rightarrow 0$, the mass is conserved. So what is the problem? The problem is that in many practical problems we cannot always have a step size that is small enough to ensure that our solution always is close enough to the analytical solution. The physical system we consider might be very complicated (e.g. a model for the earth climate), and our ODE system could be a very small part of a very big system. A very good test of any code is to investigate if the code respect the conservation laws. If we know that our implementation respect e.g. mass conservation at the discrete level, we can easily test mass conservation by summing up all the mass entering, and subtracting the mass out of and present in our system. If the mass is not conserved exactly, there is a good chance that there is a bug in our implementation.

If we now turn to our system, we know that the total amount of salt in the system when we start is $C(0)V$. The amount entering is zero, and the amount leaving each time step is $q(t)C(t)\Delta t$. Thus we should expect that if we add the amount of salt in the tank to the amount that has left the system we should always get an amount that is equal to the original amount. Alternatively, we expect $\int_{t_0}^t qC(t)dt + C(t)V - C(0)V = 0$. Adding the following code in the `while(ti <= t_final):` loop:

```
mout += 0.5*(c_old+c_new)*q*dt
mbal = (c_new*vol+mout-vol*c_init)/(vol*c_init)
```

it is possible to calculate the amount of mass lost (note that we have used the trapezoidal formula to calculate the integral). In the table below the fraction of mass lost relative to the original amount is shown for the various numerical methods.

Δt	h	Euler	RK 2. order	RK 4. order
900	0.9	-0.4500	0.3682	0.0776
500	0.5	-0.2500	0.0833	0.0215
100	0.1	-0.0500	0.0026	0.0008
10	0.01	-0.0050	2.5E-05	8.3E-06

We clearly see from the table that the Runge-Kutta methods performs better than Eulers method, but *all of the methods violates mass balance*.

This might not be a surprise as we know that our numerical solution is always an approximation to the analytical solution. How can we then formulate an algorithm that will respect conservation laws at the discrete level? It turns out that for Eulers method it is not so difficult. Eulers algorithm at the discrete level (see equation (5.6)) is actually a two-step process: first we inject the fresh water while we remove the “old“ fluid *and then we mix*. By thinking about the problem this way, it makes more sense to calculate the mass out of the tank as $\sum_k q_k C_k \Delta t_k$. If we in our implementation calculates the mass out of the tank as:

```
mout += c_old*q*dt
mbal = (c_new*vol+mout-vol*c_init)/(vol*c_init)
```

We easily find that the mass is exactly conserved at every time for Eulers method. The concentration in the tank will of course not be any closer to the analytical solution, but if our mixing tank was part of a much bigger system we could make sure that the mass would always be conserved if we make sure that the mass out of the tank and into the next part of the system was equal to $qC(t)\Delta t$.

5.5 Solving a set of ODE equations

What happens if we have more than one equation that needs to be solved? If we continue with our current example, we might be interested in what would happen if we had multiple tanks in series. This could be a very simple model to describe the cleaning of a salty lake by injecting fresh water into it, but at the same time this lake was connected to two nearby fresh water lakes, as illustrated in figure 5.8. The weakest part of the model is the assumption about complete mixing, in a practical situation we could enforce complete mixing with the salty water in the first tank by injecting fresh water at multiple point in the lake. For the two next lakes, the degree of mixing is not obvious, but salt water is heavier than fresh water and therefore it would sink and mix with the fresh water. Thus if the flow rate was slow, one might imaging that a more or less complete mixing could occur. Our model then could answer questions like, how long time would it take before most of the salt water is removed from the first lake, and how much time would it take before most of the salt water was cleared from the whole system? The answer to these questions would give practical input on how much and how fast one should inject the fresh water to clean up the system. If we had data from an actual

system, we could compare our model predictions with data from the physical system, and investigate if our model description was correct.

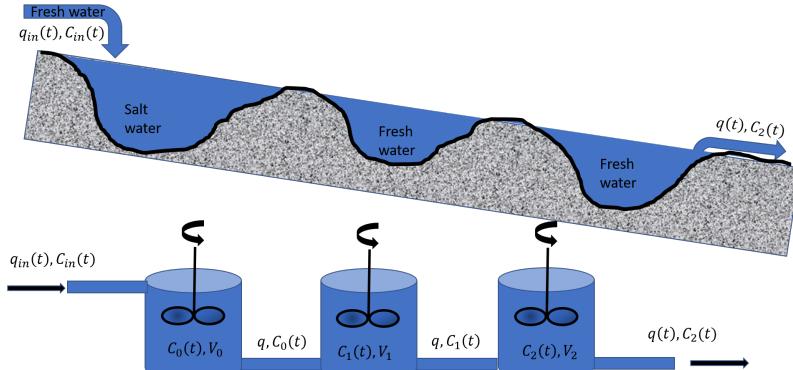


Fig. 5.8 A simple model for cleaning a salty lake that is connected to two lakes downstream.

For simplicity we will assume that all the lakes have the same volume, V . The governing equations follows as before, by assuming mass balance (equation (5.1)):

$$\begin{aligned} C_0(t + \Delta t) \cdot V - C_0(t) \cdot V &= q(t) \cdot C_{\text{in}}(t) \cdot \Delta t - q(t) \cdot C_0(t) \cdot \Delta t, \\ C_1(t + \Delta t) \cdot V - C_1(t) \cdot V &= q(t) \cdot C_0(t) \cdot \Delta t - q(t) \cdot C_1(t) \cdot \Delta t, \\ C_2(t + \Delta t) \cdot V - C_2(t) \cdot V &= q(t) \cdot C_1(t) \cdot \Delta t - q(t) \cdot C_2(t) \cdot \Delta t. \end{aligned} \quad (5.40)$$

Taking the limit $\Delta t \rightarrow 0$, we can write equation (5.40) as:

$$V \frac{dC_0(t)}{dt} = q(t) [C_{\text{in}}(t) - C_0(t)], \quad (5.41)$$

$$V \frac{dC_1(t)}{dt} = q(t) [C_0(t) - C_1(t)], \quad (5.42)$$

$$V \frac{dC_2(t)}{dt} = q(t) [C_1(t) - C_2(t)]. \quad (5.43)$$

Let us first derive the analytical solution: Only the first tank is filled with salt water $C_0(0) = C_{0,0}$, $C_1(0) = C_2(0) = 0$, and $C_{\text{in}} = 0$. The solution to equation (5.41) is, as before $C_0(t) = C_{0,0}e^{-t/\tau}$, inserting this equation into equation (5.42) we find:

$$V \frac{dC_1(t)}{dt} = q(t) [C_{0,0}e^{-t/\tau} - C_1(t)], \quad (5.44)$$

$$\frac{d}{dt} [e^{t/\tau} C_1] = \frac{C_{0,0}}{\tau}, \quad (5.45)$$

$$C_1(t) = \frac{C_{0,0}t}{\tau} e^{-t/\tau}. \quad (5.46)$$

where we have used the technique of integrating factors¹ when going from equation (5.44) to (5.45). Inserting equation (5.46) into equation (5.43), solving the equation in a similar way as for C_1 we find:

$$V \frac{dC_2(t)}{dt} = q(t) \left[\frac{C_{0,0}t}{\tau} e^{-t/\tau} - C_2(t) \right], \quad (5.47)$$

$$\frac{d}{dt} [e^{t/\tau} C_2] = \frac{C_{0,0}t}{\tau}, \quad (5.48)$$

$$C_2(t) = \frac{C_{0,0}t^2}{2\tau^2} e^{-t/\tau}. \quad (5.49)$$

The numerical solution follows the exact same pattern as before if we introduce a vector notation. Before doing that, we rescale the time $t \rightarrow t/\tau$ and the concentrations, $\hat{C}_i = C_i/C_{0,0}$ for $i = 0, 1, 2$, hence:

$$\begin{aligned} \frac{d}{dt} \begin{pmatrix} \hat{C}_0(t) \\ \hat{C}_1(t) \\ \hat{C}_2(t) \end{pmatrix} &= \begin{pmatrix} \hat{C}_{\text{in}}(t) - \hat{C}_0(t) \\ \hat{C}_0(t) - \hat{C}_1(t) \\ \hat{C}_1(t) - \hat{C}_2(t) \end{pmatrix}, \\ \frac{d\hat{\mathbf{C}}(t)}{dt} &= \mathbf{f}(\hat{\mathbf{C}}, t). \end{aligned} \quad (5.50)$$

In figure 5.9 results of an implementation using Runge-Kutta 4. order is shown (see exercises for more details).

¹ https://en.wikipedia.org/wiki/Integrating_factor

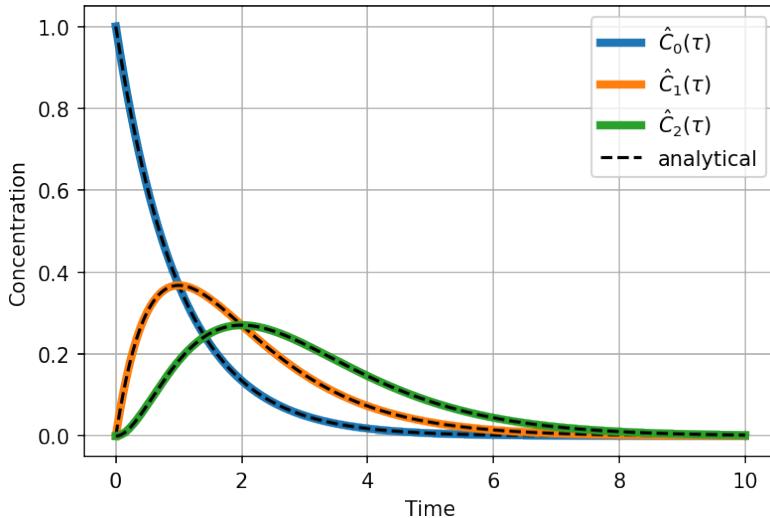


Fig. 5.9 The concentration in the tanks.

5.6 Stiff sets of ODE and implicit methods

As already mentioned a couple of times, our system could be part of a much larger system. To illustrate this, let us now assume that we have two tanks in series. The first tank is similar to our original tank, but the second tank is a sampling tank, 1000 times smaller.

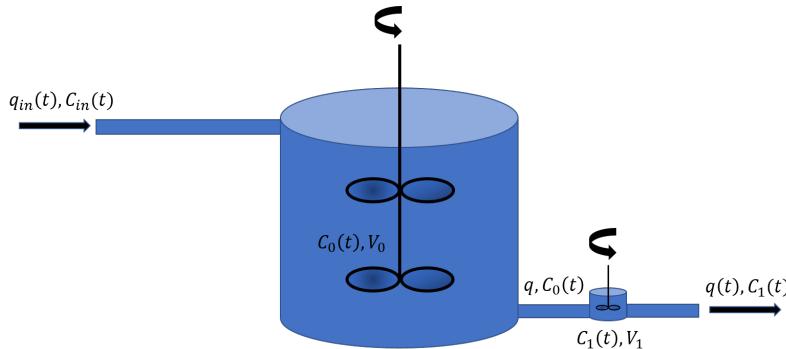


Fig. 5.10 A continuous stirred tank model with a sampling vessel.

The governing equations can be found by requiring mass balance for each of the tanks (see equation (5.1)):

$$\begin{aligned} C_0(t + \Delta t) \cdot V_0 - C_0(t) \cdot V_0 &= q(t) \cdot C_{\text{in}}(t) \cdot \Delta t - q(t) \cdot C_0(t) \cdot \Delta t. \\ C_1(t + \Delta t) \cdot V_1 - C_1(t) \cdot V_1 &= q(t) \cdot C_0(t) \cdot \Delta t - q(t) \cdot C_1(t) \cdot \Delta t. \end{aligned} \quad (5.51)$$

Taking the limit $\Delta t \rightarrow 0$, we can write equation (5.51) as:

$$V_0 \frac{dC_0(t)}{dt} = q(t) [C_{\text{in}}(t) - C_0(t)]. \quad (5.52)$$

$$V_1 \frac{dC_1(t)}{dt} = q(t) [C_0(t) - C_1(t)]. \quad (5.53)$$

Assume that the first tank is filled with seawater, $C_0(0) = C_{0,0}$, and fresh water is flooded into the tank, i.e. $C_{\text{in}} = 0$. Before we start to consider a numerical solution, let us first find the analytical solution: As before the solution for the first tank (equation (5.52)) is:

$$C_0(t) = C_{0,0} e^{-t/\tau_0}, \quad (5.54)$$

where $\tau_0 \equiv V_0/q$. Inserting this equation into equation (5.53), we get:

$$\begin{aligned} \frac{dC_1(t)}{dt} &= \frac{1}{\tau_1} [C_{0,0} e^{-t/\tau_0} - C_1(t)], \\ \frac{d}{dt} [e^{t/\tau_2} C_1] &= \frac{C_{0,0}}{\tau_1} e^{-t(1/\tau_0 - 1/\tau_1)}, \end{aligned} \quad (5.55)$$

$$C_1(t) = \frac{C_{0,0}}{1 - \frac{\tau_1}{\tau_0}} [e^{-t/\tau_0} - e^{-t/\tau_1}], \quad (5.56)$$

where $\tau_1 \equiv V_1/q$.

Next, we will consider the numerical solution. You might think that these equations are more simple to solve numerically than the equations with three tanks in series discussed in the previous section. Actually, this system is much harder to solve with the methods we have discussed so far. The reason is that there are now *two time scales* in the system, τ_1 and τ_2 . The smaller tank sets a strong limitation on the step size we can use, because we should never use step sizes larger than a tank volume. Thus if you use the code in the previous section to solve equation (5.52) and (5.53), it will not find the correct solution, unless the step size is lower than 10^{-3} . Equations of this type are known as *stiff*.

Stiff equations

There is no precise definition of "stiff", but it is used to describe a system of differential equations, where the numerical solution becomes unstable unless a very small step size is chosen. Such systems occurs because there are several (length, time) scales in the system, and the numerical solution is constrained by the shortest length scale. You should always be careful on how you scale your variables in order to make the system dimensionless, which is of particular importance when you use adaptive methods.

These types of equations are often encountered in practical applications. If our sampling tank was extremely small, maybe 10^6 smaller than the chemical reactor, then we would need a step size of the order of 10^{-8} or lower to solve the system. This step size is so low that we easily run into trouble with round off errors in the computer. In addition the simulation time is extremely long. How do we deal with this problem? The solution is actually quite simple. The reason we run into trouble is that we require that the concentration leaving the tank must be a small perturbation of the old one. This is not necessary, and it is best illustrated with Eulers method. As explained earlier Eulers method can be viewed as a two step process: first we inject a volume (and remove an equal amount: $qC(t)\Delta t$), and then we mix. Clearly when we try to remove more than what is left, we run into trouble. What we want to do is to remove or flood much more than one tank volume through the tank during one time step, this can be achieved by $q(t)C(t)\Delta t \rightarrow q(t + \Delta t)C(t + \Delta t)\Delta t$. The term $q(t + \Delta t)C(t + \Delta t)\Delta t$ now represents *the mass out of the system during the time step Δt* .

The methods we have considered so far are known as *explicit*, whenever we replace the solution in the right hand side of our algorithm with $y(t + \Delta t)$ or (y_{n+1}) , the method is known as *implicit*. Implicit methods are always stable, meaning that we can take as large a time step that we would like, without getting oscillating solution. It does not mean that we will get a more accurate solution, actually explicit methods are usually more accurate.

Explicit and Implicit methods

Explicit methods are often called *forward* methods, as they use only information from the previous step to estimate the next value. The explicit methods are easy to implement, but get into trouble if the

step size is too large. Implicit methods are often called *backward* methods as the next step cannot be calculated directly from the previous solution, usually a non-linear equation has to be solved. Implicit methods are generally much more stable, but the price is often lower accuracy. Many commercial simulators uses implicit methods extensively because they are stable, and stability is often viewed as a much more important criterion than numerical accuracy.

Let us consider our example further, and for simplicity use the implicit Eulers method:

$$\begin{aligned} C_{0n+1}V_0 - C_{0n}V_0 &= q(t + \Delta t)C_{in,n+1}\Delta t - q(t + \Delta t)C_{0n+1}\Delta t. \\ C_{1n+1}V_1 - C_{1n}V_1 &= q(t + \Delta t)C_{0n+1}\Delta t - q(t + \Delta t)C_{1n+1}\Delta t. \end{aligned} \quad (5.57)$$

This equation is equal to equation (5.51), but the concentrations on the right hand side are now evaluated at the next time step. The immediate problem is now that we have to find an expression for C_{n+1} that is given in terms of known variables. In most cases one needs to use a root finding method, like Newtons method, in order to solve equation (5.57). In this case it is straight forward to show:

$$\begin{aligned} C_{0n+1} &= \frac{C_{0n} + \frac{\Delta t}{\tau_0}C_{in,n+1}}{1 + \frac{\Delta t}{\tau_0}}, \\ C_{2n+1} &= \frac{C_{1n} + \frac{\Delta t}{\tau_1}C_{0n+1}}{1 + \frac{\Delta t}{\tau_1}}. \end{aligned} \quad (5.58)$$

In figure 5.11 the result of the implementation is shown, note that quite large step sizes can be used without inducing non physical results.

Exercise 5.1: Truncation Error in Eulers Method

In the following we will take a closer look at the adaptive Eulers algorithm and show that the constant c is indeed the same in equation (5.19) and (5.20). The true solution $y(t)$, obeys the following equation:

$$\frac{dy}{dt} = f(y, t), \quad (5.59)$$

and Eulers method to get from y_0 to y_1 by taking one (large) step, h is:

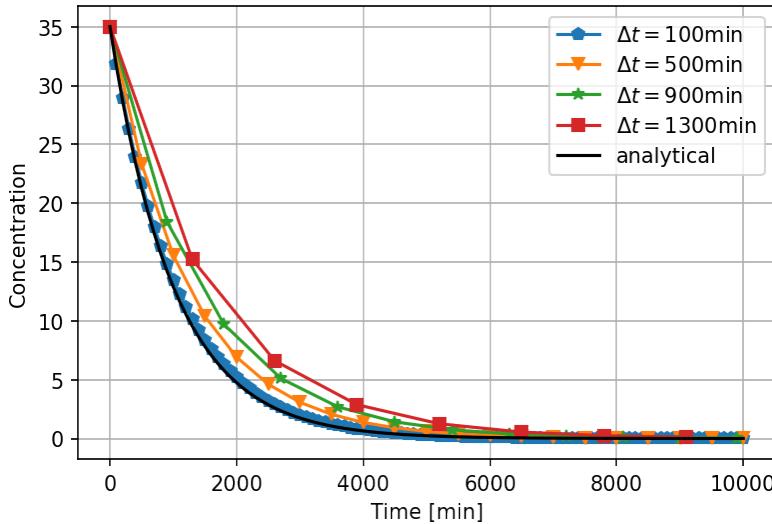


Fig. 5.11 The concentration in the tanks for $h = 0.01$.

$$y_1^* = y_0 + h f(y_0, t_0), \quad (5.60)$$

We will also assume (for simplicity) that in our starting point $t = t_0$, the numerical solution, y_0 , is equal to the true solution, $y(t_0)$, hence $y(t_0) = y_0$.

a) Show that when we take one step of size h from t_0 to $t_1 = t_0 + h$, $c = y''(t_0)/2$ in equation (5.19).

Answer. The local error, is the difference between the numerical solution and the true solution:

$$\begin{aligned} \epsilon^* &= y(t_0 + h) - y_1^* = y(t_0) + y'(t_0)h + \frac{1}{2}y''(t_0)h^2 + \mathcal{O}(h^3) \\ &\quad - [y_0 + h f(y_0, t_0 + h)], \end{aligned} \quad (5.61)$$

where we have used Taylor expansion to expand the true solution around t_0 , and equation (5.60). Using equation (5.59) to replace $y'(t_0)$ with $f(y_0, t_0)$, we find:

$$\epsilon^* = y(t_0 + h) - y_1^* = \frac{1}{2}y''(t_0)h^2 \equiv ch^2, \quad (5.62)$$

hence $c = y''(t_0)/2$.

b) Show that when we take two steps of size $h/2$ from t_0 to $t_1 = t_0 + h$, Eulers algorithm is:

$$y_1 = y_0 + \frac{h}{2}f(y_0, t_0) + \frac{h}{2}f(y_0 + \frac{h}{2}f(y_0, t_0), t_0 + h/2). \quad (5.63)$$

Answer.

$$y_{1/2} = y_0 + \frac{h}{2}f(y_0, t_0), \quad (5.64)$$

$$y_1 = y_{1/2} + \frac{h}{2}f(y_{1/2}, t_0 + h/2), \quad (5.65)$$

$$y_1 = y_0 + \frac{h}{2}f(y_0, t_0) + \frac{h}{2}f(y_0 + \frac{h}{2}f(y_0, t_0), t_0 + h/2). \quad (5.66)$$

Note that we have inserted equation (5.64) into equation (5.65) to arrive at equation (5.66).

- c) Find an expression for the local error when using two steps of size $h/2$, and show that the local error is: $\frac{1}{2}ch^2$

Answer.

$$\begin{aligned} \epsilon &= y(t_0 + h) - y_1 = y(t_0) + y'(t_0)h + \frac{1}{2}y''(t_0)h^2 + \mathcal{O}(h^3) \\ &\quad - \left[y_0 + \frac{h}{2}f(y_0, t_0) + \frac{h}{2}f(y_0 + \frac{h}{2}f(y_0, t_0), t_0 + h/2) \right]. \end{aligned} \quad (5.67)$$

This equation is slightly more complicated, due to the term involving f inside the last parenthesis, we can use Taylor expansion to expand it about (y_0, t_0) :

$$\begin{aligned} f(y_0 + \frac{h}{2}f(y_0, t_0), t_0 + h/2) &= f(y_0, t_0) \\ &\quad + \frac{h}{2} \left[f(y_0, t_0) \frac{\partial f}{\partial y} \Big|_{y=y_0, t=t_0} + \frac{h}{2} \frac{\partial f}{\partial t} \Big|_{y=y_0, t=t_0} \right] + \mathcal{O}(h^2). \end{aligned} \quad (5.68)$$

It turns out that this equation is related to $y''(t_0, y_0)$, which can be seen by differentiating equation (5.59):

$$\frac{d^2y}{dt^2} = \frac{df(y, t)}{dt} = \frac{\partial f(y, t)}{\partial y} \frac{dy}{dt} + \frac{\partial f(y, t)}{\partial t} = \frac{\partial f(y, t)}{\partial y} f(y, t) + \frac{\partial f(y, t)}{\partial t}. \quad (5.69)$$

Hence, equation (5.68) can be written:

$$f(y_0 + \frac{h}{2}f(y_0, t_0), t_0 + h/2) = f(y_0, t_0) + \frac{h}{2}y''(t_0, y_0), \quad (5.70)$$

hence the truncation error in equation (5.67) can finally be written:

$$\epsilon = y(t_1) - y_1 = \frac{h^2}{4} y''(y_0, t_0) = \frac{1}{2} ch^2, \quad (5.71)$$

Solution. The local error, is the difference between the numerical solution and the true solution:

$$\begin{aligned} \epsilon^* &= y(t_0 + h) - y_1^* = y(t_0) + y'(t_0)h + \frac{1}{2}y''(t_0)h^2 + \mathcal{O}(h^3) \\ &\quad - [y_0 + hf(y_0, t_0 + h)], \end{aligned} \quad (5.72)$$

where we have used Taylor expansion to expand the true solution around t_0 , and equation (5.60). Using equation (5.59) to replace $y'(t_0)$ with $f(y_0, t_0)$, we find:

$$\epsilon^* = y(t_0 + h) - y_1^* = \frac{1}{2}y''(t_0)h^2 \equiv ch^2, \quad (5.73)$$

where we have ignored terms of higher order than h^2 , and defined c as $c = y''(t_0)/2$. Next we take two steps of size $h/2$ to reach y_1 :

$$y_{1/2} = y_0 + \frac{h}{2}f(y_0, t_0), \quad (5.74)$$

$$y_1 = y_{1/2} + \frac{h}{2}f(y_{1/2}, t_0 + h/2), \quad (5.75)$$

$$y_1 = y_0 + \frac{h}{2}f(y_0, t_0) + \frac{h}{2}f(y_0 + \frac{h}{2}f(y_0, t_0), t_0 + h/2). \quad (5.76)$$

Note that we have inserted equation (5.74) into equation (5.75) to arrive at equation (5.76). The truncation error in this case is, as before:

$$\begin{aligned} \epsilon &= y(t_0 + h) - y_1 = y(t_0) + y'(t_0)h + \frac{1}{2}y''(t_0)h^2 + \mathcal{O}(h^3) \\ &\quad - \left[y_0 + \frac{h}{2}f(y_0, t_0) + \frac{h}{2}f(y_0 + \frac{h}{2}f(y_0, t_0), t_0 + h/2) \right]. \end{aligned} \quad (5.77)$$

This equation is slightly more complicated, due to the term involving f inside the last parenthesis, we can use Taylor expansion to expand it about (y_0, t_0) :

$$\begin{aligned} f(y_0 + \frac{h}{2}f(y_0, t_0), t_0 + h/2) &= f(y_0, t_0) \\ &+ \frac{h}{2} \left[f(y_0, t_0) \left. \frac{\partial f}{\partial y} \right|_{y=y_0, t=t_0} + \left. \frac{\partial f}{\partial t} \right|_{y=y_0, t=t_0} \right] + \mathcal{O}(h^2). \end{aligned} \quad (5.78)$$

It turns out that this equation is related to $y''(t_0, y_0)$, which can be seen by differentiating equation (5.59):

$$\frac{d^2y}{dt^2} = \frac{df(y, t)}{dt} = \frac{\partial f(y, t)}{\partial y} \frac{dy}{dt} + \frac{\partial f(y, t)}{\partial t} = \frac{\partial f(y, t)}{\partial y} f(y, t) + \frac{\partial f(y, t)}{\partial t}. \quad (5.79)$$

Hence, equation (5.78) can be written:

$$f(y_0 + \frac{h}{2}f(y_0, t_0), t_0 + h/2) = f(y_0, t_0) + \frac{h}{2}y''(t_0, y_0), \quad (5.80)$$

hence the truncation error in equation (5.77) can finally be written:

$$\epsilon = y(t_1) - y_1 = \frac{h^2}{4}y''(y_0, t_0) = \frac{1}{2}ch^2, \quad (5.81)$$

6.1 Monte Carlo Methods

Monte Carlo methods are named after the Monte Carlo Casino in Monaco, this is because at its core it uses random numbers to solve problems. Monte Carlo methods are quite easy to program, and they are usually much more intuitive than a theoretical approach.

6.2 Monte Carlo Integration "Hit and Miss"

Let us start with a simple illustration of the Monte Carlo Method (MCM), Monte Carlo integration. To the left in figure 6.1 there is a shape of a pond. Imagine that we wanted to estimate the area of the pond, how could we do it? Assume further that you did not have your phone or any other electronic devices to help you.

One possible approach is: First to walk around it, and put up some bands (illustrated by the black dotted line). Then estimate the area inside the bands (e.g. 4×3 meters). Then we would know that the area was less than e.g. 12m^2 . Finally, and this is the difficult part, throw rocks *randomly* inside the bands. The number of rocks hitting the pond divided by the total number rocks thrown should be equal to the area of the pond divided by the total area inside the bands, i.e. the area of the pond should be equal to:

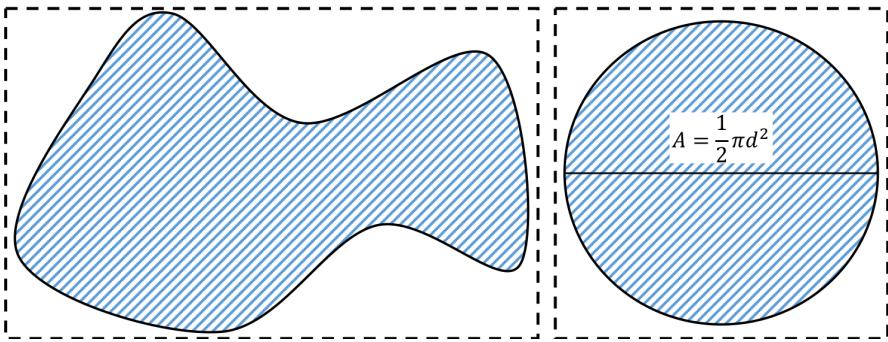


Fig. 6.1 Two ponds to illustrate the MCM.

$$A \simeq \text{Area of rectangle} \times \frac{\text{Number of rocks hitting the pond}}{\text{Number of rocks thrown}}. \quad (6.1)$$

It is important that we throw the rocks randomly, otherwise equation (6.1) is not correct. Now, let us investigate this in more detail, and use the idea of throwing rocks to estimate π . To the right in figure 6.1, there is a well known shape, a circle. The area of the circle is $\pi d^2/4$, and the shape is given by $x^2 + y^2 = d^2/4$. Assume that the circle is inscribed in a square with sides of d . To throw rocks randomly inside the square, is equivalent pick random numbers with coordinates (x, y) , where $x \in [0, d]$ and $y \in [0, d]$. We want all the x - and y -values to be chosen with equal probability, which is equivalent to pick random numbers from a *uniform* distribution. Below is a Python implementation:

```
import numpy as np

def estimate_pi(N,d):
    # random.seed(2)
    D2=d*d/4; dc=0.5*d
    A=0
    for k in range(0,N):
        x=np.random.uniform(0,d)
        y=np.random.uniform(0,d)
        if((x-dc)**2+(y-dc)**2 <= D2):
            A+=1
    # estimate area of circle: d*d*A/N
    return 4*A/N

N=1000;d=2
pi_est=estimate_pi(N,d)
print('Estimate for pi= ', pi_est,' Error=', np.pi-pi_est)
```

In the table below, we have run the code for $d = 1$ and different values of N .

MC estimate	Error	N	$1/\sqrt{N}$
3.04	-0.10159	10^2	0.100
3.176	0.03441	10^3	0.032
3.1584	0.01681	10^4	0.010
3.14072	-0.00087	10^5	0.003

We clearly see that a fair amount of rocks or numbers needs to be used in order to get a good estimate. If you run this code several times you will see that the results changes from time to time. This makes sense as the coordinates x and y are chosen at random.

A note on performance

The code above is not efficient and for MC simulations we usually have to use many random numbers. Instead of

```
for k in range(0,N):
    x=np.random.uniform(0,d)
    y=np.random.uniform(0,d)
```

one should avoid loops, and take advantage of build in functions in Numpy

```
x=np.random.uniform(0,d,size=N)
y=np.random.uniform(0,d,size=N)
```

6.2.1 Random number generators

There are much to be said about random number generators. The MCM depends on a good random number generator, otherwise we cannot use the results from statistics to develop our algorithms. Below, we briefly summarize some important points that you should be aware of:

1. Random number generators are generally of two types: *hardware random number generator* (HRNG) or *pseudo random number generator* (PRNG).
2. HRNG uses a physical process to generate random numbers, this could atmospheric noise, radioactive decay, microscopic fluctuations, which is translated to an electrical signal. The electrical signal is converted to a digital number (1 or 0), by sampling the random signal random numbers can be generated. The HRNG are often named *true random number generators*, and their main use are in *cryptography*.

3. PRNG uses a mathematical algorithm to generate an (apparent) random sequence. The algorithm uses an initial number, or a *seed*, to start the sequence of random number. The sequence is deterministic, and it will generate the same sequence of numbers if the same seed is used. At some point the algorithm will reproduce itself, i.e. it will have certain period. For some seeds the period may be much shorter.
4. Many of the PRNG are not considered to be cryptographically secure, because if a sufficiently long sequence of random numbers are generated from them, the rest of the sequence can be predicted.
5. Python uses the Mersenne Twister¹ algorithm to generate random numbers, and has a period of $2^{19937} - 1 \simeq 4.3 \cdot 10^{6001}$. It is not considered to be cryptographically secure.

In Pythons `random.uniform` function, a random seed is chosen each time the code is run, but if we set e.g. `random.seed(2)`, the code will generate the same sequence of numbers each time it is called.

6.2.2 Encryption

This section can be skipped as it is not relevant for development of the numerical algorithms, but it is a good place to explain the basic idea behind encryption of messages. A very simple, but not a very good encryption, is to replace all the letters in the alphabet with a number, e.g. A=1, B=2, C=3, etc. This is what is known as a *substitution cipher*, it does not need to be a number it could be a letter, a sequence of letters, letters and numbers etc. The receiver can solve the code by doing the reverse operation.

The weakness of this approach is that it can fairly easily be cracked, by the following approach: First we analyze the encrypted message and find the frequency of each of the symbols. Assume that we know that the message is written in English, then the frequency of symbols can be compared with the frequency of letters from a known English text (the most common is E (12%), then T (9%), etc.). We would then guess that the most occurring symbol probably is an E or T. When some of the letters are in place, we can compare with the frequency of words, and so on. By the help of computers this process can easily be automated.

A much better algorithm is *to not replace a letter with the same symbol*. To make it more clear, consider our simple example where A=1, B=2,

¹ https://en.wikipedia.org/wiki/Mersenne_Twister

C=3, If we know say that A=1 but we add a *random number*, then our code would be much harder to crack. Then the letter A could be several places in the message but represented as a complete different number. Thus we could not use the frequency of the various symbols to crack the message.

How can the receiver decrypt the message? Obviously, it can be done if both the sender and receiver have the same sequence of random numbers (or the *key*). This can be achieved quite simple with random number generators, if we know the seed used we can generate the same sequence of random numbers. If Alice where to send a message to Bob without Eve knowing what it is, Alice and Bob could agree to send a message that was scrambled using Pythons Mersenne-Twister algorithm with seed=2.

The weakness of this approach is of course that Eve could convince Alice or Bob to give her the seed or the key. Another possibility is that Eve could write a program that tested different random number generators and seeds to decipher the message. How to avoid this?

Let us assume that Alice and Bob each had their own hardware random generator. This generator generated random numbers that was truly random, and the sequence could not be guessed by any outsider. Alice do not want to share her key (sequence of random numbers) with Bob, and Bob would not share his key with Alice. How can they send a message without sharing the key? One possible way of doing it is as follows: Alice write a message and encrypt it with her key, she send the message to Bob. Bob then encrypt the message with his key, he sends it back to Alice. Alice then decrypt the message with her key and send it back to Bob. Now, Bob can decrypt it with his own key and read the message. The whole process can be visualized by thinking of the message as box with the message. Alice puts her padlock on the box (keeps her key for herself), she sends the message to Bob. Bob locks the box with his padlock, now there are two padlocks on the box. He sends the box back to Alice, Alice unlocks her padlock with her key, and sends it back to Bob. The box now only has Bob's key, he can unlock the box and read the message. The important point is that the box was never unlocked throughout the transaction, and Alice and Bob never had to share the key with anyone.

6.2.3 Errors on Monte Carlo Integration and the Binomial Distribution

How many rocks do we need to throw in order to reach a certain accuracy? To answer this question we need some results from statistics. Our problem of calculating the integral is closely related to the *binomial distribution*. When we throw a rock one of two things can happen i) the rock falls into the water, or ii) it falls outside the pond. If we denote the probability that the rock falls into the pond as p , then the probability that it falls outside the pond, q , has to be $q = 1 - p$. This is simply because there are no other possibilities and the sum of the two probabilities has to be one: $p + q = p + (1 - p) = 1$. The binomial distribution is given by:

$$p(k) = \frac{n!}{k!(n-k)!} p^k (1-p)^{n-k}. \quad (6.2)$$

$p(k)$ is the probability that an event happens k times after n trials. The mean, μ , and the variance, σ^2 , of the binomial distribution is:

$$\mu = \sum_{k=0}^{n-1} kp(k) = np, \quad (6.3)$$

$$\sigma^2 = \sum_{k=0}^{n-1} (k - \mu)^2 p(k) = np(1-p). \quad (6.4)$$

Mean and variance

The mean of a distribution is simply the *sum* divided by the *count*, the symbol μ or \bar{x} is usually used. For N observations, x_i , $\mu = \sum_i x_i / N$. The mean is just an average, it could e.g. be the sum of all the heights of students in the class divided by the number of students. The mean would then be the average height of all the students in the class.

The variance is calculated by taking the difference between each of the data points and the mean, square it, and sum over all data points. Usually the symbol σ^2 is used, $\sigma^2 = \sum_i (\mu - x_i)^2 / N$. The variance measures the spread in the data. Furthermore, it squares the distance between the mean and the individual observations, meaning that the points lying far a way from μ contributes more to the variance.

Before we proceed, we should take a moment and look a little more into the meaning of equation (6.2) to appreciate its usefulness. A classical example of the use of the binomial formula is to toss a coin, if the coin is fair it will have an equal probability of giving us a head or tail, hence $p = 1/2$. Equation (6.2), can answer questions like: "What is the probability to get only heads after 4 tosses?". Let us calculate this answer using equation (6.2), the number of tosses is 4, the number of success is 4 (only heads each time)

$$p(k=4) = \frac{4!}{4!(4-4)!} \frac{1}{2}^4 (1 - \frac{1}{2})^{4-4} = \frac{1}{2^4} = \frac{1}{16}. \quad (6.5)$$

"What is the probability to get three heads in four tosses?", using the same equation, we find:

$$p(k=3) = \frac{4!}{3!(4-3)!} \frac{1}{2}^3 (1 - \frac{1}{2})^{4-3} = \frac{4}{2^4} = \frac{1}{4}. \quad (6.6)$$

In figure 6.2, all the possibilities are shown. The number of possibilities are 16, and there are only one possibility that we get only heads, i.e. the probability is 1/16 as calculated in equation (6.5). In the figure we also see that there are 4 possible ways we can get three heads, hence the probability is 4/16=1/4 as calculated in equation (6.6).

Now, let us return to our original question, "What is the error on our estimate of the integral, when using the MCM?". Before we continue we should also clean up our notation, let I be the value of the true integral, A is our *estimate* of the integral, and I_N is the area of the rectangle. First, let us show that the mean or expectation value of the binomial distribution is related to our estimate of the area of the pond or the circle, A . In our case we draw $n = N$ random numbers, and k times the coordinate falls inside the circle, equation (6.3) tells us that the mean value is np . p is the probability that the coordinate is within the area to be integrated, hence as before p is equal to the area to be integrated divided by the area of the total domain, thus:

$$\mu = np = N \frac{A}{I_N}, \quad (6.7)$$

or

$$A = I_N \frac{\mu}{N}. \quad (6.8)$$

Equation (6.4), gives us an estimate of the variance of the mean value. Assume for simplicity that we can replace $1 - p \simeq p$, this is of course

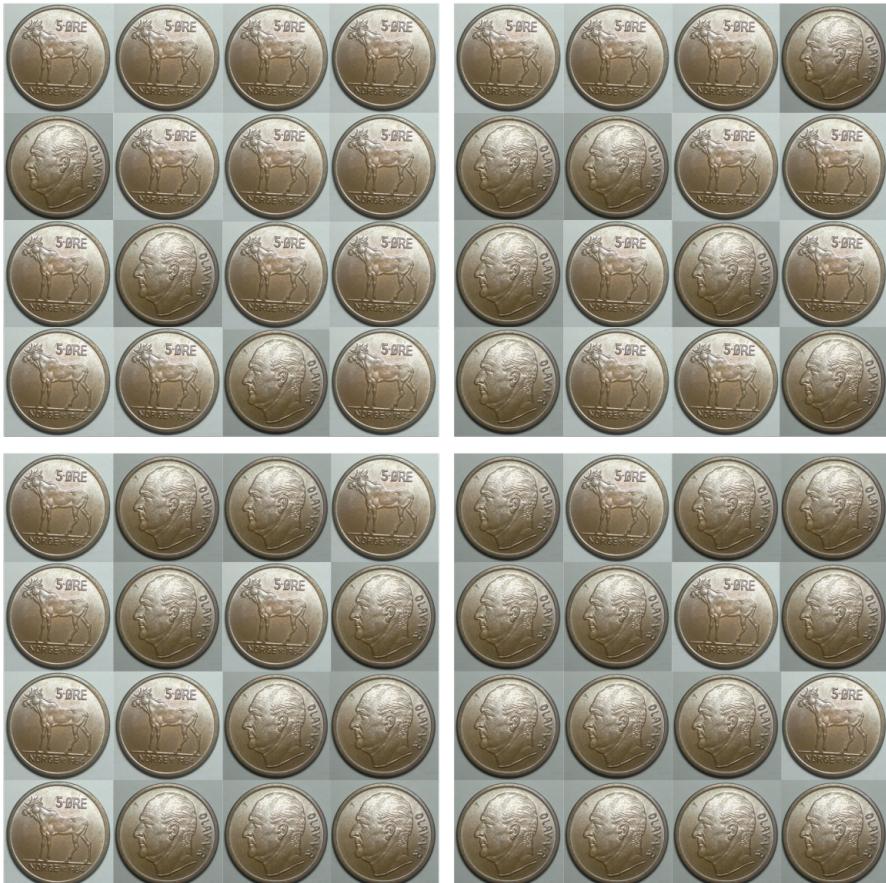


Fig. 6.2 The famous Norwegian Moose coin, and possible outcomes of four coin flips in a row.

only correct if the area of the rectangle is twice as big as our pond, but we are only interested in an estimate of the error, hence $\sigma^2 \simeq np^2$. We can now use the standard deviation as an estimate of the error of our integral:

$$\begin{aligned} I &\simeq I_N \frac{\mu \pm \sigma}{n} = I_N \frac{Np \pm \sqrt{Np}}{N} \\ &\simeq I_N(p \pm \frac{p}{\sqrt{N}}) = A \pm \frac{A}{\sqrt{N}}. \end{aligned} \quad (6.9)$$

In the last equation we have replaced p with A/I_N . Hence, the error of our integral is inversely proportional to the square root of the number of points.

6.2.4 The mean value method

How does our previous method compare with some of our standard methods, like the midpoint rule? The error for the MC method scales as $1/\sqrt{N}$, in our previous error estimates we used the step length, h , as an indicator of the accuracy, and not N . The sN is related to the number of points as $h = (b - a)/n$, where b and a are the integration limit. Thus our MCM scales as $1/\sqrt{n} \sim h^{1/2}$, this is actually worse than the midpoint or trapezoidal rule, which scaled as h .

The MCM can be improved. We will first describe the mean value method. In the last section we calculated the area of a circle by picking random numbers inside a square and estimated the fraction of points inside the circle. This is equivalent to calculate the area of a half circle, and multiply with 2:

$$I = 2 \int_{-d/2}^{d/2} \sqrt{(d/2)^2 - x^2} dx = \frac{\pi d^2}{4}. \quad (6.10)$$

The half-circle is now centered at the origin. Before we proceed we write our integral in a general form as:

$$I = \int_a^b f(x) dx. \quad (6.11)$$

Instead of counting the number of points inside the curve given by $f(x)$, we could instead use the mean of the function, which we will define as $\bar{f} = \sum_k f(x_k)/N$:

$$I = \int_a^b f(x) dx \simeq \bar{f} \int_a^b dx = (b - a)\bar{f} = \frac{(b - a)}{N} \sum_{k=0}^{N-1} f(x_k). \quad (6.12)$$

Note that this formula is similar to the midpoint rule, but now the function is not evaluated at the midpoint, but at several points and we use the average value.

Below is an implementation:

```
import numpy as np
```

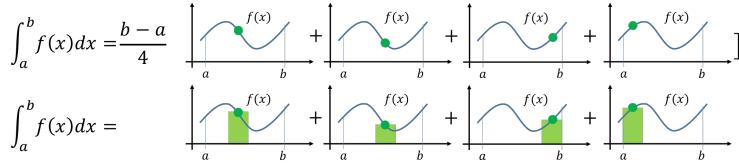


Fig. 6.3 Illustration of MC integration for $N = 4$.

```

def f(x,D2):
    return 2*np.sqrt((D2-x*x))

def mcm_mean(N,d):
    D2=d*d/4
    x=np.random.uniform(-d/2,d/2,size=N)
    A=np.sum(f(x,D2))
    # estimate for area: A/N
    return d*A/N

```

In the table below we have compared the mean value method with the "hit and miss" method. We see that the mean value method performs somewhat better, but there are some random fluctuations and in some cases it performs poorer.

MC-mean	Error	MC	Error	N
3.1706	0.0290	3.1600	0.0184	10^2
3.1375	-0.0041	3.1580	0.0164	10^3
3.1499	0.0083	3.1422	0.0006	10^4
3.1424	0.0008	3.1457	0.0041	10^5
3.1414	-0.0002	3.1422	0.0006	10^6

We also see that in this case the error scales as $1/\sqrt{N}$.

Notice

At first sight it might be a little counter intuitive that if we multiply the average value of the function with the size of the integration domain we get an estimate for the integral, as illustrated in the top figure in figure 6.3. A different, but equivalent way, of viewing

the mean value method is the lower figure in figure 6.3. For each random point we choose, we multiply with the area $(b - a)/N$, as N increases the area decreases and the mean value method approaches the midpoint algorithm. The reason the mean value method performs poorer is that we do not sample the function at regular intervals. The law of large numbers^a, ensures that our estimate approach the true value of the integral.

^ahttps://en.wikipedia.org/wiki/Law_of_large_numbers

6.2.5 Basic Properties of Probability Distributions

The MCM is closely tied to statistics, and it is important to have a basic understanding of probability density functions (PDF). In the previous section, we used a random number generator to give us random numbers in an interval. All the numbers are picked with an equal probability. Another way to state this is to say that: we *draw* random numbers from an *uniform* distribution. Thus all the numbers are drawn with an equal probability p . What is the value of p ? That value is given from another property of PDF's, all PDF's must be *normalized* to 1. This is equivalent to state that the sum of all probabilities must be equal to one. Thus for a general PDF, $p(x)$, we must have:

$$\int_{-\infty}^{\infty} p(x)dx = 1. \quad (6.13)$$

A uniform distribution, $p(x) = U(x)$, is given by:

$$U(x) = \begin{cases} \frac{1}{b-a}, & \text{for } x \in [a, b] \\ 0, & \text{for } x < a \text{ or } x > b, \end{cases} \quad (6.14)$$

you can easily verify that $\int_{-\infty}^{\infty} U(x) = 1$. In the MCM we typically evaluate *expectation values*. The expectation value, $E[f]$, for a function is defined:

$$E[f] \equiv \int_{-\infty}^{\infty} f(x)p(x)dx, \quad (6.15)$$

specializing to a uniform distribution, $p(x) = U(x)$, we get:

$$E[f] = \int_{-\infty}^{\infty} f(x)U(x)dx = \frac{1}{b-a} \int_a^b f(x)dx. \quad (6.16)$$

Rearranging this equation, we see that we can write the above equation as:

$$\int_a^b f(x)dx = (b-a)E[f] \simeq (b-a)\frac{1}{N} \sum_{k=0}^{N-1} f(x_k). \quad (6.17)$$

This equation is the same as equation (6.12), but in the previous section we never explained why the expectation value of $f(x_k)$ was equal to the integral. The derivation above shows that $\int_a^b f(x)dx$ is equal to the expectation value of $f(x)$ only under the condition that *we draw numbers from a uniform distribution*.

To make this a bit more clearer, let us specialize to $f(x) = x$. In this case the expectation value is equal to the mean:

$$E[x] = \mu = \int_{-\infty}^{\infty} xp(x) = \frac{1}{N} \sum_k x_k. \quad (6.18)$$

The mean of a distribution is a special case follows directly from the definition of the variance:

$$\sigma = \sqrt{\frac{1}{N} \sum_k (f(x_i) - \langle f \rangle)^2} \sim \frac{1}{\sqrt{N}}, \quad (6.19)$$

the reason that the mean value method usually performs better is that the leading coefficient is smaller.

Why would we or anyone use MC integration?

Monte Carlo integration performs much poorer than any of our previous methods. So why should we use it, or when should we use it? The strength of MC integration is only apparent when there is a large number of dimensions.

6.2.6 Example: Monte Carlo Integration of a Hyper Sphere

The volume of a hyper sphere is known:

$$V(R) = \frac{\pi^{D/2}}{\Gamma(D/2 + 1)} R^D, \quad (6.20)$$

where D is the number of dimensions $\Gamma(D/2 + 1)$ is the gamma function, if n is an integer then $\Gamma(n) = (n - 1)!$ and $\Gamma(n + 1/2) = (2n)!/(4^n n!) \sqrt{\pi}$.

You can easily verify that for $D = 2, 3$, $V(R) = \pi R^2, 4/3\pi R^3$, respectively.

In the case of MC integration, we simply place the sphere inside a cube, and then count the number of points that hits inside the hypersphere:

```
def mc_nballII(N=1000,D=3,R=1):
    """
    Calculates the volume of a hypersphere using accept and reject
    N: Number of random points
    D: Number of dimensions
    R: Radius of hypersphere
    """
    r=0
    for d in range(D):
        xi=np.random.uniform(-R,R,size=N)
        r+=xi*xi
    r=np.sqrt(r)
    vol = np.sum(r<=R)
    print("Number of points inside n-ball: ", vol)
    return vol/N*(2*R)**D
```

Notice how easy it is to do MC integration in any number of dimensions. How can we extend our previous one dimensional methods to more dimensions? One way of doing it is to call a one dimensional integration routine several times. The volume of a hypersphere is

$$V(R) = \int_{-R}^R \int_{-\sqrt{R^2-x_0^2}}^{\sqrt{R^2-x_0^2}} \int_{-\sqrt{R^2-x_0^2-x_1^2}}^{\sqrt{R^2-x_0^2-x_1^2}} \cdots \int_{-\sqrt{R^2-x_0^2-x_1^2-\cdots-x_{n-2}^2}}^{\sqrt{R^2-x_0^2-x_1^2-\cdots-x_{n-2}^2}} dx_0 dx_1 dx_2 \cdots dx_{n-1}. \quad (6.21)$$

To simplify the notation lets look a little bit closer at $D = 3$ ($n = 2$). We can always do the last integration regardless of the number of dimensions

$$V(R) = 2 \int_{-R}^R \int_{-\sqrt{R^2-x_0^2}}^{\sqrt{R^2-x_0^2}} \sqrt{R^2 - x_0^2 - x_1^2} dx_0 dx_1. \quad (6.22)$$

This equation can be rewritten as

$$\begin{aligned} V(R) &= 2 \int_{-R}^R F(x_0) dx_0, \\ F(x_0) &\equiv \int_{-\sqrt{R^2-x_0^2}}^{\sqrt{R^2-x_0^2}} \sqrt{R^2 - x_0^2 - x_1^2} dx_1, \end{aligned} \quad (6.23)$$

when integrating $F(x_0)$, we do it by dividing the x-axis from $-R$ to R into N equal slices as before. We also need to evaluate $F(x_0)$ for each value of x_0 , which is slightly more tricky, see figure 6.4 for an illustration.

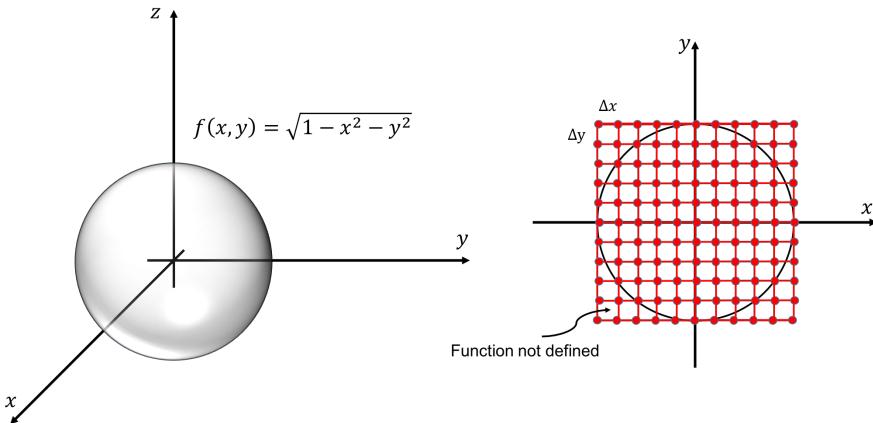


Fig. 6.4 Illustration of a 2D integration to evaluate the volume of a sphere.

The multi dimensional integral is done by placing a box around the sphere, and divide this box into $N \times N$ equal boxes. If start the integration at $x = -R$, $F(-R) = 0$, because the integrand is zero. If we move one step to the left, we need to integrate from $y = -R$ to $y = R$. We see from the figure to the right in figure 6.4 that the function is not defined for two first points. Thus we need to make sure that if we are outside the integration bounds the function is zero. Below is an implementation that uses recursive function calls

```
def dd_trapez(lower_limit,upper_limit,func,x,i,N,D):
    h = (upper_limit-lower_limit)/N
    if(i == D-1):
        funci=d1_trapez
    else:
        funci=dd_trapez
    x[i] = lower_limit
    area = funci(lower_limit, upper_limit,func,x,i+1,N,D)
    x[i] = upper_limit
    area += funci(lower_limit, upper_limit,func,x,i+1,N,D)
    area *= 0.5
    x[i] = lower_limit
    for k in range(1,N): # loop over k=1,...,N-1
        x[i] += h # midpoint value
        area += funci(lower_limit, upper_limit,func,x,i+1,N,D)
    return area*
```

Recursive functions

Recursive implementation is very elegant, and more transparent, but it comes with a price. The reason is that when a function is called additional memory is allocated to store the local variables. If we were to calculate $100!$, 100 copies of the variable n are created, whereas using a loop only one variable is created. Each time a function is called more memory is allocated, and if the recursive calls are too many it might cause memory overflow. If you try to call `fact_rec(1000)`, Python will give an error, because the maximum number of recursions are reached, it can be changed by:

```
import sys  
sys.setrecursionlimit(1500)
```

Error Analysis in higher dimensions

In the chapter about numerical integration, we did an error analysis on the trapezoidal rule and found that it scaled as h^2 . As we see from the example above, a higher order integration is simply to do a series of 1D integrations in all the dimensions, thus the error term should be $h_{x_0}^2 + h_{x_1}^2 + \dots + h_{x_{d-1}}^2$. If we use the same spatial resolution in all dimensions, then the overall error scale as h^2 . If we let n denote the number of points in each directions, $h \sim 1/n$, the total number of points used is $N = n \times n \cdots n = n^d$. Thus, the error term scales as $h^2 \sim N^{-2/d}$, and we see that if $d \geq 4$, the MC integration is expected to perform better.

6.3 Importance Sampling (To be completed)

What would be the optimal shape of the function for our MC method?

6.4 Accept Reject (To be completed)

6.5 Example: Random Walk (To be completed)

6.6 Simulated Annealing (To be completed)

Exercise 6.1: The central limit theorem

The central limit theorem is a corner stone in statistics, and it is the reason for why the normal distribution is so widely used. The central limit theorem states that if we calculate the average of an independent random variable, the *average will be distributed according to a normal distribution*. Note that the central limit theorem does not state anything about the distribution of the original variable. We will not prove the central limit theorem, but illustrate it with two examples.

- a)** First we will investigate a random variable that follows a *uniform distribution*. Write a Python function that returns the average of N uniformly distributed numbers in $[0, 1]$.

```
def average(N):
    x=[np.random.uniform() for _ in range(N)]
    return np.mean(x)

# or alternatively, and equally fast

def average2(N):
    x=0
    for i in range(N):
        x+=np.random.uniform()
    return x/N

# or much faster:
def average3(N):
    x=np.random.uniform(size=N)
    return np.mean(x)
```

- b)** Calculate the average M times and make a histogram of the values.

```
def hist(M,N=100):
```

- c)** Repeat the above exercise for a Poisson distribution.

```

def average3(N):
    x=np.random.uniform(size=N)
    return np.mean(x)

def hist(M,N=100):
    y=[average3(N) for _ in range(M)]
    plt.hist(x=y, bins='auto', color='#0504aa', alpha=0.7, rwidth=0.85)
    plt.show()

def average4(N):
    x=[np.random.poisson() for _ in range(N)]
    return np.mean(x)

```

Remarks. It is quite remarkable that the distribution of the average values from both a uniform and Poisson distribution follows a normal distribution. The general proof² is not that complicated, but the ramifications are large. The central limit theorem explains why it makes sense to use the standard deviation as a measure of confidence for the mean value.

Exercise 6.2: Birthday Paradox

The human mind is not good at logical thinking, and if we use our intuition we often get into trouble. A well known example is the "Birthday Paradox", it is simply to answer the following question: "How many randomly selected people do we need in order that there is a 50% chance that two of them have birthday on the same date?"

a) Write a Python function that pick a random date

Solution. Below are two examples, the first one picks a date, while the second one just picks a random day at year.

```

from datetime import date
import numpy as np

def get_date():
    """ return a random date in the current year """
    start_dt = date.today().replace(day=1, month=1).toordinal()
    end_dt = date.today().replace(day=31, month=12).toordinal()
    random_day = date.fromordinal(np.random.randint(start_dt, end_dt))
    return random_day

def get_day():
    """ return a random day in a year """
    return np.random.randint(1,365)

```

²https://en.wikipedia.org/wiki/Central_limit_theorem

- b)** Write a function that takes as argument, number of persons in a group, and returns 1 if two of them has birthday on the same date and 0 otherwise.

Solution. .

```
def NoPeople(p):
    """ pick random dates in a year, return 1 if two
        is in the same date before p is reached """
    dates=[]
    for n in range(p):
        date=get_day()
        if date in dates:
            return 1
        else:
            dates.append(date)
    return 0
```

- c)** Write a function that returns the probability that two people in a group of p persons have birthday on the same day, and determine how many people we need to have a probability of 50%.

Solution. In order to get some statistics, we need to sample N groups and return the fraction of groups that had two persons with the same birthday.

```
def BP(p, N):
    prob=0.;
    for i in range(N):
        prob += NoPeople(p)
    return prob/N

print(BP(23,1000))
```

By trial an error, we find that 23 persons is needed in order to have a probability of

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